STIC-Biotech/Ch mLib

5984

From:

T :

Chan, Christina

Sent:

Thursday, February 07, 2002 11:19 AM Chen, Shin-Lin

Cc: Subject: STIC-Biotech/ChemLib

RE: Rush sequence search: 09/391,606

Please rush. Thanks Chris

----Original Message----

Fr m:

Chen, Shin-Lin

Sent:

Wednesday, February 06, 2002 6:03 PM

To: Cc:

Chan, Christina STIC-Biotech/ChemLib

Subject:

Rush sequence search: 09/391,606

09/391,606 is an amended case due next bi-week and require sequence search. Could you approve the following Rush Sequence Search for 09/391,606? Thanks!

SEQ ID Nos. 1-4, 7-9 and 12-16.

Shin=Lin Chen ! AU 1632 CM1 12A15

Mail Box # 12E12 (703)305-1678

> POINT OF CONTACT: BARB O'BRYEN TECH. INFORMATION SPECIALIST 308-4291 STIC CM1 12014 6A05

Phone: Location: Date Picked Up: Date Completed: 2-8-02 Searcher Prep/Review: _____ Clerical: Online time: _____

TYPE OF SEARCH:	VENDOR/COST(where applic.)
NA Sequences:	STN:
AA Sequences:	DIALOG:
Structures:	Questel/Orbit:
Bibliographic:	DRLink:
Litigation:	Lexis/Nexis:
Full text:	Sequence Sys.:
Patent Family:	WWW/Internet:
Other:	Other (specify):

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2002, 21:34:38; Search time 137.02 Seconds (without alignments)
212.997 Million cell updates/sec February Run on:

US-09-391-606-15 2103 1 MLPVGNPSDPSLLIDGTIWE.....QKLISEEDLNSAVDHHHHHH 394 Perfect score: Sequence:

Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

522463 Total number of hits satisfying chosen parameters: 522463 seqs, 74073290 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

/SIDSZ/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDSZ/gcgdata/geneseqg/AA1981.DAT:*
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/SIDSZ/gcgdata/geneseqg/AA1987.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1996.DAT:* /SIDS2/gcgdata/geneség/geneségp/AA1989 /SIDS2/gcgdata/geneseg/genesegp/AA1990 /SIDS2/gcgdata/geneseq/geneseqp/AA1991. /SIDS2/gcgdata/geneseq/geneseqp/AA1992. /SIDS2/gcgdata/geneseq/geneseqp/AA1993 A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS2/gcgdata/geneseq/genesecp/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:*

SUMMARIES

		Description	Chlamydia pheumoni	C. trachomatis ser	Chlamydia psittaci	Chlamydia psittaci	C. pneumoniae sero	Protein encoded by	Chlamydia psittaci	C. trachomatis ser	C. trachomatis ser		C. trachomatis ser
		ΠD	AAY35319	AAY56771	AAW98188	AAW98189	AAB13645	AAG83213	AAW98187	AAY56767	AAY56768	AAW76366	AAY56766
		DB	20	20	20	20	21	22	20	20	20	19	20
		Match Length DB	391	343	389	402	525	525	402	387	404	376	397
p o	Query	Match	91.5	78.3	73.0	67.0	67.0	67.0	6.99	64.5	64.1	64.0	63.6
		Score	1925	1647	1534.5	1408	1408	1408	1407	1356.5	1349	1345.5	1338.5
	Result	No.	-	7	æ	4	₂	9	7	80	6	10	11

C. trachomatis ser	C. trachomatis ser	C. trachomatis ser	C. trachomatis JM1	C. trachomatis ser	C. trachomatis ser		Chlamydia trachoma	C. trachomatis JM1	C. trachomatis ser	C. trachomatis JM1	Chlamydia trachoma	Chlamydia trachoma	Chlamydia trachoma	Chlamydia trachoma	C. trachomatis ser	C. trachomatis ser	C. trachomatis ser	Chlamydia trachoma	Sequence of a majo	C. trachomatis ser	C. trachomatis MOM	C. trachomatis MOM	C. trachomatis ser	C. trachomatis MOM	C. trachomatis MOM	trachor	Chlamydia psittaci	Chlamydia psittaci			ㅌ	Chlamydial major o	Chlamydial major o
AAY56763	AAY56764	AAY56765	AAW76363	AAY56757	AAY56759	AAW76365	AAE06646	AAW76364	AAY56762	AAW76362	AAW15149	AAW73141	AAY81268	AAW57775	AAY56761	AAY56760	AAY56758	AAY37494	AAP60004	AAY56769	AAY82388	AAY82389	AAY56770	AAY82391	AAY82390	AAY82392	AAW98184	AAW98186	AAW98183	AAW98185	AAY82393	AAW95307	AAW95295
20	20	20	19	20	20	19	22	19	20	19	18	19	21	19						20					21	21	20	20	20	20	21	20	20
397	396	397	376	393	393	372	393	374	395	373	394	394	394	394	394	392	394	394	394	343	457	484	356	514	454	349	228	225	222	215	277	100	100
3.6	3.1	2.8	2.8	2.5	2.4	2.2	2.2	2.1	2.1	1.8	1.6	1.6	1.6	1.5	1.5	1.3	1.2	1.1	6.0	60.1	9.3	7.8	6.2	3.9	1.6	0.1	3.4	3.1	0.1	6.3	6.5	4.7	3.3
1336.5	1326	1321.5	1320.5	1313.5	1312.5	1308.5	1308.5	1306.5	1305.5	1300	1295	1295	1295	1294	1293	1289	1287	1284	1280	1264.5	1248	1214.5	1182	1134.5	1085.5	1053	913	507	842.5	825.5	7.67	519	489
17	13	7	5	1.6	17	18	£	20	2.1	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 =-
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ALIGNMENTS

RESULT

Chlamydia pneumoniae transmembrane protein seguence. AAY35319 standard; Protein; 391 AA (first entry) 13-SEP-1999 AAY35319; AAY35319

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccinė; neutralising epitope. 98WO-IB01890 98US-0107078 97FR-0014673 Chlamydia pneumoniae. WO99271.05-A2. 20-NOV-1998; 21-NOV-1997; 04-NOV-1998; 03-JUN-1999

(GEST) GENSET Griffais R;

WPI; 1999-357842/30

Page 1130-1131; Disclosure; 1912pp; English. Genome sequence of Chlamydia pneumoniae

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    AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Major outer membrane protein; MOMP; Chlamydia; vaccine; immune response; cellular response; immunogen; Thl-like CD4 response; mucosal immunity.
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                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                  Length 391;
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                                                                                                                                                                                                                Score 1925; DB 20;
Pred. No. 2.3e-182;
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                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                91.5%;
98.9%;
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Best Local Similarity
                                                                                                                                                                           391 AA;
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386 sgqfrf 391
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The invention provides a non-replicating vector that comprises, linked to a promoter, a nuclectide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly callular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Thh-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAYS6757-71 represent MOMP sequences from a variety
                                                                     Non-replicating vector encoding fragments of the outer membrane protein of Chlamydia, useful in vaccines and as immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
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                                                                                                                                                                                                                                                                                                                                                                        Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                    Score 1647; DB 20;
Pred. No. 7.2e-155;
2; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                              Disclosure; Fig 10 A-F; 52pp; English.
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                                                                                                                                                                                                                                                                                               of serovars of C. trachomatis.
                                                                                                                                                                                                                                                                                                                                                                     78.38;
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Best Local Similarity 86.3
Matches 316; Conservative
                                      WPI; 1999-620205/53
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nsgfrf
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05-JUL-1999 (first entry)

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                                                                                                                                                                                                                                                                           The present sequence is the major outer membrane protein (MOMP) of Chlamydia psittaci strain B577. A claimed MOMP polypeptide (see AAM98184) comprises regions VD3 and VD4 of B577 MOMP, i.e. it lacks regions VD1 and VD2. A claimed vaccine composition includes MOMP polypeptide lacking VD1 and VD2, optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG
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                                                                                                                                               Kousoulas KG, Tully TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.0%; Score 1534.5; DB 2075.7%; Pred. No. 1.3e-143; Live 39; Mismatches 49;
                                                                                                                                                                                                                    A new vaccine for Chlamydia psittaci infections
                                                                                                                (LOUU ) UNIV LOUISIANA & AGRIC & MECH COLLEGE
                                                                                                                                                                                                                                                Disclosure; Page 60-61; 72pp; English.
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                                                          98WO-US17943
                                                                                    97US-0057147
                                                                                                                                               Baghian A, Chouljenko VN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
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mnagfrf 389
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WO9910005-A1
                                                        28-AUG-1998;
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AAW98189

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62 S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCALWECGCATLCAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN 290
                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the major outer membrane protein (MOMP) of Chlämydia psittaci strain 6BC. Claimed MOMP polypeptides (see AAM98183 and AAW98184) comprise regions VD3 and VD4 of an MOMP, i.e. Lakey lack regions VD1 and VD2. Claimed vaccine compositions include such MOMP polypeptides, optionally fused to a maltose binding protein. Also claimed are isolated muclaic acids encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide a vectors encoding MOMP polypeptides lacking regions volumed volume vaccine containing the vectors encoding work polypeptides acking regions volume volume vaccine vaccine to prevent C. psittaci infection, especially in birds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 402;
                                                                   protein; MOMP; psittacosis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                 Tully TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.0%; Score 1408; DB 20; 70.3%; Pred. No. 4.7e-131; iive 38; Mismatches 61;
                                       Chlamydia psittaci major outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                  A new vaccine for Chlamydia psittaci infections
                                                                                                                                                                                                                                                     (LOUU ) UNIV LOUISIANA & AGRIC & MECH COLLEGE.
                                                                                                                                                                                                                                                                                 Kousoulas KG,
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 65-66; 72pp; English
                                                                  Major Outer membrane protein; vaccine; genetic immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAEARLINERAAHVSGQFRF 367
                                                                                                                                                                                            98WO-US17943.
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                                                                                                                                                                                                                                                                              Chouljenko VN,
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Best Local Similarity 70.3
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                        WPI; 1999-254214/21.
                                                                                                          Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX25048
                                                                                                                                                                                            28-AUG-1998;
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                                                                                                                                    WO9910005-A1
                                                                                                                                                                  04-MAR-1999.
                                                                                                                                                                                                                                                                               Baghian A,
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GASNGYIRGNSTAFNLVGLFGVKG----TTVNANELPNVSLSNGVVELYTDTSFSWSVGA 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamidiae are intracellular bacterial pethogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is a laso thought to play a role in the pathogenesis of atherosclerosis and coronary heart disease. The present sequence is a protein isolated in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stromberg EJ;
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38; Mismatches
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                                                                                                                                                                                                 AA.
                                                                                                                                                                                           AAB13645 standard; Protein; 525
99US-0288594.
99US-0410568.
99US-0426571.
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01-OCT-1999;
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                                                                                                                                                                                                                                                         AAB13645;
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Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease
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231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN 290
                                                                                                                                                                                                                                                                                        445
                                                                                                                                                                                                                                                                                                                                                        LTAWNPSLLGNATAL---STTDSFSDFWQIVSCQINKFKSRKACGVTVGATLVDADKWSL 347
                                                                                                                                                                                                                                                                                                                                                                                          compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of Chlamydia antigens and DNA sequences encoding such polypeptides. They are useful for vaccinating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease.
                                                                                                                                                                                                                                                             RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
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19-APR-2000; 2000US-0556877.
20-JUN-2000; 2000US-0598419.
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                                                                                                  402 AA;
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                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the major outer membrane protein (MOMP) of Chlamydia psittaci strain LSUWTCK, a cockatiel isolate (the MOMP gene sequence of this isolate is identical to that of C. psittaci Avian Type C). A claimed MOMP polypeptide (see ARW98183) comprises regions VD3 and VD4 of LSUWTCK MOMP, i.e. it lacks regions VD1 and VD2. A claimed vaccine composition includes MOMP
                                                        S-MGAKPT---GSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL
                                                                                                GASNGY I RGNSTAFNLVGLFGVKG - - - - TTVNANELPNVSLSNGVVELYTDTSFSWSVGA
                                                                                                                                         LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
                                                                                                                                                                     RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
                                                                                                                                                                                                            231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN
                                                                                                                                                                                                                                                     LTAWNPSLLGNATAL --- STTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL
                            14;
         Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Major outer membrane protein; MOMP; psittacosis; infection; vaccine; genetic immunisation.
                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tully
         DB 22;
                            61;
Score 1408; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia psittaci major outer membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine for Chlamydia psittaci infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LOUU ) UNIV LOUISIANA & AGRIC & MECH COLLEGE.
                           38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 56-57; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kousoulas
                                                                                                                                                                                                                                                                                                                                                                 Protein; 402 AA.
                                                                                                                                                                                                                                                                                            TAEARLINERAAHVSGQFRF 367
                                                                                                                                                                                                                                                                                                                525
        67.08;
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                   70.38;
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                                                                                                                                                                                                                                                                                                        (first entry)
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-254214/21
                                                                                                                                                                                                                                                                                                                                                                 standard;
                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX25046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9910005-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1999
                           267;
                                                                                                                                                                                                                                                                                                                                                               AAW98187
                                                                                                                                                                                                                                                                                                                                                                                    AAW98187;
        Query Match
                    Local
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                  Best Loca
Matches
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response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GASNGYIRGNSTAFNLVGLFGVKG----TTVNANELPNVSLSNGVVELYTDTSFSWSVGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || |||||| ||||||| ::|| teatdtksatikyhewqvglalsyrlnmlvpyjgvnwsratfdadtiriaqpklkseiln 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Major outer membrane protein; MOMP; Chlamydia; vaccine; immune respon:
cellular response; immunogen; Thl-like CD4 response; mucosal immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide lacking VD1 and VD2, optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOPP polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in
                                                                                                                                                                                                                                                                                                                                                                                             LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
                                                                                                                                                                                                                                                                                                                                                                                                                       gasngyfkassaafnlvgligfsaassistdlptqlpnvgitqgvvefytdtsfswsvga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTAWNPSLLGNATAL - - - STTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                 Length 402;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                   /;
6e-131;
61;
                                                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                                                                                                                     Pred. No. 6e-1
39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. trachomatis serovar MoPn MOMP sequence
                                                                                                                                                                                                                                                                                                 Score 1407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY56757 standard; Protein; 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAEARLINERAAHVSGOFRF 367
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0%;
Matches 266; Conservative 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0055765,
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07-APR-1999;
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                                                                                                                          useful
                                                                The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vectores to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunicanien response (mainly cellular) in standard immunoassays. Immunization with the vector induces a broad superture immune responses, including Thi-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAN56757-71 represent MOMP sequences from a variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outer membrane protein; MOMP; Chlamydia; vaccine; immune response; lar response; immunogen; Th1-like CD4 response; mucosal immunity.
          Non-replicating vector encoding fragments of the outer membrane protein
                                                                                                                                                                                                                                                                                                                              62 SMGAKPIGSAAANYTIA---VDRPNPAYNKHLHDAEWFINAGFIALNIWDRFDVFCTLGA 118
                                                                                                                                                                                                                                                                                                                                                                           SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
                                                                                                                                                                                                                                                                                                                                                                                                                         CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS 238
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                        82
                                                                                                                                                                                                                                                                                   2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
                                                                                                                                                                                                                                                                                                                                            ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA
                                                                                                                                                                                                                                       DB 20; Length 387;
                                                                                                                                                                                                                                                              7;
                       in vaccines and as immunogen
                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                      64.5%; Score 1356.5; DB 2
66.4%; Pred. No. 5.8e-126;
                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trachomatis serovar SFPD MOMP sequence.
                                           52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY56768 standard; Protein; 404 AA.
                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                of serovars of C. trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cellular response; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                              Conservative
                                           Disclosure; Fig 10 A-F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis.
                     Chlamydia, useful
                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 ahvnaqfrf 387
                                                                                                                                                                                                      387 AA;
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                                                                                                                                                                                                                                                   Local Sim
tes 245;
                                                                                                                                                                                                       Sequence
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Matches
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to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used (a) in vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Thi-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAX56757-71 represent MOMP sequences from a variety
                                                                                                                                                                                                                                                      membrane protein
                                                                                                                                                                                                                                                                                                                                                                              The invention provides a non-replicating vector that comprises, linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMGAKPTGS---AAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNGYIRGNSTAFNLVGLFGVKG-----TTVNANELPNVSLSNGVVELYTDTSFSWSV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GARGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTAWNPSLLGNAT ----ALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADK 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                      outer
                                                                                                                                                                                                                                                    n-replicating vector encoding fragments of the Chlamydia, useful in vaccines and as immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.1%; Score 1349; DB 20;
64.8%; Pred. No. 3.4e-125;
iive 51; Mismatches 66;
                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 10 A-F; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 yavtvetrlideraahvnagfrf 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 WSLTAEARLINERAAHVSGQFRF 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serovars of C. trachomatis.
                                                 98US-0055765.
99WO-CA00292
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                                                                                                                                                                                                                                                    Non-replicating vector
                                                                                                  MANITOBA
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                                                                                                  (UYMA-) UNIV
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Best Local Simil
Matches 248; C
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                                                                                                                                                    Bruhnam RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Conservative
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383 lideraahvnaqfrf 397
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                                          Chlamydia trachomatis.
                                                                                                                                                UYMA-) UNIV MANITOBA
                                                                                                                                                                                         WPI; 1999-620205/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 243; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              397 AA;
                                                             W09951745-A2
                                                                                                       07-APR-1999;
                                                                                                                           07-APR-1998;
                                                                                   14-0CT-1999
                                                                                                                                                                      Bruhnam RC;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                AAW76362-W76366 are major outer membrane proteins isolated from Chlamydia trachomatis which are used for the measurement of an antibody against Chlamydia trachomatis, by using it as an antigen in the form of a reagent. The method can give a diagnostic method for Chlamydia trachomatis-infected diseases with high specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
                                                                                                                                                                                                                                                                                                                                                                       Preparation of major outer membrane protein of Chlamydia trachomatis - by cloning and recombinant expression of the gene, for use as a diagnostic of Chlamydia infections
                                                                                                                                                                                                                                                                                                                                                       Gaps
Major outer membrane protein; antibody; antigen; diagnosis; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSMGAKPTGSAAANY ----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNPSLLGNAT - - ALSTIDSFSDFMQIVSCQINKFKSRKACGVIVGATLVDADKWSLTAEA
                                                                                                                                                                                                                                                                                                                                 Length 376;
                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                               64.0%; Score 1345.5; DB 19; Lengt
65.2%; Pred. No. 6.8e-125;
ive 51; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. trachomatis serovar H MOMP sequence
                                                                                                                                                                                                              Claim 2; Page 15-16; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELED ) DENKI KAGAKU KOGYO KK
                                                                                 97JP-0040780
                                                                                                      97JP-0040780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 65.2 hes 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLINERAAHVSGQFRF 367
                    Chlamydia trachomatis.
                                                                                                                                               WPI; 1998-535045/46.
                                                                                                                                                                                                                                                                                                 376 AA;
                                        JP10234395-A
                                                                                 25-FEB-1997;
                                                                                                      25-FEB-1997;
                                                             08-SEP-1998,
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches 245;
                                                                                                                                                                                                                                                                                                 Sequence
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The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in yaccines to generate a protective immune response (mainly cellular) equalist MOMP, and (b) as Immunogens to raise anti-MOMP and thodales, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immuno responses, including Th1-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAY5675771 represent MOMP sequences from a variety of servars of C. trachomatis.
Major outer membrane protein; MOMP; Chlamydia; vaccine; immune response; èellular response; mucogen; Th1-like CD4 response; mucosal immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outer membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPSLLGNAT - - ALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEAR 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LEVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.6%; Score 1338.5; DB 20; Length 397; 64.8%; Pred. No. 3.7e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-replicating vector encoding fragments of the o of Chlamydia, useful in vaccines and as immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3.7e-124;
; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10 A-F; 52pp; English.
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standard; Protein; 397

AAY56763

AAY 56763

12

RESULT

AAY56763;

(first entry)

22-FEB-2000

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NPSLL--GNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEAR 352
             323
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LINERAAHVSGQFRF 367 353 δy Db

11:11111: 1|1| 383 lideraahvnagfrf 397

13 RESULT AAY56764 standard; Protein; 396 AA.

ÁAY56764 ID AAY5

AAY56764;

(first entry) 22-FEB-2000

C. trachomatis serovar A MOMP sequence.

MOMP; Chlamydia; vaccine; immune response; Th1-like CD4 response; mucosal immunity. Major outer membrane protein; cellular response; immunogen;

Chlamydia trachomatis

WO9951745-A2

14-OCT-1999.

99WO-CA00292 07-APR-1999;

98US-0055765 07-APR-1998;

MANITOBA (UYMA-) UNIV

Bruhnam RC;

WPI; 1999-620205/53

Non-replicating vector encoding fragments of the outer membrane protein of Chlamydia, useful in vaccines and as immunogen

Disclosure; Fig 10 A-F; 52pp; English.

The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used (a) in vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Th1-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAY56757-71 represent MOMP sequences from a variety C. trachomatis. serovars of

396 AA; Seguence

SMGAKPTGSAAANY ----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117

62

118

2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61 175 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT 234

ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174

GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294

235

263

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Gaps

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Indels

DB 20; Length 397;

63.6%; Score 1336.5; DB 20 64.8%; Pred. No. 5.8e-124; ive 50; Mismatches 73;

Similarity 64.8

243;

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Query Match Best Local Si Matches 243;

Gaps 61 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF Length 396; Indels 63.1%; Score 1326; DB 20; 64.7%; Pred. No. 6.3e-123; ive 48; Mismatches 76; Conservative Similarity Local Sim Query Match Matches δ

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82 62 SMGAKPIGSAAANY----TTAVDRPNPAYNKHLHDAEWFINAGFIALNIWDRFDVFCTLG

q οy qmgaapttsdtaglekdpvanvarpnpaygkhmqdaemftnaaymalniwdrfdvfctlg

117

118 ASNGYIRGNSTAFNLVGLFGVKGTTV --- NANELPNVSLSNGVVELYTDTSFSWSVGARG 174

q δy Db

useful The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Th1-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences ANYESSS:7-71 represent MOMP sequences from a variety Non-replicating vector encoding fragments of the outer membrane protein of Chlamydia, useful in vaccines and as immunogen outer membrane protein; MOMP; Chlamydia; vaccine; immune respons« Lar response; immunogen; Th1-like CD4 response; mucosal immunity. C. trachomatis serovar L3 MOMP sequence. Disclosure; Fig 10 A-F; 52pp; English. cellular response; immunogen; trachomatis. 99WO-CA00292 98US-0055765 Chlamydia trachomatis. MANITOBA WPI; 1999-620205/53 serovars of C. .397 AA; (UYMA-) UNIV WO9951745-A2 07-APR-1999; 07-APR-1998; 14-0CT-1999 Bruhnam RC; Seguence Major

23 lpvgnpaepsimidgilwegfggdpcdpcttwcdaismrvgyygdfvfdrvlktdvnkef 82

SMGAKPTGSAAANY - - - - TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG

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The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP and antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Th1-like CD4 responses and challenge. Sequences AAY5675771 represent MOMP sequences from a variety of serovars of C. trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOMP; Chlamydia; vaccine; immune response; Th1-like CD4 response; mucosal immunity.
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                                                                                                                                                                                                            295 NPSLLGNATALSTTDS-FSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARL 353
                      GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW
                                                                                                                                                                                                                                           ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-replicating vector encoding fragments of the cof Chlamydia, useful in vaccines and as immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY56765 standard; Protein; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer membrane protein;
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383 ideraahvnaqfrf 396
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                                                                                                                                                                                                                                                                                                                    354 INERAAHVSGQFRF 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis.
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                                                                                                      235
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'AAW76362-W76366 are major outer membrane proteins isolated from Chlamydia trachomatis which are used for the measurement of an antibody against Chlamydia trachomatis, by using it as an antigen in the form of a reagent. The method can give a diagnostic method for Chlamydia trachomatis-infected diseases with high specificity.
                                   ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
                                               GİKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
                                                                                                                                               NPSLLGNATALS--TTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEAR 352
                                                                                                                                                                                              Preparation of major outer membrane protein of Chlamydia trachomatis - by cioning and recombinant expression of the gene, for use as a diagnostic of Chlamydia infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                     membrane protein; antibody; antigen; diagnosis; disease.
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ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
                                                                                               Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                             C. trachomatis JM109 pCT33-C major outer membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.8%; Score 1320.5; DB 19;
ilarity 64.4%; Pred. No. 2.1e-122;
Conservative 49; Mismatches 76; II
                                                                                                                                                                                                                                                                                                                    AAW76363 standard; protein; 376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 12; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELED ) DENKI KAGAKU KOGYO KK
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-535045/46.
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Best Local Similarity
Matches 242; Conserv
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20; Length 397;

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62.8%; Score 1321.5; DB 20 64.0%; Pred. No. 1.8e-122; ive 51; Mismatches 75;

Local Similarity 64.0 es 240; Conservative

Best Loca Matches

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Query Match

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RLINERAAHVSGQFRF 367
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Search completed: February 7, 2002, 21:34:40 Job time: 20759 sec

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Sequence Sequence Sequence Sequence Sequence

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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER, OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCHWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19.0VV.1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                     US-09-371-913A-7
US-09-208-74-2
US-09-322-295-4
US-08-627-907A-2
US-08-471-043-21
US-08-471-044-21
US-08-471-046A-21
US-08-471-046A-21
US-08-471-046A-21
US-08-469-344-21
US-08-469-344-21
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US-08-262-220-8
US-08-750-494-8
                                                                                                                                                                                                                                                                                                                                                          US-08-856-253-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 110 08/911,312
PRIOR APPLICATION NUMBER: 110 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 611, Application US/08974549A Patent No. 6166178 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: TWO ENLANCE CITY: San Francisco cmarE: California
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San
STATE: Ca
COUNTRY:
ZIP: 9411
(without alignments)
103.204 Million cell updates/sec
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Appli
Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 45, 8 Sequence 45, 8 Sequence 22, 8 Sequence 24, 8 Sequence 24, 8 Sequence 58, 8 Sequence 11, 8 Sequence 41, 8 Sequen
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                                                                                                                                                                      Search time 85.91 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-374-560-1

US-08-446-6923-3

US-08-446-6923-3

US-08-488-351A-45

PCT-US93-10871-17

US-09-411-329C-22

US-09-411-329C-22

US-09-411-329C-26

US-08-446-692-24

US-08-446-692-24

US-08-446-692-24

US-08-133-428D-57

US-09-433-428D-57

US-09-433-428D-57

US-09-433-428D-57

US-09-434-488-61-6

US-08-188-682-16

US-08-188-682-16

US-08-188-682-16

US-08-188-681-63

US-08-188-681-63

US-09-163-683-63

US-09-171-710-41

US-08-911-710-41

US-08-911-710-41

US-08-911-710-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     212252 seqs, 22503292 residues
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                                                                                                                                                                   7, 2002, 21:36:24
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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1 MLPVGNPSDPSLLIDGTIWE.
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                         US-09-391-606-15
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length: 2000000000
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Match Length
                                                                                                                                                                      February
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Minimum DB seq Maximum DB seq

Database

Result Š.

Searched:

Perfect score: Sequence: Scoring table:

Run on:

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APPLICANT: The Government of the United States of America
APPLICANT: as represented
APPLICANT: as represented
APPLICANT: as represented
APPLICANT: by the Secretary of the Department of Health and Human Services
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINE FOR
TITLE OF INVENTION: TRACHOMATIS
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 RATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALSTTD-SFSDFMQIVSCQINKFKS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 61;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08739
                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.5%; Score 136.5; DB 3
Best Local Similarity 47.5%; Pred. No. 3.4e-07,
Matches 29; Conservative 10; Mismatches 23
                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9215780.9
FILING DATE: 24-JUL-1992
ATTORNEY AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTATION NUMBER: 24,735
REFERENCE/DOOKET NUMBER: P/365-302
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,671 US
FILING DATE: 18 SEP
INFORMATION FOR SEQ 1D NO: 3:
                                                                                                      UMBER: US/08/374,560
13-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application PC/TUS9308739 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 382-0700
(212) 382-0888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 61 amino acids
                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US93-08739-3
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TELEX: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 LNVICNVSQ--FSVNKPK-----GYKGVAFPLPTDAGVATATGTKSATINYHEWQVGAS 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 LSYRLN----SLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALST 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.8%; Score 142.5; DB 4; Length 1154; 26.1%; Pred. No. 9.3e-06; Live 19; Mismatches 37; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "fusion protein composed of hTRT protein sequence, vector sequences, the Myc epitope and His6 tag"
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION WUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
ATTORNEY AGENT INFORMATION:
NAME: APPLE, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEFONMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1078 FLLKLTRHRVTYVPLLG------SLRTAQTQL-
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APPLICANT: GIBBONS, William Anthony
ITILE OF INVENTION: PEPTIDE COMPOUNDS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 RYQAYVEQKLISEEDLNSAVDHHHHH 394
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; Patent No. 5882645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.85
Best Local Similarity 26.15
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: 974 - 540x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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10036-8403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-974-549A-611
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US-08-374-560-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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Immunogenic LHRH peptide constructs
and synthetic universal immune stimulators for vaccines
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APPLICANT: The Government of the United States of America
APPLICANT: By the Secretary of the Department of Health and Human Services
APPLICANT: By the Secretary of the Department of Health and Human Services
TITLE OF INVENTION: SINTHEIR PORTIES
TITLE OF INVENTION: TRACHOMATIS
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 124; DB 2;
Pred. No. 1.7e-06;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9308739 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 21-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
                                                                                              ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%;
Best Local Similarity 84.0%;
Matches 21; Conservative
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide
US-08-488-351A-45
                                                     NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                       10154-0053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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PCT-US93-08739-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
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                                                                                            Query Match 5.9%; Score 125; DB 5; Length 42
Best Local Similarity 61.9%; Pred. No. 3.1e-06;
Matches 26; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                    103 ALNIWDRFDVFCTLGASNGYIRGNSTAFNLVGLFGVKGTTVN 144
                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
CLASSIFICATION:
NAME: MAILS C.H. Lin
RESISTRATION NUMBER: 29,323
RESISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 124; DB 1; I
Pred. No. 1.7e-06;
3; Mismatches 1;
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US-08-488-351A-45
; Sequence 45, Application US/08488351A
; Patent No. 5843446
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                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/08446692
Patent No. 575951
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALNIWDRFDVFCTLGATTGYLKGNS 25
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TELECOMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 45:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 25 amino acids
amino acid
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Best Local Similarity 84.0
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: peptide US-08-446-692-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
      ; FRAGMENT TYPE:
PCT-US93-08739-3
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US-08-446-692-45
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                                                                                              Query Match
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; OTHER INFORMATION: Analog form of native pro-fibrolase of Agkistrodon contortrix US-09-411-329C-26
                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature; OTHER INFORMATION: Native pro-fibrolase of Agkistrodon contortrix US-09-411-329C-22
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      Length 25;
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Pred. No. 1.9e-06;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              APPLICANT: DOWN HOLD APPLICANT: DOWN HOLD APPLICANT: Mann, Michael TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE FILE REFERENCE: 45.596
CURRENT APPLICATION NUMBER: US/09/411,329C
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEO ID NOS: 29
SOFTWARE: PatentIn version 3.0
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE FILE REFERENCE: A-596
    5.9%; Score 124; DB 5;
84.0%; Pred. No. 1.7e-06;
live 3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/411,329C
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 26
LENGTH: 27
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0S-09-411.329C-26
1 Sequence 26, Application US/09411329C
2 Patent No. 6261820
                                                                                                                                                                                                                      Sequence 22, Application US/09411329C Patent No. 6261820
                                                                                103 ALNIWDRFDVFCTLGASNGYIRGNS 127
                                                                                                     1 ALNIWDREDVECTLGATTGYLKGNS 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Agkistrodon contortrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.9%;
Best Local Similarity 87.5%;
Matches 21; Conservative
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Best Local Similarity 87.5%;
Matches 21; Conservative
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Boone, Thomas
APPLICANT: Li, Huimin
APPLICANT: Mann, Michael
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Boone, Thomas
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                        Similarity
                                                                                                                                                                                               US-09-411-329C-22
      Query Match
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                            Best Local
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                                             Matches
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GENERAL INFORMATION:
APPLICANT: United Biomedical Inc; Walfield, Alan M.;
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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Pred. No. 1.7e-06;
3; Mismatches 1; Indels
APPLICATION NUMBER: PCT/US93/08739 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/US95/13841
25-OCT-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           103 ALNIWDRFDVFCTLGASNGYIRGNS 127
                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,671
FILING DATE: 18 SEP 93.
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/328,519
FILING DATE: 25-0CT-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
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                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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Best Local Similarity 84.0°
Matches 21; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                              ; FRAGMENT TYPE: internal PCT-US93-08739-1
                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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                                                                                                                                                LENGTH: 25 ammure 1 amino acid
                                         CLASSIFICATION:
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Gaps
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OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus:
CTHER INFORMATION: Sequence
US-09-433-428D-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: De Leys, Robert J.
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP O
FILE REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
CURRENT TILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 439
TYPE: PRT
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Pred. No. 0.00017;
3; Mismatches 10; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION VUMBE: US/08/488,351A
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.9%; Score 124; DB 2; Best Local Similarity 84.0%; Pred. No. 3.2e-06; Matches 21; Conservative 3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1151-4146 US2
                                                                                                                                                    FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
                                                                      FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-433-428D-57; Sequence 57, Application US/09433428D; Patent No. 6149910
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                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.8%;
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 ERAAHVSGQFRFRYQAYV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-488-351A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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Patent No. 584346
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Ladd, Anna
APPLICANT: Lamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                 immune stimulators for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 3.2e-06;
3; Mismatches 1; Indels
                                                                                  APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang YI
APPLICANT: Wang, Chang YI
APPLICANT: Zanb, Timchhy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimu
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-UN-1995
CLASSIFICATION: 42
ATTORNEY/AGENT INFORMATION:
NAME: MARIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 ALNIWDRFDVFCTLGASNGYIRGNS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ALNIWDRFDVFCTLGATTGYLKGNS 25
                  Sequence 24, Application US/08446692
Patent No. 5759551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                         345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.9
Best Local Similarity 84.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-08-446-692-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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10154-0053
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                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      STREET: 345 Par
CITY: New York
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US-08-446-692-24
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                                                                                                                                                                                                                                                                                                                   STATE:
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 DMVWIVGGSSVY----OEAMNOPGHLRLFVTRI-------MOEFESDIFF---- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 ------PEIDLGKYKLLPEYPGVLSEVQEEKGIKYKFEVYEKKGSRSARLL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 5.8%; Score 121; DB 4; Length 368;
Best Local Similarity 21.2%; Pred. No. 0.00027;
Matches 82; Conservative 43; Mismatches 131; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 MGRKTWFSIPEKNRPLKDRINIVLSRELKEPP--RCAHFLAKSLDDALRLIEQPELASKV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 DVFCTLGASNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 GARGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQ------FSVNKPKGYKGVAFP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 LPTDAGVA----- 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 L---SGIVQQQNNLLRAIEAQQHMLQLTAWGIKQLRARLQALETLMQNQQRLNSWGCKGR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 LVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW-NPSL---LGNATALSTTDSFSDF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 MQIVSCQINKFKSRKACGVTVGATLVDADKW-SLTAEARLINERAAHVSGQFRFFRYQAYV 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 SSIIYDKILEAQDQQEENV---RELLELDKWASLWNWFDITN-------WLWYIKIFI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ASWSNKSLEDIWDNMTWMQWDQQVNNV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:HIV Consensus; OTHER INFORMATION: Sequence
US-09-433-428D-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Antigenic Peptides Of Chlamydia trachomatis
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: De Leys, Robert J.
APPLICANT: Zheng, Jian
APPLICANT: Zheng, Jian
APPLICANT: Leys, Robert J.
APPLICANT: Leys, Robert J.
APPLICANT: Leys, Robert J.
APPLICANT: Cheng, Jian
TITLE OF INVENTION: PEPTIDES FOR THE DETECTION OF HIV-1 GROUP INTLES REFERENCE: CDS-207
CURRENT APPLICATION NUMBER: US/09/433,428D
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 70
395 ERDRDTSGRLVHGFLAIIWVDLGPEQKLISEEDLNSAVDHHHHHH 439
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STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 ----EQKLISEEDLNSAVDHHHHH 394
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APPLICANT: DEMars, Robert I.
APPLICANT: Ortiz, Linette (n.m.i.)
                                                                                                      US-09-433-428D-58
; Sequence 58, Application US/09433428D
; Patent No. 6149910
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Patent No. 6001372
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US-08-519-385B-1
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Gaps
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COUNTRY: U.S.A.

ZIP: 53202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PACCOMPATIBLE
SOFTWARE: PACCOMPATIBLE
SOFTWARE: PACCOMPATIBLE
CURRENT APPLICATION DATA:
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5; Mismatches
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                                                                                                                                                                                                                                                                                     960296.93456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.7%; Score 119; Best Local Similarity 64.5%; Pred. No. 8: Matches 20; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 TINYHEWQVGASLSYRLNSLVPYIGVQWSRA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/519,385B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/100,409A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOMP Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51, Application US/09100409A Patent No. 6090388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                       NAME: Schwartz, Carl R. REGISTRATION NUMBER: 29,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5715
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Chang 1
TITLE OF INVENTION: PREP
TITLE OF INVENTION: PREP
TITLE OF INVENTION: IMM
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: #1.25
CURRENT APPLICATION DATA
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ZIP: 10154-0054
COMPUTER READABLE FORM:
                                                                                                                                                                                                    CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ou
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REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 1151-4154
FELECOMMUICATION INFORMATION:
FELEPHONE: 212-758-4800
FELEPAX: 212-751-6849
FINFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acids
TYPE: amino acids
FOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-409A-51
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Query Match 5.5%; Score 115; DB 3; Length 25; Best Local Similarity 80.0%; Pred. No. 1.5e-05; Matches 20; Conservative 4; Mismatches 1; Indels

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Search completed: February 7, 2002, 21:36:25 Job time: 20494 sec

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1779 IPONTEYRTRVRKNADSKNNLNAERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSF 1838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I-----DSEDDLLQECISS-----AMPKKKKPSRLKGDNEKHSPRNMGGILGED-LTLDL 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1659 DLITESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKA 1718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 GKLTSFDLLQTALLQSVANNNKAAELLKEM----QDNPVVPGKTPAIAQSLVDQTDATAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 QIƏKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1977 -- QENNN--- KENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 PPTSDDYKTQAQTAYDT-----IFT-----STSLADIQAALVSLQDAV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144;
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                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                         MEDIUM TYPE: Floppy .....
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                  32,141
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     2843 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS LENGTH: 2843 amino ac
                                                                                                                                                                                                                                                                                NAME: Kagan, Sarah A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 ERWSILRSAVNALM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-940-2
                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMINO ACID
      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                             20001-4598
                                                                                                                                                                                                                    FILING DATE: 19 CLASSIFICATION:
                                               USA
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US-08-289-548A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---STSLADIQAALVSLQDAV---- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                    Score 138; DB 1; Length 2842;
Pred. No. 0.11;
!) Mismatches 194; Indels 144;
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TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                              11 DETERTPPADLSA-QGLEASAANKSAEAQRIAGAEAKPKE----SKTDSV
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1001 G Street, NW
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                                                                                                                                                                                                                                                       82;
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20.0%;
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HEDGE, PHILIP J.
JOSLYN, GEOFF
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                         Conservative
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ADDRESSEE: Banner, B
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                                                                                                ORGANISM: HOMO
IMMEDIATE SOURCE:
CLONE: APC
US-08-452-654-7
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Matches 105;
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Best Local 3
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23;

Gaps

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2032 I----DSEDDLLQECISS----AMPKKKKPSRLKGDNEKHSPRNMGGILGED-LTLDL 2080
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                                                                                                                       356 VSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAAL 415
                                     --QGSSIGSIR 355
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llarity 20.0%; Pred. No. 0.11;
Conservative 82; Mismatches 194; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERERS, ANDREW
TITLE OF INVERTION: INTERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVERTION: GENE IN COLORECTAL CANCER IN HUMANS
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                                       308 ILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Banner, Birch, McKie & Beckett
1001 G Street, NW
---FAIENTPVCFSHNSSLSSLSDID-
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APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/452,654
25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINZLER, KENNETH
MARKHAM, ALEXANDER F.
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08452654
Patent No. 5691454
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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FILING DATE: 25-MAY
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1947 TDEKLON---
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STATE: D.C
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US-08-452-654-2
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Matches 105;
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Pred. No. 0.11;
2; Mismatches 194; Indels 144;
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                                                                                                                                                                                                              APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GRBE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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PR: 1107.46943
                                                                                                                                                                                                                                                                                                                                            3: Banner & Allegretti, LTD 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,548A
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Scur
20.0%; Pred
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MARKHAM, ALEXANDER F.
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NAME: KAGAN, SATAh A.
REGISTRATION NUMBER: 32.141
REFERENCE/DOCKET NUMBER: 1107
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-9299
                                            ALBERTSEN, HANS
ANAND, RAKESH
                                                                                                      GRODEN, JOANNA
HEDGE, PHILIP J
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Best Local Similarity 20.0%
Matches 105; Conservative
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                                                                                      CARLSON, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-289-548A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
  Patent No. 5648212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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APPLICANT:
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20.0%; Pred. No. 0.11;
.ive 82; Mismatches 194; Indels 144;
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                                                                           NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEPHONE: 202-508-9299
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     US 07/741,940
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GRODEN, JOANNA
HEDGE, PHILLP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
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                                                                                                                                                                                                     TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 0 FILING DATE: 08-AUG-1991 ATTORNET/AGENT INFORMATION: NAME: Kagan, Sarah A.
                                                                                                                                                                                                                                                                                    2843 amino acids
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Best Local Similarity 20.0%
Matches 105; Conservative
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US-08-452-655B-7
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                           APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
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                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,655B
FILING DATE: 25-MAY-1995
CLASSIFICATION: 530
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APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERNCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                            ADDRESSEE: Banner & Witcoff, Ltd. STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
NAKAMURA, YUSUKE
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Best Local Similarity 20.0%
Matches 105; Conservative
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                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Search completed: February 7, 2002, 21:36:24 Job time: 20493 sec

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February 7, 2002, 21:38:09; Search time 96.2 Seconds (without alignments) 311.983 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	major outer membra
SUMMARIES	
	A43587 140864 140864 14038 MMCWP3 A60109 A60109 A6034 140747 140747 170947 S16034 MMCWTE S10005 S12799 MMCWTE S06259 H71484 H71484 MMCWTE S06259 H71484 MMCWTE S10005
DB	аааанааанаааааааааааанааанааа
% Query Match Length	388 388 388 388 388 388 388 402 402 402 403 303 303 303 303 303 303 303
% Query Match	99.20 90.20 90.20
Score	1947-1 19
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	2 2	Specie	N; Alceinate names: MOMP C; Species: Chlamydophila	dophila	meud t	noni	ae, Chlamy	ydia pneumoniae	
		Date: Access	29-Jan-1	993 #sec 587: A40	quence,	rev A492	ision 29-0	Jan-1993 #text_change 11-May-2000 4: FR1619	
	W. F	Perez	Melcosa,	M., Kuc	, C.C	Ü	ampbell, I	R: Perez Melcosa, M.; Kuo, C.C.; Campbell, L.A.	
	A:	Title:	Sequence	oviene e	is of	1 y y	ı major out	ter membrane protein gene of Chlamudia	dia nno
	A;]	Refere	nce numbe	er: A43	587; MI	UID:	91244474		
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	A;(Cross-	reférence	35: GB:	469230	IN :	D:9144540;	; PIDN:AAA73071.1; PID:g144541	
	ж.+	Carter	M.W.	۱۱-Mahd،	awi, S	H.A.	.; Giles,	I.G.; Treharne, J.D.; Ward, M.E.; C	Clarke,
		Gen. Pitde.	MICFODIO.	L. 137, ide segi	465-4	/ \chi	1991 Favonomio	walte of the major outer membrase arctoin	0,000
•	A; 1	Refere	nce numbe	er: A497	51; M	UID:	91237311	vatue of the major outer membrane ;	nranoid
	A;	Access	ion: A49	751					
		Status	: prelim.	inary					
	A	Residu	es: 1-389	UNA 3 <car></car>					
	A;(Cross-	reference	S: GB:	164064	; GB	:M34942; 1	NID:9144534; PIDN:AAA23143.1; PID:91	144535
	A;	Note:	isolate	FOL-207		4	i i	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
	Ini	sayuus fect.	Immün. 60	, 5319.	5323,	199	7 r.U.1 2	noadydos, c.a.; Valin, 1.C.; Bobo, L.D.; Elden, J.J. Infect. Immun. 60, 5319-5323, 1992	
•	A;	ritle:	Similar	ity of (hlamy	dia	pneumoniae	e strains in the variable domain IV	region
	:	Kerere	ion: A493	er: A49.	216; M	OID:	93084388		
	A);	Status	: prelimi	inary					
	A;1	Mollecu	le type:	DNA					
	A:0	Tross-	reférence	35: GB: 8	350607	ÎN.	.2760972.	: PIDN.AAB24363 1: PID.G260973	
	A; I	Note:	sednence	extract	ed fr	N E	CBI backbo	A: Note: sequence extracted from NCBI backbone (NCBIN:120604, NCBIP:120605)	
	R;I	Kalman	, S.; Mit	chell,	W.; W.	arati	he, R.; La		Grimwood,
	A A	ritle:	Comparat	ive der	SA, LY	יה היה	lamydia pr	neumoniae and C trachomatic	
_	A; I	Refere	nce numbe	er: A720	000; MI	UID:	99206606		
	Z. K	Access	ion: G72(044					
	A	Residu	te cype: es: 1-389	DNA <arn></arn>					
	A;(Tross-	reference	ss: GB:1	AE0016!	52; (3B:AE00136	63; NID:94376997; PIDN:AAD18834.1; E	PID:943
	A; D	Experi	mental so	ource: :	train	CWL	029	o o tide of the second of the	1
		7.; Do	dson, R.;	Gwinn, Gwinn,	Σ.	Nelse	on, W.; De	i, s.r.; neideibeig, J.f.; Mille, O. eBoy, R.; Kolonay, J.; McClarty, G.;	Salzb:
- 12	Nuc	cleic	Acids Res	3. 28,]	1397-1	406,	2000		
	AA	ricie: Refere	denome :	sequence ir: A815	S OI (JID:	nyala trac 20150255	A;IIIIE: benome sequences of Chlamydia trachomatis MoPh and Chlamydia pneumoniae AR3 A;Reference number: A81500; MUID:20150255	iae AR3
	A; 2	Access	ion: F816	519					
	A A	Status	A;Status: preliminary A:Molecule type: DNA	Lnary					
· , ma)	. O. J. P. O.						

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major outer
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C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
C;Accession: 140864; S3465
R;Girjes, A.A.; Carrick, F.N.; Lavin, M.F.
Gene 138, 139-142, 1994
A;Title: Remarkable sequence relatedness in the DNA encoding the major outer
A;Reference number: 140864; MUID:94171025
A;Accession: 140864
A;Accession: 140864
A;Accession: 1389
A;Molecule type: DNA
A;Actus: 1389
A;Accession: 1389
A;Cross-references: EMBL;X72023; NID:9313844; PIDN:CAA50906.1; PID:9313845
C;Superfamily: Chlamydia major outer membrane protein
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                      NID:97188982; PIDN:AAF37944.1; PID:9718899
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C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Caccession: D86577
R; Shiral, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID:20330349
A; Reference number: A86491; MUID:20330349
A; Molecule type: DNA
A; Residues: 1-389 <STO>
A; Coss references: GB:BA000008; NID:98979067; PIDN:BAA98902.1; GSPDB:GN00142
A; Experimental source: strain J138
C; Genetics:
A; Gene: ompA
C; Superfamily: Chlamydia major outer membrane protein
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A;Residues: 1-389 <REA>
A;Cross-references: GB:AE002168; GB:AE002161; NID:g7188982; PIDN:AAF379
A;Cross-references: strain AR39, HL cells
C;Genetics: cmpA; CP0051
G;Superfamily: Chlamydia major outer membrane protein
C;Keywords: membrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-389/Product: major outer membrane protein #status predicted <MAT>
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Pred. No. 2.7e-148;
0; Mismatches 0;
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100.0%; Pre
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Gaps

Length Indels

DB 1;

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300 322

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Accession A60109
R;Zhang, Y.X.; Morrison, S.G.; Caldwell, H.D.; Baehr, W.
Infect. Immun. 57, 1621-1625, 1989
A;Title: Cloning and sequence analysis of the major outer membrane protein genes of A;Reference number: A60109; MUID:89212917
A;Reference number: A60109; MUID:89212917
A;Retatus: not compared with conceptual translation
A;Accession: A60109
A;Residues: 1-389 < 2MA>
C;Superfamily: Chlamydia major outer membrane protein
C;Superfamily: Chlamydia major outer membrane protein
F;1-22/Domain: signal sequence #status predicted <NAT>
F;23-389/Product: major outer membrane protein #status predicted <NAT>
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C; Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
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                                                       A;Cross-references: EMBL:X51859; NID:g40600; PIDN:CAA36152.1; PID:g40601
C;Superfanily: Chlamydia major outer membrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F;23-389/Product: major outer membrane protein #status predicted <MAT>
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                                                                                                                                                                                                                                                 Query Match 73.0%; Score 1534.5; DB 1
Best Local Similarity 75.7%; Pred. No. 2.9e-115;
Matches 278; Conservative 39; Mismatches 49;
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es 272; Conserv
      type: DNA
1-389 <HER>
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                                                                                                                                            Major outer membrane protein precursor - Chlamydophila pneumoniae (strain equine/N16)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
Avariety: strain equine/N16
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Apr-2000
C;Accession: 140739 #sequence_revision 16-Aug-1996 #text_change 20-Apr-2000
C;Accession: 140739 #sequence_revision 16-Aug-1996 #text_change 20-Apr-2000
C;Accession: 140739 #sequence of non-human origin.
A;Reference number: 140739; MUID: 94103736
A;Accession: 140739
A;Accession: 140739
A;Accession: 140739
A;Bealdue; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-389 csrpo
A;Residues: 1-389 csrpo
A;Cross-references: GB:L04982; NID: 9288840; PIDN: AAA17397.1; PID: 9289841
C;Comment: On the basis of the major outer membrane protein the authors classified the content of the genome strain CWL029 and strain strain IOL-207. See PIR: A43587.
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A;Gene: momp
C;Superfamily: Chlamydia major outer membrane protein
C;Superfamily: Chlamydia major outer membrane protein
C;Keywords: membrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-389/Product: major outer membrane protein #status predicted <MAT>
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Best Local Similarity 94.5%; Pred. No. 4.3e-143;
Matches 346; Conservative 15; Mismatches 5;
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SGQFRF 389
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C; Species: Chlamydophila psittaci, Chlamydia psittaci
C; Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
C; Accession: 140740
R; Storey, C.; Lusher, M.; Yates, P.; Richmond, S.
J. Gen. Microbiol. 139, 2621-2626, 1993
A; Title: Evidence for Chlamydia pneumoniae of non-human origin.
A; Reference number: 140739; MUID:94103736
A; Status: nucleic acid sequence not shown; translation not shown; translated from A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translation not shown; translated from A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translation not shown; translated from A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translated from A; Molecule type: DNA
A; Residues: 1-402 < RES>
A; Cross-references: GB:L04980; NID:9144544; PIDN:AAA17396.1; PID:9144545
C; Genetics:
A; Gene: momp
C; Superfamily: Chlamydia major outer membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.5%; Score 1419; DB 2; 70.5%; Pred. No. 5.3e-106; iive 37; Mismatches 61;
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Matches 268; Conservative
       RAAHVSGQFRF
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382 RAAHINAQFRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       major outer membrane protein precursor - Chlamydophila psittaci (strain Fpn/pring)
C;Species: Chlamydophila psitaci, Chlamydia psittaci
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 31-Mar-2000
C;Accession: 140859; A40371; Si6137
R;Stocesy. C:; Lusher, M.; Yates, P.; Richmond, S.
J. Gen. Microbiol. 139, 2621-2626, 1993
A;Title: Evidence for Chlamydia pneumoniae of non-human origin.
A;Reference number: 140739; MUID:94103736
A;Reference number: 140739; MUID:94103736
A;Retus: nucleic acid sequence not shown; translation not shown; translated from GB/EME
A;Residues: 1-392 <RES
A;Cross-references: EMBL:X61096; NID:940564; PIDN:CAA43409.1; PID:940565
C;Genetics:
A;Genetics:

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                                                  201
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23 LPVGNPAEPSLLIDGTM#EGASGDPCDPCATWCDAISIRAGFYGDYVFDRILKVDVNKTI
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                                                                                                                                                                                                                                                                                             GNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAA
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Pred. No. 1.2e-110;
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                                       23 LFVGNPAEPSLLIDGTMWEGASGDPCDPCATWCDAISIRAGYYGDYVFDRVLKVDVNKTF
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             RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA - - FPLPTDAGV
                                                                                                                                                                                                                                                                  LTAWNPSLLGNATAL - - - STTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GASNGYIRGNSTAFNLVGLFGVKGTTVNANE----LPNVSLSNGVVELYTDTSFSWSVGA 172
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                                       predicted <MAT>
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; Pred. No. 2.8e-105;
38; Mismatches 61;
                                                                                                                              Score 1415; DB 1;
Pred. No. 1.1e-105;
                                                                                                                                                                                         37; Mismatches
F;1-22/Domain: signal sequence #status F;23-402/Product: major outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAEARLINERAAHVSGQFRF 367
                                                                                                                              67.3%;
70.3%;
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70.3%;
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hes 267; Conservative
                                                                                                                                                               Best Local Similarity 70.3 Matches 267; Conservative
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Best Local Similarity
Matches 244; Conserv
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C;Superfamily: C
C;Keywords: memb
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D
                                                                                                                                                                                                                                                                                    major outer membrane protein, porin TC0052 [imported] - Chlamydia muridarum (strain Nigg C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C; Species: Tay Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000 (SAccession: C81747 (Saccession: C81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: GB:AE002272; GB:AE002160; NID:g7190083; PIDN:AAF38941.1; PID:g719009
A,Experimental source: strain Nigg (MoPn)
A,Genetics
A,Genetics
C,Superfamily: Chlamydia major outer membrane protein
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140741
major outer membrane protein - Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 16-Aug-1996 #Sequence_revision 16-Aug-1996. #text_change 20-Aug-1999
C;Accession: 140741
R;Zhang, Y.X.; Fox, J.G.; Ho, Y.; Zhang, L.; Stills, H.F.; Smith, T.F.
Mol. Biol. Evol. 10, 1327-1342, 1993
A;Title: Comparison of the major outer-membrane protein (MOMP) gene of mouse A;Reference number: A49379; MUID:94104488
323 ITTWNPSLIGSTTALPNNSGKDVLSDVLQIASIQINKMKSRKACGVAVGATLIDADKWSI 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 ASIDYHEWQASLALSYRLNMFTPYIGVKWSRASFDADTIRIAQPXLETSILXMTTWNPTI 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SMGAKPTGSAAANYTTA---VDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS
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                                                                                                                            348 TAEARLINERAAHVSGOFRF 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245; Conservative
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Best Local Similarity
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mouse pneumonitis major outer membrane protein - Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999
C;Accession: JT0947
B;Fielder, T.J.; Pal, S.; Peterson, E.M.; de la Maza, L.M.
R;Fielder, T.J.; Pal, S.; Peterson, E.M.; de la Maza, L.M.
R;Fielder, T.J.; Pal, S.; Peterson, E.M.; de la Maza, L.M.
R;Fielder, T.J.; Pal, S.; Peterson, E.M.; de la Maza, L.M.
R;Fielder, T.J.; Pal, S.; Peterson, E.M.; de la Maza, L.M.
A;Reference number: JT0947; MUID:92039057
A;Rocession: JT0947; MUID:92039057
A;Rocession: JT0947; MUID:92039057
A;Rocession: JT0947; MUID:92039057
A;Rocession: JT0947
A;Rocession: JT0947; MUID:92039057
A;Rocession: JT0947; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 SMGAKPTGS---AAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201
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A;Accession: I40741
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-404 <RES>
A;Cross-references: GB:L19221; NID:g410146; PIDN:AAA16615.1; PID:g410147
C;Genetics:
A;Gene momp
C;Superfamily: Chlamydia major outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || || : || : || : || || || || || EMGPVPTTTDTDAAADITTSTPRENPAYGKHMQDAEMFTNAAYMALNIWDRFDVFCTLGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
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66.1%; Pred. No. 1.9e-100;
ive 50; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                           64.2%; Score 1351; DB 2;
65.0%; Pred. No. 1.5e-100;
iive 50; Mismatches 66;
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382 YAVTVETRLIDERAAHVNAQFRF 404
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Best Local Similarity 65.09
Matches 249; Conservative
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239 ATINYHEWOVGASLSYRLNSLVPYIGVOWSRATFDADNIRIAOPKLPTAVLNLTAWNPSL 298
                299 LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA 358
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C;Species: Chreb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1996
C;Accession: S16034, A43875
R;Zhang, Y.X.; Zhang, L.
S;Submitted to the EMBL Data Library, July 1991
A;Bescription: The nucleotide sequence of major outer membrane protein gene of mouse bic
A;Reference number: S16034
A;Accession: S16034
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                299 LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA 358
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                                                                                                                      179 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS 238
                                                                                                                                                                                   ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
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A;Experimental source: mouse pneumonitis strain A;Note: sequence extracted from NCBI backbone (NCBIP:62877) C;Superfamily: Chlamydia major outer.membrane protein
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66.1%; Pred. No. 1.9e-100;
iive 50; Mismatches 68;
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Matches 244; Conservative
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379 AHVNAQFRF 387
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 protein search, using sw model OM protein

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US-09-391-606-15 2103 1 MLPVGNPSDPSLLIDGTIWE......QKLISEEDLNSAVDHHHHHH 394 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 Total number of hits satisfying chosen parameters:

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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ALIGNMENTS

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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White C., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Elsen J., Fraser C.M.; Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAING-102-200;
MEDLINE-91237311, PubMed-2033374;
Carter M.W. Al-Mahdawi S.A.H., Giles I.G., Treharne J.D.,
Ward M.E., Clarke I.N.;
"Nuclectide sequence and taxonomic value of the major outer membrane protein gene of Chlamydia pneumoniae IOL-207.";
J. Gen. Microbiol. 137:465-475(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perez Melgosa M., Kuo C.-C., Campbell L.A.;
"Sequence analysis of the major outer membrane protein gene of
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MEDLINE-99206606; PubMed=10192388;
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MEDLINE-20150255; PubMed-10684935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-TWAR;
MEDLINE-91244474; Pubmed-1840574;
                                                                                                                     STANDARD;
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RESULT 1
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NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN 301
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=83558;
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384 SGQFRF 389
 362 SGQFRF 367
 OMPA OR OMP1
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Q07430;
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SEQUENCE
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 J. Infect. Dis. 181 Suppl 3:S524-S527(2000).

-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.

-!- SUBJUNT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-!- SUBJURTAL LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 84 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 143
 122 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 121
 Shiral M., Hirakawa H., Ouchi K., Tabuchi M., Kishi F., Kimoto M., Takeuchi H., Nishida J., Shibata K., Fujinaga R., Yoneda H., Matsushima H., Tanaka C., Furukawa S., Miura K., Nakazawa A., Ishia T., Hattori M., Kuhara S., Nakazawa T., "Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States.";
 Gaps
 24 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 83
 61
 Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWLO29 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 membrane; Transmembrane; Porin; Signal; Complete proteome.
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 92.6%; Score 1947; DB 1; Length 389; 100.0%; Pred. No. 1.6e-153; ive 0; Mismatches 0; Indels
 24 389 MAJOR OUTER MEMBRANE PROTEIN.
389 AA; 41620 MW; 15D984151E41F8F2 CRC64;
 nicrico i PR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
MEDLINE-20330349; PubMed-10871362;
 MEDLINE=20298986; PubMed=10839753;
 EMBL; M64064; AAA23143.1; -.
EMBL; M69230; AAA73071.1; -.
 Local Similarity 100.
nes 366; Conservative
 PIR; A43587; A43587.
PIR; A49751; A49751.
TIGR; CP0051; -
 SEQUENCE FROM N.A.
 SEQUENCE
 Query Match
 SIGNAL
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 62
 Matches
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 OLIGOMERS.
 Storey C., Lusher M., Yates P., Richmond S.;
"Evidence for Chlamydia pneumoniae of non-human origin.";
"Gen. Microbiol. 139:2621-2626(1993).

1. Gen. Microbiol. 139:2621-2626(1993).

1. FUNCTION: STROTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFESION OF SOLUTES THROUGH
THE INTRACELLUIAR RETICULARE BODY MEMBRANE.

1. SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.

1. SUBCELLUIAR LOCATION: INTEGRAL WEMBRANE PROTEIN. OUTER MEMBRANE.

1. SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 121
 122 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
 361
 83
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 24 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDKILKIDAPKTF
302 ATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV
 0;
 Length 389;
 Indels
 MAJOR OUTER MEMBRANE PROJ
801622F05D841967 CRC64;
 Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 5
 89.5%; Score 1882; DB 1; 94.5%; Pred. No. 3.9e-148;
 Promission Pro1308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
SIGNAL 1 23 BY SIMILARITY.
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP).
 389 AA
 15; Mismatches
 InterPro; IPR000604; Chlamydia_OMP.
 PRT;
 MEDLINE=94103736; PubMed=8277245;
 41628 MW;
 EMBL; L04982; AAA17397.1; -
 346; Conservative
 STANDARD;
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389 AA;
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 noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
 MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 ACTAINMENTING ABORTION ISOLATE BAI;
MEDLINE-9618955; PubMed-8605581;
MEDLINE-96189655; PubMed-8605581;
MIDLINE-96189655; PubMed-8605581;
MIDLINE-96189655; PubMed-8605581;
MIDLINE-9618965; PubMed-8605581;
MIDLINE ROYLING N.C., Dawson M.;
MIDLINE Chamydia psittaci isolate and antibody response.";
MIDLINE STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR REPICTUATE BODY MEMBRANE.

-1 - SUBUNIT: DISCULLIDE BOND INTERACTIONS WITHIN AND BETPEER MOMP
61 NPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNGYIKGNSTAFNLVGLFGVKGTS 120
 VAANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQSKPKVEELNV 180
 IGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALSTTDSFSDFWQIVSCQI 322
 203 ICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPY
 SEQUENCE FROM N.A.
STRAIN=OVINE ENZOCTIC ABORTION ISOLATE $26/3;
MEDLINE=90128177; PubMed=2612883;
Herring A.J., Tan T.W., Baxter S., Inglis N.F., Dunbar S.;
"Sequence analysis of the major outer membrane protein gene of voine abortion strain of Chlamydia psittaci.";
FEMS Microbiol. Lett. 53:153-158(1989).
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83554;
 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP)
 Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 389 AA
 NKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 or send an email to license@isb-sib.ch)
 entities requires a license agreement
 InterPro; IPR000604; Chlamydia_OMP.
 EMBL; X51859; CAA36152.1; -.
 L39020; AAB02850.1;
 STANDARD;
 PIR; S08770; MMCWP3
 SEQUENCE FROM N.A.
 OMPA OR OMP1
 OMIA_CHLPS
 121
 181
 263
 OM1A_CHLPS
 323
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 MEDLINES STRUCTURE OF TRUNCH COLLEGE STRUCKS STRUCTURES OF AND ADDRESS OF ELEMENTARY BACTERIOL. 175:487-502(1933).

-1. FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFICISION OF SOLUTES THROUGH THE INTERACELULAR RETICULATE BODY MEMBRANE.

-1. SUBUNIT: DISULFIDE BOND INTERACTIONS MITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.

-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN 301
 83 NPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNGYIRGNSTAFNLVGLFGVKGTT 142
 Gaps
 23 AGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTFSMGAKPTGSAAANYTTAVDRP 82
 1 AGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTFSWGAKPTGSATANYTTAVDRP
 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATI
 302 ATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV
 ;
 Length 333;
 Indels
 35811 MW; 204604512C4C3B3F CRC64;
 Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 Score 1732; DB 1;
Pred. No. 7.8e-136;
4; Mismatches 5;
 OWAY-2000 (Rel. 39, CIELLE
30-MAY-2000 (Rel. 39, Last sequence ur. 30-MG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN (MOMP) (FRAGMENT).
 333 AA
 Porin.
 InterPro; IPR000604; Chlamydia_OMP. Pfam; PF01308; Chlamydia_OMP; 1. ProDom; PD001717; Chlamydia_OMP; 1.
 PRT;
 STRAIN-KOALA TYPE I;
MEDLINE-93123168; Pubmed-8419295;
 membrane; Transmembrane;
 82.4%;
 EMBL; M73038; AAD38210.1; -.
 Local Similarity 97.3 ies 324; Conservative
 STANDARD;
 333 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=83558;
 362 SGQFRF 367
 384 SGQFRF 389
 OM1K_CHLPN
 NON_TER
NON_TER
SEQUENCE
 Query Match
 RESULT 3

OMIK_CHLPN

ID 730-MAX

DT 30-MAX

DT 30-MAX

DT 30-MAX

DT 30-MAX

DT 20-Aug

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RR KALLEN

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CC -1-SU

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Best Local
 P10332;
 SIGNAL
 RESULT 6
OMIE_CHLPS
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 179
 297
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 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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 1;
 300
 S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG 180
 202
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 23 LPVGNPAEPSLLIDGTWWEGASGDPCDPCSTWCDAISIRAGYYGDYVFDRVLKVDVNKTI 82
 CATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSAT
 INYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLG
 263 IKYHEWQVGLALSYRLNMLVPYISVNWSRATFDADAIRIAQPRLAAAVLNLTTWNPTLLG
 NATALSTTDSFSDFWQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAH
 1;
 DB 1; Length 389;
MAJOR OUTER MEMBRANE PROTEIN.
741B5A23ACDBB447 CRC64;
 Indels
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 49;
 Score 1534.5; DB Pred. No. 2e-119;
 01-DEC-1992 (Rel: 24, Created)
01-DEC-1992 (Rel: 24, Last sequence update)
02-DEC-2001 (Rel: 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP).
 392 AA
 39; Mismatches
 STRAIN=FPN/PRING;
MEDLINE=94103736; PubMed=8277245;
 41883 MW;
 73.0%;
75.7%;
 EMBL; X61096; CAA43409.1; -.
 Matches 278; Conservative
 STANDARD;
 ¥;
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=83554;
 :: |||||
MNAQFRF 389
 361 VSGQFRF 367
23
389 A
 01-DEC-1992
01-DEC-1992
20-AUG-2001
 OMPA OR OMP1
 CHLPS
 SEQUENCE
 Query Match
 Local
 200087;
 RESULT 5
OM1P_CHLPS
 62
 83
 121
 143
 181
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 383
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 Pickett M.A., Everson S.J., Clarke I.N.;

"Chlamydia psittaci wea abortion agent: complete nucleotide sequence
"Chlamydia psittaci wea bortion agent: complete nucleotide sequence
of the major outer membrane protein gene.";

FEMS Microbiol. Lett. 55:229-234 (1988).

-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF SOLUTES THROUGH
THE INTRACELLULAR RETICULATE BODY MEMBRANE.

-!- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP
MOLECULES A OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- SUBCELLULAR ELOCATION: INTEGRAL MEMBRANE PROTEIN.
 178
 356
 236
 261
 296
 381
 S-MGAKPTGSA--AANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 201
 321
 23 LPVGNPAEPSLLIDGTWWEGASGDPCDPCATWCDAISIRAGFYGDYVFDRILKVDVNKTI 82
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 SLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINE
 119 SNCYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE
 143 SNGYFKASSDAFNLVGLIGLAGTDF-ANQRPNVEISQGIVELYTDTAFSWSVGARGALWE
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDÅDNIRIAQPKLPTAVLNLTAWNP
 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATGT
 ..
ن
 Length 392;
 MAJOR OUTER MEMBRANE PROTEIN.
 Indels
 88B3C5D90BBA26DB CRC64
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria, Chlamydiales; Chlamydiaceae; Chlamydophila.
 70.2%; Score 1477; DB 1;
74.1%; Pred. No. 1.1e-114;
ive 38; Mismatches 52;
 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP)
PIR; A40371; A40371.

PIR; S16137; S1637.

InterPro; IPR000604; Chlamydia_OMP.

Prom; PF01308; Chlamydia_OMP; 1.

Propom; P001777; Chlamydia_OMP; 1.

Outer membrane; Transmembrane; Porin; Signal.
 ¥.
 402
 42069 MW;
 74.18;
 Matches 275; Conservative
 STANDARD;
 392
 RAAHVSGOFRF 367
 23 3
392 AA;
 Similarity
 SECUENCE FROM N.A.
 NCBI_TaxID=83554;
 STRAIN=EAE A22/M;
 |||||::|||||
||RAAHINAQFRE
 OMPA OR OMP1
 OM1E_CHLPS
 SEQUENCE
 Query Match
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MEDLINE=94104488; PubMed=8277858;
 STRAIN-MOPN;
 CONFLICT
 CONFLICT
 PIGR;
 gene.
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 9
 MEDILINE-9239057; PubMed=1937036;
Fielder T.J., Pal S., Peterson E.M., la Maza L.M.;
"Sequence of the gene encoding the major outer membrane protein of the
mouse pneumonitis biovar of Chlamydia trachomatis.";
Gene 106:137-138(1991).
 S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 GASNGYIRGNSTAFNLVGLFGVKGTTVNANE----LPNVSLSNGVVELYTDTSFSWSVGA 172
 Gaps
 61
 23 LPVGNPAEPSLLIDGTWWEGASGDPCDPCATWCDAISIRAGYYGDYVFDRVLKVDVNKTF 82
 RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 14;
 Length 402;
 MAJOR OUTER MEMBRANE PROTEIN.
E6CF00D9DF1EE87A CRC64;
 Indels
 62;
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
 Score 1415; DB 1;
Pred. No. 1.5e-109;
 OMP1_CHLMU STANDARD; PRT; 387 AA. P75024; Q04063; Q9X718; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP).
 membrane; Transmembrane; Porin; Signal.
 37; Mismatches
 EMBL; X12647; CAA31177.1; -.
EMBL; M36703; AAA23146.1; -.
PIR; S05954; MMCWPM.
InterPro; IPR000604; Chlamydia_OMP.
 Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP;
 43277 MW;
 TAEARLINERAAHVSGQFRF 367
 67.3%;
70.3%;
 Query Match 67.3%
Best Local Similarity 70.3%
Matches 267, Conservative
 OMPA OR OMP1 OR TC0052.
 Chlamydia muridarum.
 402 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
 STRAIN-MOPN
 SEQUENCE
 Outer m
SIGNAL
 CHLMU
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 BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
THE INTRACELLULAR RETICULATE BODY MEMBRANE.
-! SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP
MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-! SUBCELLULAR LOCATION: CELL WALL SURFACE.
-! MISCELLARGOS: MOMP IS RESPONSIBLE FOR THE STRUCTURAL INTEGRITY OF
THE EXTRA-CELLULAR INFECTIOUS ELEMENTARY BODY & THE DEVELOPMENTAL
CONVERSION TO THE PLASTIC AND FRAGILE INTRACELLULAR RETICULATE
 MEDLINE=93123168; PubMed=8419295;
Kaltenboeck B., Kousoulas K.G., Storz J.;
"Structures of and allelic diversity and relationships among the major outer membrane protein (ompA) genes of the four chlamydial species.";
J. Bacteriol. 175:487-502(1993).
--- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY
Zhang Y.X., Fox J.G., Ho Y., Zhang L., Stills H.F., Smith T.F., "Comparison of the major outer-membrane protein (MOMP) gene of mouse pneumonitis (MOPN) and hamster SFPD strains of Chlamydia trachomatis with other Chlamydia strains ".
 (In) Mardh P.A., la Placa M., Ward M. (eds.);
Proceedings of the european society for chlamydia research and the
second international symposium of Uppsala university centre for std
research, pp.38-38, University of Uppsala, Uppsala (1992).
 membrane protein
 Signal; Complete proteome.
 Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C. Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty Salzberg S.L., Eisen J., Fraser C.M.; Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39."
 InterPro; IPR006604; Chlamydia_OMP.
Pfam; FF01308; Chlamydia_OMP; 1.
Probom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal; Complete pro SIGNAL
2 BY SIMILARITY.
CHAIN 23 387 MAJOR OUTER MEMBRANE PROTEIN.
 -! - SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY
 SEQUENCE FROM N.A.
STRAIN-SSP. BV. MOUSE / NIGG II;
CATEN S. M. Giles I. Bverson J.S., Clarke I.N.;
"Chlamydia trachomatis mouse biovar: major outer r
 F -> Y (IN REF. 5
Y -> F (IN REF. 5
L -> F (IN REF. 1
A -> P (IN REF. 1
 with other Chlamydia strains.";
Mol. Biol. Evol. 10:1327-1342(1993)
 SEQUENCE FROM N.A.
STRAIN-MOPN / NIGG;
MEDLINE-20150255; Pubmed-10684935;
 EMBL; AE002272; AAF38941.1; -.
 EMBL; M64171; AAA23144.1; -. EMBL; U60196; AAB07068.1; -. EMBL; X63409; CAA45006.1; -.
 SEQUENCE OF 37-375 FROM N.A.
 EMBL; N73044; AAD29101.1;
 22
387
118
123
123
204
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. 23 3
397 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A. STRAIN=404 / SERON
 OMIN_CHLTR
P23114;
 SEQUENCE
 SIGNAL
 RESULT 9
OMIN_CHLTR
 235
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 -!- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-!- SUBCELLULAR LOCATION FINTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 SMGAKPTGSAAANYTTA---VDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS 238
 Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.
 of
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 82
 (OmpA)
 "Nucleotide sequence of the major outer membrane protein gene from Chlamydia trachomatis serovar \mathrm{H.\,''};
 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL
 LGNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA
 7;
 Length 387;
 "Sequence analysis of the major outer membrane protein gene Chlamydia trachomatis.",
 (Rel. 13, Created)
(Rel. 17, Last sequence update)
(Rel. 10, Last annotation update)
MEMBRANE PROTEIN, SEROVAR H PRECURSOR (MOMP).
 Indels
 4FD6FDC23248E0A2 CRC64;
 DB 1;
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 Score 1358.5; DB 1 Pred. No. 6.8e-105;
 64.6%; Scur.
66.7%; Pred. No. v..
... 50; Mismatches
 397 AA
 Chlamydia trachomatis serovar H.";
Nucleic Acids Res. 17:8366-8366(1989).
 PRT;
 SEQUENCE FROM N.A.
STRAIN-SEROVAR H;
MEDLINE-90045958; PubMed-2813066;
 Hamilton P.T., Malinowski D.P.;
 42009 MW;
 Query Match
Best Local Similarity 66.7
Matches 246; Conservative
 STANDARD;
 AA;
 379 AHVNAQFRF 387
 359 AHVSGQFRF 367
 SEQUENCE FROM N.A.
 387
 NCBI_TaxID=813;
 STRAIN-H/UW-4;
 OMPA OR OMP1H
 OUTER
 01-FEB-1991
 20-AUG-2001
 OMIH_CHLTR
P13467;
 Dean D.A.;
 SEQUENCE
 RESULT 8
OM1H_CHLTR
 239
 62
 83
 119
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 3;
 DECORDER 1.0...

STRAIN-404 / SEROYAR L3;
MEDLINE-91285429; PubMed=2060793;
MEDLINE-91285429; PubMed=2060793;
Fielder T.J., Peterson E.M., de la Maza L.M.;
"Nucleotide sequence of DNA encoding the major outer membrane protein of Chlamydia trachomeais serovar L3.";
Gene 101:159-160(1991).
-: FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
 117
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 352
 118 ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR H. 478ACE3808BF37BA CRC64;
 Gaps
 82
 61
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCATWCDAISMRVGYYGDFVFDRVLKTDVNKREP
 62 SMGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFINAGFIALNIWDRFDVFCTLG
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 175 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
 295 NPSLLGNAT--ALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEAR
 6
 63.7%; Score 1340.5; DB 1; Length 397;
65.1%; Pred. No. 2.2e-103;
ive 51; Mismatches 71; Indels 9;
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR L3 PRECURSOR (MOMP).
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBL_TaxID=813;
 Outer membrane; Transmembrane; Porin; Signal.
 397 AA.
 51; Mismatches
 InterPro; IPR000604; Chlamydia_OMP. Pfam; PF01308; Chlamydia_OMP; 1. ProDom; PD001717; Chlamydia_OMP; 1.
 PRT;
 42946 MW;
 EMBL; X16007; CAA34145.1; -. EMBL; AF304857; AAG41415.1; -PIR; S06589; MMCWTH.
 Matches 244; Conservative
 353 LINERAAHVSGQFRF 367
 ||:||||||
LIDERAAHVNAQFRF 397
 STANDARD;
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MEDLINE=91045088; PubMed=2235504;
 23
396 AA;
 P17451;
01-AUG-1990
01-AUG-1990
20-AUG-2001
 OM1E_CHLTR
 SEQUENCE
 RESULT 11
OMIE_CHLTR
ID OMIE_C
AC P17451
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 έ,
 SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES. & OTHER COMPONENTS FORM HICH MOLECULER-WEIGHT OLIGOMERS. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE. SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 BY STATLARITY.
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR L3.
FIDDCF09535C2595 CRC64;
 62 SMGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
 ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
 Gaps
 61
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISMRVGYYGDFVFDRVLKTDVNKEF 82
 203 ALWECGCATLGASFOYAQSKPKVEELNVLCDASEFTINKPKGYVGAEFPLDITAGTEAAT
 NPSLL--GNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEAR
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
 6
 DB 1; Length 397;
 V-1991 (Rel. 20, Last sequence update)
G-2001 (Rel. 40, Last annotation update)
OUTER MEMBRANE PROTEIN, SEROVAR A PRECURSOR (MOMP).
 73; Indels
 Chlamydiales; Chlamydiaceae; Chlamydia
 ; Score 1338.5; DB 1; Pred. No. 3.1e-103; 49; Mismatches 73;
 THE INTRACELLULAR RETICULATE BODY MEMBRANE
 PIR; JE0413; JE0413.
InterPro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
Probom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 396 AA
 PRT;
 (Rel. 20, Created)
(Rel. 20, Last sequ
(Rel. 40, Last anno
 42885 MW;
 63.6%;
65.1%;
 EMBL; X55700; CAA39226.1; -
 Query Match
Best Local Similarity 65.1%
Matches 244; Conservative
 353 LINERAAHVSGQFRF 367
 ||:||||||||
LIDERAAHVNAQFRF 397
 STANDARD;
 [1]
SEQUENCE FROM N.A.
STRAIN=SA1/OT / SEROVAR
 397
 Chlamydia trachomatis
 397 AA;
 NCBI_TaxID=813;
 OMPA OR OMP1A
 01-NOV-1991
 01-NOV-1991
 20-AUG-2001
 SEQUENCE
 OM1A_CHLTR
 SIGNAL
 RESULT 10
OMIA_CHLTR
1D OMIA_CHLTR
AC P23732
DT 01-NOV
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 Chlamydia trachomatis strain A/Sal/or.";
Nucleic Acids Res. 18:6136-6136(1990).
-!- PUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY
BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
THE INTRACELLULAR RETICULATE BODY MEMBRANE.
 MOMP
OLIGOMERS
 117
 118 ASNCYIRGNSTAFNLVGLFGVKGTTV---NANELPNVSLSNGVVELYTDTSFSWSVGARG 174
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT 234
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 263 GTKDASIDYHEWQASLALSYRLMMFTPYIGVKWSRVSFDADTIRIAQPKLAKPVLDTTTL 322
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR A. 2F9D3B0CE2D08162 CRC64;
 8; Gaps
 -1- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH WOLECULAR-WEIGHT OLIGOMER -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.-1- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 23 LEVGNPAEPSLAIDGILWEGFGGDPCDPCTTWCDAISMRMGYYGDFVFDRYLKTDVNKEF
 62 SMGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG
 295 NPSLLGNATALSTTDS-FSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARL
Hayes L.J., Clarke I.N.; "Nucleotide sequence of the major outer membrane protein gene of
 Length 396;
 Indels
 63.0%; Score 1325; DB 1;
64.7%; Pred. No. 4.1e-102;
iive 47; Mismatches 77;
 (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 40, Last annotation update)
 PIR; S12799; S12799.
InterPro; IPR000664; Chlamydia_OMP.
Pfam; FF01308; Chlamydia_OMP; 1.
Pr00m; P0001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 PRT;
 42877 MW;
 EMBL; M58938; AAA23141.1; -. EMBL; M33635; AAA92785.1; -.
 Query Match 63.0%
Best Local Similarity 64.7%
Matches 242; Conservative
 STANDARD;
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383 IDERAHVNAQFRF 396
 354 INERAAHVSGQFRF 367
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 4;
 MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-1- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 NUCLEIC ACIGS RES. 18:3414-3414(1990).
-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING. PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.
-!- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP
 62 SMGAKP---TGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFG--VKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 WECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGT 236
 SLLGNATALSTTD-SFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR E.
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 MEDLINE-90287737; Pubmed-2356137;
Peterson E.M., Markoff B.A., de la Maza L.M.;
"The major outer membrane protein nucleotide sequence of Chlamydia
 23 LPVGNPAEPSLAIDGILWEGFGGDPCDPCTTWCDAISMRMGYYGDFVFDRVLKTDVNKEF
 SSGYLKGNSASFNLVGLFGDNENQSTVKTNSVPNMSLDQSVVELYTDTAFSWSVGARAAL
 202 WECGCATLGASFQYAQSKPKVEELNVLCNAAEFTINKPKGYVGQEFPLALIAGTDAATGT
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP
 7;
 DB 1; Length 393;
 76; Indels
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR E PRECURSOR (MOMP).
 AB2B82D16027B361 CRC64;
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
 ; Score 1315.5; DB 1; Pred. No. 2.5e-101; 46; Mismatches 76;
 Outer membrane; Transmembrane; Porin; Signal.
 InterPro; IPR000604; Chlamydia_OMP. Pfam; PF01308; Chlamydia_OMP; 1. ProDom; PD001717; Chlamydia_OMP; 1.
 393 AA; 42424 MW;
 62.6%;
 EMBL; X52557; CAA36791.1; -.
 Query Match
Best Local Similarity 65.3%
Matches 243; Conservative
 393
 ||||||||| |||||
ERAAHVNAQFRF 393
 ERAAHVSGQFRF 367
 S10201; MMCWTE.
 [1]
SEQUENCE FROM N.A.
 SEQUENCE
 SIGNAL
 119
 142
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 237
 262
 297
 322
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 Stephens R.S., Sanchez-Pescador R., Wagar E.A., Inouye C., Urdea M.S.; "Diversity of Chlamydia trachomatis major outer membrane protein
 INTECT. DIST. 182:909-916(2000).
FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH BODIES AND PORIN REFICULAR DEPENDENCE BODY MEMBRANE.
SUBUNIT: DISULPIDE BOND INTERACTIONS WITHIN AND BETWEEN NOMP MOLECULES. & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 MEDLINE=20467420; PubMed=10950788;
Dean D., Suchland R.J., Stamm W.E.;
"Evidence for long-term cervical persistence of Chlamydia trachomatis by omp1 genotyping."; ISS-916(2000).
 118 ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSOFSVNKPKGYKGVAFPLPTDAGVATAT 234
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR C. 0047BCDB108E5309 CRC64;
 62 SMGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISMRVGYYGDFVFDRVLKTDVNKRF
 MEMBRANE PROTEIN, SEROVAR C PRECURSOR (MOMP).
 Indels
 62.6%; Score 1315.5; DB 1; 64.3%; Pred. No. 2.5e-101; tive 49; Mismatches 76;
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
 Outer membrane; Transmembrane; Porin; Signal.
 (Rel. 09, Last sequence update) (Rel. 40, Last annotation update)
397, AA
 PIR; S11011; MMCWTC.
InterPro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
 PRT;
 Bacteriol. 169:3879-3885(1987).
 SEQUENCE FROM N.A. MEDLINE-87307955; PubMed=3040664;
 EMBL; M17343; AAA23156.1; -.
EMBL; AF202455; AAG09443.1; -.
 09, Created)
 42892 MW;
 Matches 241; Conservative
 STANDARD;
 01-NOV-1988 (Rel. 09, 1
20-AUG-2001 (Rel. 40, 1
MAJOR OUTER MEMBRANE PI
OMPA OR OMPI OR OMPIC.
 397 AA;
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=813;
OM1C_CHLTR
P08780;
01-NOV-1988 (
 SEQUENCE
 Query Match
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14.2 TSGYLKGNSASFNLVGLFGDNENGSTVKKDAVPNMSFDQSVVELYTDTTFAWSVGARAAL 201
 393 AA
 SEQUENCE FROM N.A.
STRAIN-D/IU-71960;
MEDLINE-98339860; Pubmed-9673241;
 STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
 MEDLINE=93013014; PubMed=1398119;
 determinants.";
infect. Immun: 66:3618-3625(1998)
 Chlamydia trachomatis.";
Science 282:754-759(1998).
 STANDARD;
 Gene 120:129-130(1992)
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382 ERAAHVNAOFRF 393
 ERAAHVSGOFRF 367
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 OMID_CHLTR STA
Q46409;
30-MAY-2000 (Rel.
 NCBI_TaxID=813;
 STRAIN=D/B-120;
 Davis R.W.;
 356
 OMID_CHLTR
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 4;
 PICKEL M.A., Ward M.E., Clarke I.N.;
Pickett M.A., Ward M.E., Clarke I.N.;
Pickett M.A., Ward M.E., Clarke I.N.;
Pickett M.A., Ward M.E., Clarke I.N.;
Percenter incledited sequence of the major outer membrane protein
gene from Chlamydiat trachomatis serovar II.";
FEMS Microbiol. Lett. 42:185-190(1987).
-! FOWTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY
BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
THE INTRACELLULAR RETICULATE BODY MEMBRANE.
-! SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP
MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-! SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR L1.
7A952839408EE2DF CRC64;
 203 ALWECGCATLGASFQYAQSKPKVEELNVLCNASEFTINKPKGYVGAEFPLNITAGTEAAT 262
 SMGAKP---TGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 119 SNGYIRGNSTAFNLVGLFG--VKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVOWSRATFDADNIRIAQPKLPTAVLNLTAW
 7;
 DB 1; Length 393;
 (Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
MEMBRANE PROTEIN, SEROVAR L1 PRECURSOR (MOMP).
 74; Indels
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 62.5%; Score 1313.5; DB 1 64.5%; Pred. No. 3.6e-101; iive 51; Mismatches 74;
 InterPro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD0017; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 393 AA
 (Rel. 17, Created)
 42543 MW;
 EMBL; M36533; AAA23142.1; -
 Matches 240; Conservative
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|LIDERAAHVNAQFRF 397
 LINERAAHVSGQFRF 367
 STANDARD;
 393 AA;
 Best Local Similarity
 NCBI_TaxID=813;
 OMPA OR OMP1L1
 01-FEB-1991
 MAJOR OUTER
 01-FEB-1991
 20-AUG-2001
 OMIL_CHLTR
P19542;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR CUTER MEMBRANE PROTEIN, SEROVAR D PRECURSOR (MOMP). Chlamydia trachomatis. Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

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Query Match
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Chlamydia trachomatis serovar F.";
Nucleic Acids Res. 18:1061-1061(1990).

1- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY
BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
THE INTRACELLULAR RETICULATE BODY MEMBRANE.

1- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP
MOLECOLIES & OTHER COMPONENTS FORM HIGH MOLECULAR WEIGHT OLICOMERS.

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 WECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGT 236
 262 KDASIDYHEWQASLALSYRLNMFTPYIGVKWSRASFDADTIRIAQPKSATAIFDTTTLNP 321
 62 SMGAKP---TGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFG - VKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP 296
 SLLGNATALSTID-SFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 Gaps
 23 LPVGNPAEPSLAIDGILWEGFGGDPCDTWCDAISMRVGYYGDFVFDRVLKTDVNKEF 82
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 MEDIINE-90192102; PubMed-2315025; Zhang Y.X., Morrison S.G., Caldwell H.D.; The nucleotide sequence of major outer membrane protein gene of
 7;
 (Rel. 14, Last sequence update)
(Rel. 40, Last annotation update)
MEMBRANE PROTEIN, SEROVAR F PRECURSOR (MOMP).
 Indels
 16;
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 ; Score 1308.5; DB 1
; Pred. No. 9.3e-101;
48; Mismatches 76;
 395 AA
 PRT;
 (Rel. 14, Created)
(Rel. 14, Last sequence)
(Rel. 40, Last anno
 62.2%;
64.8%;
 / SEROVAR F;
 Query Match 62.2%
Best Local Similarity 64.8%
Matches 241; Conservative
 STANDARD;
 356 ERAAHVSGQFRF 367
 [||||||: ||||
ERAAHVNAQFRF 393
 SEQUENCE FROM N.A.
 NCBI_TaxID=813;
 STRAIN-IC-CAL3
 OMPA OR OMP1F
 01-APR-1990
01-APR-1990
 MAJOR OUTER
 20-AUG-2001
 OMIF_CHLTR
P16155;
 RESULT 15
OMIF_CHLTR
1D OMIF_CH
AC P16155,
DT 01-APR-DT 01-APR-DT 20-AUG
GN OMIP_CT 01-APR-DT 01
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 EMGEALAGASGNTTSTLSKLVERTNPAYGKHMQDAEMFTNAACMTLNIWDRFDVFCTLGA 142
 263 KDASIDYHEWQASLSLSYRLNMFTPYIGVKWSRASFDSDTIRIAQPRLVTPVVDITTLNP 322
 SMG---AKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLF - - GVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 WECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGT 236
 203 WECGCATLGASFQYAQSKPKIEELNVLCNAAEFTINKPKGYVGKEFPLDLTAGTDAATGT 262
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP 296
 SL--LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLI 354
 Gaps
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR 7F90FFDEEC264ACF CRC64;
 7;
 Length 395;
 76; Indels
SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 62.2%; Score 1307.5; DB 1;
63.5%; Pred. No. 1.1e-100;
ive 53; Mismatches 76;
 PIK; SUGAGA; MMCWTF.
INTERPRO; IPROUGOG4; Chlamydia_OMP.
TREATH; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 7, 2002, 21:42:47
 42586 MW;
 EMBL; X52080; CAA36299.1; -.
 237; Conservative
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DERAAHVNAQFRF 395
 Search completed: February
Job time: 601 sec
 395
 355 NERAAHVSGQFRF 367
 23
395 AA;
 PIR; S08463; MMCWTF
 Similarity
 SEQUENCE
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chlamydophi chlamydophi chlamydia p

070050 069307 069306 Q9xbf6 Q9xbf5 069305 Q9aii8

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chlamydia chlamydia

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chlamydia

046407 0090114 0090115 0090115 0090115 0090110 0090110 00901110 0090110

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046406 09a1i7 052924

chlamydia s chlamydia t chlamydia s chlamydia t chlamydia t

Scoring table:

Searched:

Sequence:

protein

Run on:

Minimum DB Maximum DB

Database

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MEDLINE-94171025; PubMed-8125292;
Girjes A.A., Carrick F.N., Lavin M.F.;
"Remarkable sequence relatedness in the DNA encoding the major outer
membrane protein of Chlamydia psittaci (koala type I) and Chlamydia
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 PROJUSTY, Chiempria_OMP; 1.
PD001717; Chiempria_OMP; 1.
PD001717; Chiempriane; Porin; Signal.
1 23 BY SIMILARITY.
1 389 MAJOR OUTER MEMBRANE PROFEIN.
E 389 AA; 41579 MW; 5DC50E85A6F4E50F CRC64;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBRANE PROTEIN PRECURSOR (WOMP).
Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 Score 1910; DB 2;
Pred. No. 2.1e-146;
5; Mismatches 4;
 A
 ALIGNMENTS
 389
 Q9XBF6
Q9XBF5
 069305
09AII8
046407
 Q9AII4
069093
 Q9A115
069094
 069095
09AIJ0
 PRT;
 Q9XBF2
 Pfam; PF01308; Chlamydia_OMP; 1.
PRINTS; PR01334; CHLAMIDIAOMP.
 90.8%;
llarity 97.5%;
Conservative 5
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 387
 Gene 138:139-142(1994)
 SEQUENCE FROM N.A.
STRAIN-KOALA TYPE 1;
 Local Similarity
es 357; Conserv
NCBI_TaxID=83554
 Outer membrane;
 pneumoniae
 1382
1371.5
1367.5
1363.5
1362.5
1352.5
 1351
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1342
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 1327.5
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 (without alignments)
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 MLPVGNPSDPSLLIDGTIWE......QKLISEEDLNSAVDHHHHH 394
 7, 2002, 21:41:19; Search time 172 Seconds
 Description
 09apm4
09alk1
046235
09alk0
09alj0
09aj15
09aj15
09aj12
09aj12
09aj19
09aj19
09aj19
 008085
 47.3505
 version 4.5
- 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 473505 seqs, 146272329 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Q46235
Q9AIK0
Q9AIH9
 Q9AIJ4
Q9AII2
Q9AIJ5
Q99QB0
 09AIJ2
09X717
046193
 sp_vertebrate:*
sp_unclassified:*
 GenCore (c) 1993
 sp_fungi:*
sp_human:*
sp_invertebrate:*
 sp_organelle:*
 seq length: 0 seq length: 2000000000
 sp_bacteria:*
 US-09-391-606-15
 sp_rodent:*
 SPTREMBL_17:*
: sp_archea:*
 sp_mammal:*
 sp_plant:*
 sp_virus:*
 sp_phage:*
 protein search,
 Length
 388
389
392
381
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380
391
 sp_mhc:*
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1529.5
1501.5
1497.5
1487
1487
1487
 Title:
Perfect score:
 Score
 1910
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Gaps

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Length 389

1469.5

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CATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSAT
 41573 MW;
 Conservative
 PRELIMINARY;
 19
388
 <1
20
388 AA;
 Similarity
 SEQUENCE FROM N.A.
 :: |||||
383 MNAQFRF 389
 361 VSGQFRF 367
 STRAIN-VS225
 281;
 Query Match
Best Local Si
Matches 281;
 SEQUENCE
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CHAIN
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 Q9AIK1
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 202
 Vretou E., Psarrou E., Kaisar M., Vlisidou I., Salti-Montesanto V., Longbottom D.; "Identification of protective epitopes by sequencing of the major outer membrane protein gene of a variant strain of Chlamydia psittaci
 S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 ATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV 361
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 121
 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN 301
 Gaps
 61
 23 LPVGNPAEPSLLIDGTWWEGASGDPCDPCSTWCDAISIRAGYYGDYVFDRVLKVDVNKTI 82
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG
72.8%; Score 1531.5; DB 2; Length 389; illarity 75.7%; Pred. No. 8.2e-116; Conservative 38; Mismatches 50; Indels 1;
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20513C69C7DBAAF5 CRC64;
 Chlamydophila abortus.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83555;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR.
 Ą
 389
 POTENTIAL.
 PRT;
 MEDLINE-20569239; PubMed-11119563;
 Infect. Immun. 69:607-612(2001).
EMBL; AF272945; AAG53881.1; -.
 41897 MW;
 PRELIMINARY;
 22
389
 1
23 3
389 AA;
 Query Match
Best Local Similarity
Matches 278; Conserv
 SEQUENCE FROM N.A. STRAIN=LLG;
 389
 SGQFRF 367
 serotype 1.";
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 CHAIN
SEQUENCE
 09APM4
09APM4;
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238
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 121 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALMECG 180
 199
 260 ATLKYHEWQVGLALSYRLNMLVPYIGVNWSRATFDADSIRIAQPKLAAAVLNLTTWNPTL 319
 300
 S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 323 EATTLDINNKFADFLQIASIQINKMKSRKACGVAVGATLIDADKWSITGEARLINERAAH 382
 301 NATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAH 360
 20 LPVGNPAEPSLLIDGTMWEGASGDPCDPCATWCDAISIRAGYYGDYVFDRVLKVDVNKTI 79
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 181 CATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATGTKS
 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL
 LGNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA
203 CATLGAEFQYAQSNPKIEMLNVVSSPAQFVVHKPRGYKGTAFPLPLTAGTDQATDTKSAT
 INYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLG
 .,
m
 72.7%; Score 1529.5; DB 2; Length 386;
76.2%; Pred. No. 1.2e-115;
Live 35; Mismatches 50; Indels 3;
 POTENTIAL.
MAJOR OUTER MEMBRANE PROTEIN.
8E232D22C9B9948D CRC64;
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83554;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL. AF269259; AAR00240.1; -.
 388 AA
 PRT;
 MEDLINE=21078680; PubMed=11211261;
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046235

RESULT

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S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG 180
 CAILGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPIDAGVATATGTKS 238
 200 CATLGAEFQYAQSNPKIEMLNVISSPAQFVVHKPRGYKGTSANFPLPANAGTEAATDTKS 259
 20 LPVGNPAEPSLLIDGTMWEGASGDPCDPCSTWCDAISIRAGYYGDYVFDRVLKVDVNKTF 79
 Gaps
 LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL
 3;
 DB 2; Length 388;
 MAJOR OUTER MEMBRANE PROTEIN.
96E675B3F69F708B CRC64;
 Indels
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83554;
 Chlamydophila caviae.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_FaxID=83557;
 (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR CUTER MEMBRANE PROTEIN PRECURSOR.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 71.2%; Score 1497.5; DB 2; 72.9%; Pred. No. 4.6e-113; ive 49; Mismatches 48;
 "Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL; AF269260; AAK00241.1;
 388 AA
 389. AA
 POTENTIAL
 PRT;
 PRT;
 SEQUENCE FROM N.A.
STRAIN-CALIFORNIN TURKEY 1, CT1;
MEDIINE-210/5660; Pubmed-11211261;
Bush R.M., Everett K.D.;
 42053 MW;
 Query Match
Best Local Similarity 72.98
Matches 259; Conservative
 PRELIMINARY;
 PRELIMINARY;
 \begin{array}{c} 1 \\ 19 \\ 388 \end{array}
 388 AA;
 380 AHMNAQERE 388
 AHVSGQFRF 367
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SIGNAL
 09AIH9;
 Q9AIK0
 Q9AIKO
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 62 S-MGAKPIGSAAANYTIAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVCARGALWECG 180
 181 CATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATGTKS 238
 203 CATLGAEFQYAOSNPKIEMLNVISSPAQFVVHKPRGYKGTSANFPLPANAGTEAATDTKS 262
 Gaps
 23 LPVGNPAEPSLLIDGTMWEGASGDPCDPCSTWCDAISIRAGYYGDYVFDRVLKVDVNKTF 82
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 LGNATALSTTDSFSDFWQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA
 239 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL
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ش
 DB 2; Length 391;
 MAJOR OUTER MEMBRANE PROTEIN
D98A8F5E76362A00 CRC64;
 Indels
 Storey C.C.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBI_TaxID=83554;
 Last sequence update)
 48;
 Bush R.M., Everett K.D.;

"Molecular evolution of the Chlamydiaceae.";

Int. J. Syst. Evol. Microbiol. 51:203-220(2001).

EMBL; AF263261; AAA23147.1;

EMBL; AF269261; AAK00242.1;

InterPro; IPR000604; Chlamydia_OMP.

Pfam; PF01308; Chlamydia_OMP.

ProDom; PD001314; CHLAMIDIAOMP.

ProDom; PD001717; Chlamydia_OMP; 1.
 71.4%; Score 1501.5; DB 2
73.2%; Pred. No. 2.2e-113;
Live 48; Mismatches 48;
 Ā
 391
 046235.
01-NOV-1996 (TTEMBLELOI, 01, Created)
01-NOV-1996 (TTEMBLELOI, 01, Last sequen
01-NOV-2001 (TTEMBLELOI, 17, Last annota
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR.
 POTENTIAL.
 STRAIN=GERMAN DUCK;
MEDLINE=21078680; PubMed=11211261;
 22
391
42427 MW;
 Conservative
 PRELIMINARY:
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23 3
391 AA;
 Local Similarity
les 270; Conserv
11:: |||||
380 AHMNAQFRF 388
 SEQUENCE FROM N.A. STRAIN-AVIAN TYPE
 AHVSGQFRF 367
 ||:: ||||
383 AHMNAQFRF 391
 SEQUENCE FROM N.A
 MOMP OR OMPA.
 SEQUENCE
 Query Match
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Signal

Best Loca Matches

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MEMBRANE PROTEIN.

POTENTIAL.
MAJOR OUTER MEMBRANE PRO:
; FC31FC051955246C CRC64

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EMBL; AF269267; AAK00248.1;
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23
392 AA;
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Best Local Similarity
Matches 276; Conserv
 09A112;
01-JUN-2001 (
01-JUN-2001 (
01-JUN-2001 (
 STRAIN-1710S;
 STRAIN=1710S
 CHAIN
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 122 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
 182 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATGTKSA 239
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 121
 261
 GNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAA 359
 Gaps
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 Zhang Y.X., Morrison S.G., Caldwell H.D., Baehr W.;
"Cloning and sequence analysis of the major outer membrane protein genes of two Chlamydia psittaci strains.";
Infect. Immun. 57:1621-1625(1989).
 240 TINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLL
 3;
 Length 389;
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STRAIN-GUINEA PIG INCLUSION CONJUNCTIVITIS, GPIC, ATCC VR813;
MEDLINE-21078680; Pubmed-11211261;
SEQUENCE FROM N.A.
STRAIN-GUINEA PIG INCLUSION CONJUNCTIVITIS, GPIC, ATCC VR813;
MEDLINE-89212917; PubMed-2707861;
 MAJOR OUTER MEMBRANE PROTEIN.
2527A820C76F8310 CRC64;
 50; Indels
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 Last sequence update)
Last annotation update)
 DB 2;
 71.2%; Score 1497.5; DB 2 73.9%; Pred. No. 4.6e-113;
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL. AF269282; AAK00263.1;
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
 43; Mismatches
 POTENTIAL
 01-JUN-2001 (TIEMBLIEL 17, Last annoted MAJOR OUTER MEMBRANE PROTEIN PRECURSOR
 (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last seq
(TrEMBLrel. 17, Last ann
 STRAIN-TEXAS TURKEY 3, TT3;
MEDLINE-21078680; PubMed-11211261;
 22 PO
389 MA
41932 MW;
 Similarity 73.972; Conservative
 389 AA;
 [1]
SEQUENCE FROM N.A.
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|HVNAQFRF 389
 360 HVSGQFRF 367
 NCBI_TaxID=83554;
 Query Match
Best Local Sim
Matches 272;
 01-JUN-2001
01-JUN-2001
 SEQUENCE
 Signal.
SIGNAL
 09AIJ4;
 Q9AIJ4
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major
 SMGAK ---- PTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
 ECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATG 235
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 PSLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
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 Gaps
 82
 MEDLINE-93123168; PubMed=8419295;
Kaltenboeck B., Kousoulas K.G., Storz J.;
"Structures of and allelic diversity and relationships among the majouter membrane protein (ompA) genes of the four chlamydial species. J. Bacteriol. 175:487-502(1993).
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 .;
8
 Indels
 Length
 Everett K.D.E., Hambly W.A., Andersen A.A.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF269279; AAK00260.1;
 Chlamydophila pecorum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 49;
70.7%; Score 1487; DB 2; 74.2%; Pred. No. 3.3e-112;
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
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 356 ERAAHVSGQFRF 367
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 OMPA.
Chlamydophila
 STRAIN=1710S;
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CHAIN SEQUENCE

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Signal. NON\_TER SIGNAL

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118 ASNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALW 177
 178 ECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATG 235
 236 TKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWN 295
 296 PSLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 S-MGAKPTGSA--AANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATGT 236
 21 LPVGNPAEPSLLIDGTMWEGASGDPCDPCATWCDAISIRAGYYGDYYFDRVLKVDVNKTF 80
 Gaps
 SMGAK - - - - PTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG
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MAJOR OUTER MEMBRANE PROTEIN.
88B3C09C1FEE26DB CRC64;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83556;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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 52;
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 "Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL; AF269257; AAK00238.1; -.
 392 AA
 FP CELLO;
 PRT;
 SEQUENCE FROM N.A.
STRAIN-FP BAKER, ATCC VR120, AND FI
MEDLINE-21078680; Pubmed-11211261;
Bush R.M., Everett K.D.;
 22 PC
392 M2
42051 MW;
 EMBL; AF269258; AAK00239.1;
Signal.
SIGNAL
 PRELIMINARY;
 379 ERAAHMNAQERF 390
 356 ERAAHVSGOFRF 367
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23
392 AA;
 CHAIN
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 RESULT 10
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 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG 180
 301 NATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAH 360
 SMGAKPTG-SAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 Gaps
 61
 Gaps
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 INYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLG
 ;;
 8;
 Length 381;
 Length 390
 POTENTIAL.
MAJOR OUTER MEMBRANE PROTEIN.
B62858403DBFA4E6 CRC64;
 POTENTIAL.
MAJOR OUTER MEMBRANE PROTEIN.
29406725CF9D3512 CRC64;
 51; Indels
 Indels
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBI_TaxID=83554;
 01-JUN-2001 (TIEMBLED. 17, Last sequence update) 01-JUN-2001 (TremBLrel. 17, Last annotation update) MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 49;
 70.4%; Score 1480; DB 2;
nilarity 72.8%; Pred. No. 1.2e-111;
Conservative 47; Mismatches 51;
 70.3%; Score 1479; DB 2;
73.7%; Pred. No. 1.4e-111;
:lve 41; Mismatches 49;
 SECUENCE FROM N.A.
STRAIN-MED JERSEY 1, NJ1;
MEDLINE-21078680; Pubbed=11211261;
Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL; AF269266; AAK00247.1;
 390 AA
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390
42042 MW; b
 15 PO
381 MA
41332 MW;
 (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 17,
 Local Similarity 73.7
 PRELIMINARY;
 Query Match
Best Local Similarity
Matches 267; Conserv
 390 AA;
 375 LSAQCRF 381
 361 VSGQFRF 367
 01-JUN-2001
01-JUN-2001
01-JUN-2001
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Q9AIJ5

61

SEQUENCE

Signal. NON\_TER SIGNAL

RESULT
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10 0941JS
AC 0991
AC 099

Query Match

Best Loca Matches

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255 INYHEWQVGAALSYRLNMLVPYIGIQWSRATFDADTIQVAQPKLASPIFNLTTWNPTLLG
INYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLG
 42056 MW;
 PRELIMINARY;
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378 INERAAHMNAQFRF 391
 354 INERAAHVSGQFRF 367
 \begin{array}{c} 1 \\ 17 \\ 391 \end{array}
 391 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=83554;
 LSAQCRF 380
 361 VSGQFRF 367
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Matches 266;
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Q9AIJ2;
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 RESULT 12
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 Kaltenboeck B., Kousoulas K.G., Storz J.; "Storz B." Structures of and allelic diversity and relationships among the major outer membrane protein (ompA) genes of the four chlamydial species."; J. Bacteriol. 175:487-502(1933).
 62 SMGAKPTG-SAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG 180
 CATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSAT 240
 254
 Gaps
 75
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 16 LPVGNPAEPSLLIDGTIWEGMSGDPCDPCATWCDAISLRVGFYGDYVFDRVLKTDVSKMF
 262 KSATVKYHEWQVGLALSYRLNMLVPYIGVNWSRATFDADTIRIAQPKLASAILNLTTWNP
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP
 3;
 DB 2; Length 380;
 MAJOR OUTER MEMBRANE PROTEIN 829A18D3C5A85008 CRC64;
 48; Indels
 STRAIN=L71;
Everect K.D.E., Hambly.W.A., Andersen A.A.;
Submitted (MAY-2000) to the EMBL/Genbank/DDBJ databases.
EMBL; AF269280; AAK00261.1; -
 Chlamydophila pecorum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
 01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
 Query Match 69.9%; Score 1469.5; DB Best Local Similarity 71.4%; Pred. No. 8.1e-111 Matches 262; Conservative 54; Mismatches 48
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 POTENTIAL.
 STRAIN=L71;
MEDLINE=21078680; PubMed=11211261;
 MEDLINE=93123168; PubMed=8419295;
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15 PC
380 MA
41047 MW;
 SEQUENCE OF 40-352 FROM N.A.
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382 RAHINAQFRF 392
 357 RAAHVSGQFRF 367
 380 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=85991;
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 STRAIN-L71;
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233
 S-MGAKPTGSA--AANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 119 SNGYIRGNSTAFNLVGLFGVKGTT-VNA--NELPNVSLSNGVVELYTDTSFSWSVGARGA 175
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 18 LPVGNPAEPSLLIDGTMWEGASGDPCDPCATWCDAISIRAGYYGDYVFDRVLKVDVNKTF
 LWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATA
 TGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTA
 WNPSLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARL
 ..
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 Length 391;
 POTENTIAL.
MAJOR OUTER MEMBRANE PROTEIN.
B58A73D4980408BF CRC64;
 Indels
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
 01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 26;
 STRAIN-WC;
MEDLINE-21078680; PubMed=11211261;
Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL; AF269269; AAK00250.1; -.
 tch 67.7%; Score 1423; DB 2; al Similarity 71.1%; Pred. No. 4.8e-107; 266; Conservative 44; Mismatches 56;
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391
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Q9X717

RESULT 13

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S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 GASNGYIRGNSTAFNLVGLFGVKGTTVNANE----LPNVSLSNGVVELYTDTSFSWSVGA 172
 230
 203 RGALWECGCATLGAEFQYAQSNPKIEVLNVTSSPAQFVIHKPRGYKGASSNFPLPITAGT 262
 291 LTAMNPSLLGNATALSTT --- DSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL 347
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 23 LFVGNPAEPSLLIDGTMWEGASGDPCDPCATWCDAISIRAGYYGDYVFDRVLKVDVNKTF
 263 TEATDTKSATIKYHEWQVGLALSYRLNMLVPYIGVNWSRATFDADTIRIAQPKLKSEILN
 RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
 231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN
 14;
MEDLINE-94103736; PubMed-8277245;
Storey C., Lusher M., Yates P., Richmond S.;
Storey C., Lusher M., Yates P., Richmond S.;
Feyidedice for Chlamydia pneumoniae of non-human oxigin.";
Gen. Microbiol. 139:2621-2626(1993).

EMBL; E04980; AAA17396.1;
FinterPeo, IPR000604; Chlamydia_OMP.

Fran: FF01308; Chlamydia_OMP;
FRINTS; PR01334; CHLAMIDIAOMP.

FroDom; PD001717; Chlamydia_OMP; 1.
 MAJOR OUTER MEMBRANE PROTEIN.
E36ABCB5AF04820A CRC64;
 PROTEIN.
 Indels
 MAJOR OUTER MEMBRANE PROT
6917171A9A69303B CRC64;
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
 01-JUN-2001 (TrEMBLrel. 17, Created)
(1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
(1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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 61;
 SEQUENCE FROM N.A.
STRAIN-MENINGOPNEUMONITIS, MN. ATCC VR122;
MEDLINE-21076860; Pubmed-11211261;
Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
 67.5%; Score 1419; DB 2; 70.5%; Pred. No. 1.1e-106;
 382 AA.
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 43261 MW;
 Int. J. Syst. Evol. Microbiol.
EMBL; AF269262; AAK00243.1; -.
 41231 MW;
 383 TGEARLINERAAHMNAOFRF 402
 348 TAEARLINERAAHVSGQFRF 367
 PRELIMINARY;
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402 AA;
 382 AA;
 Similarity
 NCBI_TaxID=83554;
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 CHAIN
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"Structures of and allelic diversity and relationships among the major outer membrane protein (omph) genes of the four chlamydial species.";
J. Bacteriol. 175:487-502(193).

EMBL; M73040; AAD29103.1;

InterProt. IPRO00604; Chlamydia_OMP.
Probom; PD001717; Chlamydia_OMP; 1.
Probom; PD001717; Chlamydia_OMP; 1.
Probom; PR01308; Chlamydia_OMP; 1.
NON_TER 341

SEQUENCE 341 AA; 36762 MW; B5933C9BF6AAF171 CRC64;
 241 RLNMLVPYIGVNWSRATFDADAIRIAQPKLAAAVLNLTTWNPTLLGEATALDTSNKFADF 300
 255 RLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALSTTDSFSDF 314
 Gaps
 75 YTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNGYIRGNSTAFNLVG 134
 135 LFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQSK 194
 16 GTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTFS-MGAKPTGSAAAN 74
 195 PKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSY
 DB 2; Length 341;
 Indels
 Chlamydophila abortus.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83554;
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 , Last sequence update), Last annotation update)
 315 MQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 301 LQIASIQINKMKSRKACGVAVGATLIDADKWSITGEARLIN 341
 67.5%; Score 1420.5; DB 2.75.4%; Pred. No. 6.4e-107; iive 35; Mismatches 48;
 341 AA
 402 AA
 01-NOV-1996 (TrEMBLrel. 01, Last sequen 01-JUN-2001 (TrEMBLrel. 17, Last annota MAJOR OUTER MEMBRANE PROTEIN PRECURSOR.
 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seq)
 PRT;
 STRAIN-LW508;
WEDLINE-93123168; PubMed-8419295;
 Matches 257; Conservative
 PRELIMINARY;
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=83555
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Query Match

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RESULT 14
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9
 RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV 230
 231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN 290
 303 ITTWNPSLLGSTTTLPNNGGKDVLSDVLQIASIQINKMKSRKACGVAVGATLIDADKWSI 362
 S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 GASNGYIRGNSTAFNLVGLFGVKGTTVNANE----LPNVSLSNGVVELYTDTSFSWSVGA 172
 LTAWNPSLLGNATALSTT---DSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL 347
 Gaps
 Indels 14;
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 TAEARLINERAAHVSGQFRF 367
 173
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Search completed: February 7, 2002, 21:41:21 Job time: 4650 sec

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 7, 2002, 21:34:40 ; Search time 137.02 Seconds Run on:

(without alignments)
198.401 Million cell updates/sec

US-09-391-606-16 1952 1 MLPVGNPSDPSLLIDGTIWE.....TAEARLINERAAHVSGQFRF 367 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 Total number of hits satisfying chosen parameters:

522463 segs, 74073290 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_1101:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|   |        | DOSAL PROTOCOL |          |          |         |         |         | 3 Protein encoded by |         |         |          |         |         |
|---|--------|----------------|----------|----------|---------|---------|---------|----------------------|---------|---------|----------|---------|---------|
|   | 1      |                | AAY35319 | AAY5677. | AAW9818 | AAW9818 | AAB1364 | AAG83213             | AAW9818 | AAY5676 | AAY56768 | AAW7636 | AAY5676 |
|   | g      | ;              | 20       | 20       | 20      | 20      | 21      | 22                   | 20      | 20      | 20       | 19      | 20      |
|   | Query  |                | 391      | 343      | 389     | 402     | 525     | 525                  | 402     | 387     | 404      | 376     | 397     |
| æ | Query  |                | 98.6     | 84.4     | 78.6    | 72.1    | 72.1    | 72.1                 | 72.1    | 69.5    | 69.1     | 68.8    | 68.6    |
|   | Score  | ) !            | 1925     | 1647     | 1534.5  | 1408    | 1408    | 1408                 | 1407    | 1356.5  | 1349     | 1345.5  | 1338.5  |
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C.        | Ω.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | W76362 C. trachomatis JM1                                                                                                          | Chl                                                                                                                                                                         |                                                                                                                                                                             | Chlamydia                                                                                                                                                                                                 | 5 Chlamydia                                                                                                                                                                                                                                                      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                                               | Y56758 C. trachomatis ser                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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|        | 20 AA130703 | 20 AAY56764 | 20 AAY56764 | 20 AAYS6764 C. 20 AAYS6765 C. 21 AAYS6757 C. 20 AAYS6757 C. 20 AAYS6757 C. 22 AAE06646 C. 22 AAE06646 C. 19 AAW76365 C. 21 AAW76364 C. 21 AAW7646 C. 21 AAW7 | 20 AAYS6764<br>20 AAYS6765<br>19 AAW76363<br>20 AAXS6757<br>20 AAXS6759<br>22 AAR6565<br>22 AAR66646<br>23 AAR76664<br>20 AAX56762 | 20 AAY 56764<br>20 AAY 56765<br>19 AAY 76363<br>20 AAY 56757<br>21 AAY 7355<br>22 AAF 66646<br>22 AAF 66646<br>23 AAF 66646<br>24 AAY 656762<br>26 AAY 56762<br>27 AAY 6562 | 20 AAYS6764<br>20 AAYS6765<br>20 AAXS6756<br>20 AAXS6757<br>20 AAXS6757<br>21 AAAXS685<br>22 AAXS6766<br>22 AAXS6762<br>23 AAXS6762<br>24 AAXS6762<br>25 AAXS6762<br>26 Chl | 20 AAYS6764 C. 20 AAYS6765 C. 20 AAXS6765 C. 20 AAXS6757 C. 20 AAXS6757 C. 22 AAE006646 C. 22 AAE006646 C. 20 AAX56762 C. 19 AAW76362 C. 19 AAW76362 C. 19 AAW76362 C. 19 AAW763141 Chl. 19 AAW73141 Chl. | 20 AAY 56764 20 AAY 56765 21 AAY 56765 22 AAY 56759 22 AAY 56759 23 AAY 56759 24 AAY 56762 25 AAB 06646 26 AAY 56762 26 AAY 56762 27 AAY 56762 28 AAY 56762 29 AAY 56762 20 AAY 56762 21 AAY 5482 21 AAY 81268 22 AAY 81268 23 AAY 81268 24 AAY 81268 25 AAY 81268 26 AAY | 20 AAY 56764 20 AAY 56765 20 AAY 56765 20 AAY 56757 20 AAY 56757 21 AAW 56365 22 AAY 56765 22 AAY 56762 23 AAY 56762 24 AAW 56762 25 AAY 56762 26 AAY 56762 27 AAY 56762 28 AAY 56762 29 AAY 56762 20 AAY 56762 21 AAY 61268 21 AA | 20 AAYS6764 20 AAYS6765 20 AAXS6765 20 AAXS6757 20 AAXS6757 21 AAW76365 22 AAE06646 20 AAX56762 21 AAX81268 21 AAX81268 21 AAX81268 22 AAX5775 20 AAX56761 21 AAX81268 22 AAX56761 23 AAX81268 24 AAX56777 26 Chl | 20 AAY 56764 20 AAY 56765 21 AAY 56765 22 AAY 56759 22 AAY 56759 23 AAY 56759 24 AAY 56762 25 AABO 6646 26 AAY 56762 26 AAY 56762 27 AAW 75149 28 AAW 55149 29 AAW 55149 21 AAW 55149 21 AAW 5775 20 AAY 56761 21 AAW 57775 20 AAY 56761 20 AAY 56761 21 AAW 57775 20 AAY 56761 20 AAY | 20 AAY 56764 20 AAY 56765 20 AAY 56765 20 AAY 56757 20 AAY 56757 21 AAN 6366 22 AAY 56762 22 AAY 56762 23 AAY 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AAY56760<br>24 AAY56760<br>25 AAY56760<br>26 AAY56760<br>27 AAY56760<br>28 AAY56760<br>29 AAY56760<br>20 AAY56760<br>20 AAY56760<br>21 AAY56760 | 20 AAY56764 20 AAY56765 21 AAY56765 22 AAX56757 22 AAX56759 22 AAX56759 23 AAX56762 24 AAW76364 25 AAW76364 26 AAW76364 27 AAW873141 21 AAW87775 20 AAX56761 20 AAX56761 20 AAX56761 21 AAX86788 21 AAX86789 21 AAX86789 21 AAX86789 21 AAX86789 21 AAX86388 | 20 AAY56764 20 AAY56765 20 AAY56765 20 AAY56757 20 AAY56757 20 AAY56759 21 AAW76364 22 AAW76364 21 AAW76362 21 AAW73141 21 AAW75775 20 AAY56760 21 AAX82388 21 AAX82388 21 AAX82388 | 20 AAY56764 20 AAY56764 20 AAY56765 20 AAY56755 20 AAY56755 21 AAW76364 19 AAW76364 19 AAW73141 21 AAW73141 21 AAW57775 20 AAY56760 20 AAY56760 20 AAY56760 20 AAY56760 21 AAY82389 21 AAY82389 21 AAY82389 21 AAY82389 21 AAY82389 | 20 AAY56764 20 AAX56765 21 AAX56765 22 AAX56757 22 AAX56759 22 AAX56759 23 AAX56762 24 AAX6364 25 AAX6364 26 AAX56762 27 AAX6775 20 AAX56761 20 AAX56761 21 AAX82388 21 AAX82388 21 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## ALIGNMENTS

AAY35319 standard; Protein; 391 AA AAY35319; AAY35319

RESULT

13-SEP-1999 (first entry) 

Chlamydia pneumoniae transmembrane protein sequence.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.

Chlamydia pneumoniae.

WO9927105-A2.

03-JUN-1999.

98WO-IB01890. 20-NOV-1998;

98US-0107078. 97FR-0014673. 21-NOV-1997; 04-NOV-1998;

(GEST ) GENSET

Griffais R;

WPI; 1999-357842/30.

Genome sequence of Chlamydia pneumoniae

Page 1130-1131; Disclosure; 1912pp; English.

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 Major outer membrane protein; MOMP; Chlamydia; vaccine; immune response; cellular response; immunogen; Th1-like CD4 response; mucosal immunity
 brochitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent ofitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
 AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and
 301
 265
 Gaps
 62 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 121
 122 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
 85
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN
 182 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATI
 266 nyhewqvgaslsyrlnslvpyigvqwsratfdadniriaqpklptavlnltawnpsllgn
 302 ATALSTTDSFSDFMOIVSCOINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV
 ;
0
 Length 391;
 Indels
 Score 1925; DB 20;
Pred. No. 2e-182;
0; Mismatches 4;
 0; Mismatches
 C. trachomatis serovar HuPn MOMP sequence.
 AAY56771 standard; Protein; 343
 98.6%;
98.9%;
 99WO-CA00292.
 98US-0055765.
 (first entry)
 Matches 362; Conservative
 Chlamydia trachomatis
 (UYMA-) UNIV MANITOBA.
 Best Local Similarity
 391 AA;
 362 SGQFRF 367
 386 sqqfrf 391
 22-FEB-2000
 WO9951745-A2
 07-APR-1999;
 07-APR-1998;
 14-0CT-1999.
 Sequence
 AAY56771;
 Query Match
 242
 AAY56771
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to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Th1-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAV5675771 represent.MOMP sequences from a variety of serovars of C. trachomatis.
 outer membrane protein
 The invention provides a non-replicating vector that comprises, linked
 337
 301
 361
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 121
 Gaps
 61
 83
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN
 ATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATI
 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC
 Length 343;
 Major outer membrane protein; MOMP; psittacosis; infection; vaccine; genetic immunisation.
 Indels
 Non-replicating vector encoding fragments of the cof Chlamydia, useful in vaccines and as immunogen
 Score 1647; DB 20;
Pred: No. 6.4e-155;
2; Mismatches 2;
 Chlamydia psittaci major outer membrane protein.
 Disclosure; Fig 10 A-F; 52pp; English.
 AAW98188 standard; Protein; 389 AA.
 84.4%;
86.3%;
 (first entry)
 Best Local Similarity 86.3
Matches 316; Conservative
 WPI; 1999-620205/53.
 Chlamydia psittaci
 343 AA;
 343
 SGQFRF 367
 : |||
nsqfrf
 05-JUL-1999
 Bruhnam RC;
 Sequence
 AAW98188;
 Query Match
 7
 84
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AAW98188
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protein; MOMP; psittacosis; infection;

(first entry)

Tully TN;

Kousoulas KG,

98WO-US17943

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Chlamydia psittaci major outer membrane protein
 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE.
 Disclosure; Page 65-66; 72pp; English.
 vaccine; genetic immunisation
 Baghian A, Chouljenko VN,
 Major cuter membrane
 WPI; 1999-254214/21.
 Chlamydia psittaci
 N-PSDB; AAX25048
 WO9910005-A1
 28-AUG-1998;
 28-AUG-1997;
 05-JUL-1999
 04-MAR-1999.
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 62 S-MGAKPIGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 The present sequence is the major outer membrane protein (MOMP) of Chlamydia psittaci strain B577. A claimed MOMP polypeptide (see AAM98184) comprises regions VD3 and VD4 of B577 MOMP, i.e. it lacks regions VD1 and VD2. A claimed vaccine composition includes MOMP polypeptide lacking VD1 and VD2, optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing consistant infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in
 61
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 CATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSAT
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG
 241 INYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLG
 301 NATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLIAEARLINERAAH
 DB 20; Length 389;
 Indels
 Chouljenko VN, Kousoulas KG, Tully TN;
 ed. No. 1.1e-143;
Mismatches 49;
 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE.
 78.6%; Score 1534.5; 75.7%; Pred. No. 1.1e
 Disclosure; Page 60-61; 72pp; English.
 AAW98189 standard; Protein; 402
 39;
 98WO-US17943.
 97US-0057147
 Conservative
 WPI; 1999-254214/21
 Similarity
 389 AA;
 :: ||||
383 mnaqfrf 389
 361 VSGQFRF 367
 N-PSDB; AAX25047
 28-AUG-1997;
WO9910005-A1
 28-AUG-1998;
 04-MAR-1999
 Baghian A,
 Best Local Sir
Matches 278;
 Sequence
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 AAW98189
 121
 181
 203
 AAW98189
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AC AAW9
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S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 LTAWNPSLLGNATAL---STTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL 347
 Gaps
 82
 2 LFVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
The present sequence is the major outer membrane protein (MOMP) of Chlamydia psittaci strain 6BC. Claimed MOMP polypeptides (see AAM98183 and AAW98184) comprise regions VD3 and VD4 of an MOMP, i.e. they lack regions VD1 and VD2. Claimed vaccine compositions include such MOMP polypeptides, optionally fused to a maltose binding protein. Also claimed are isolated nucleic acids encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide a vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in birds.
 GASNGY IRGNSTAFNLVGLFGVKG----TTVNANELPNVSLSNGVVELYTDTSFSWSVGA
 RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN
 14;
 Length 402;
 Indels
 72.1%; Score 1408; DB 20; 70.3%; Pred. No. 4.2e-131; live 38; Mismatches 61;
 TAEARLINERAAHVSGOFRF 367
 Best Local Similarity 70.3
Matches 267; Conservative
 402 AA;
 Sequence
 Query Match
Best Local S
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; 9

GASNGYIRGNSTAFNLVGLFGVKG----TTVNANELPNVSLSNGVVELYTDTSFSWSVGA 172

347

367

q

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LTAWNPSLLGNATAL - - - STTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL
 348 TAEARLINERAAHVSGQFRF
 117
 AAG83213
 oy
Db
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 9
 The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can
 lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is also thought to play a role in the pathogenesis of atherosclerosis and coronary heart disease. The present sequence is a protein isolated in the
 Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 Stromberg EJ;
 Chlamydial infection; sexually transmitted disease; pelvic inflammatory disease; PID; tubal obstruction; infertility; trachoma; blindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial.
 14;
 Length 525;
 pneumoniae serovar MOMPS pmp gene Ral2 fusion protein.
 Indels
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 Jen
 3; DB 21;
6.3e-131;
 Skeiky YAW, Fling SP,
 Pred. No. 6.3e; Mismatches
 72.1%; Score 1408; 70.3%; Pred. No. 6.
 Claim 2; Pages 221-222; 256pp; English.
 AAB13645 standard; Protein; 525 AA.
 38;
383 tgearlineraahmnaqfrf 402
 98US-0208277.
99US-0288594.
99US-0410568.
99US-0426571.
 99WO-US29012
 (first entry)
 Best Local Similarity 70.3
Matches 267; Conservative
 Bhatia A,
 Chlamydia pneumoniae
 (CORI-) CORIXA CORP.
 WPI; 2000-431303/37
 525 AA;
 coronary heart dis
present invention.
 WO200034483-A2
 02-FEB-2001
 08-DEC-1999;
 08-APR-1999;
01-OCT-1999;
 08-DEC-1998;
 15-JUN-2000
 22-OCT-1999;
 Probst P,
 AAB13645;
 Sequence
 Query Match
 RESULT
AAB13645
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Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease
 Chlamydia; vaccine; infection; fusion protein; antigen; pelvic inflammatory disease; tachoma; atheroscierosis; heart disease; acute respiratory tract infection; Capl; CT529; OWCB; polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
 The present sequence is provided in a specification relating to compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of chlamydia antigens and DNA sequences encoding such polypeptides. They are useful for vaccinating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease.
 Protein encoded by Chlamydia trachomatis serovar MOMPS pmp gene.
 Scholler J;
 Skeiky YAW, Fling SP,
 Claim 2; Page 226-227; 295pp; English.
 AAG83213 standard; Protein; 525 AA
 04-DEC-2000; 2000WO-US32919.
 03-DEC-1999; 99US-0454684.
19-APR-2000; 2000US-0556877.
20-JUN-2000; 2000US-0598419.
 (first entry)
 Chlamydia trachomatis.
 Bhatia A,
 WPI; 2001-374831/39.
 (CORI-) CORIXA CORP.
 WO200140474-A2.
 05-SEP-2001
 07-JUN-2001
 Probst P,
 AAG83213;
 Sequence
9
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S-MGAKPT---GSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116 

62 206

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Gaps

14;

Length 402; Indels

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Major outer membrane protein; MOMP; Chlamydia; vaccine; immune response; cellular response; immunogen; Thl-like CD4 response; mucosal immunity.
 62 S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 GASNGYIRGNSTAFNLVGLFGVKG----TTVNANELPNVSLSNGVVELYTDTSFSWSVGA 172
 ||||||| : :| |||||||| |
143 gasngyfkassaafnlvgligfsaassistdlptqlpnvgitggvvefytdtsfswsvga 202
 RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV 230
 231 AȚATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN 290
 LPAWNPSLLGNATAL --- STTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL 347
 polypeptide lacking VD1 and VD2, optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking irequos, VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in
 72.1%; Score 1407; DB 20; 70.0%; Pred. No. 5.3e-131; 11ve 39; Mismatches 61;
 C. trachomatis serovar MoPn MOMP sequence
 AAY56767 standard; Protein; 387 AA.
 348 TAEARLINERAAHVSGOFRF 367
 99WO-CA00292
 98US-0055765
 22-FEB-2000 (first entry)
 Query Match
Best Local Similarity 70.09
Matches 266; Conservative
 Chlamydia trachomatis
 (UYMA-) UNIV MANITOBA
 WPI; 1999-620205/53
 402
 W09951745-A2
 07-APR-1998;
 07-APR-1999;
 14-OCT-1999
 Sequence
 AAY56767;
 birds.
 æ
 323
 383
 173
 203
 117
 AAY56767
 9
 231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN 290
 GASNGYIRGNSTAFNLVGLFGVKG----TTVNANELPNVSLSNGVVELYTDTSFSWSVGA 172
 S-MGAKPT---GSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 LTAWNPSLLGNATAL --- STTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSL 347
 61
 Gaps
 of Chlamydia psittaci strain LSUWTCK, a cockatiel isolate (the MOMP gene sequence of this isolate is identical to that of C. psittaci Avian Type C). A claimed MOMP polypeptide (see AAW98183) comprises regions VD3 and VD4 ESUWTCK MOMP, i.e. it lacks regions VD1 and VD2. A claimed vaccine composition includes MOMP
 RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 14;
 The present sequence is the major outer membrane protein (MOMP)
Length 525;
 protein; MOMP; psittacosis; infection;
 Indels
 Tully TN;
DB 22;
 61;
72.1%; Score 1408; DB 22; 70.3%; Pred. No. 6.3e-131;
 Chlamydia psittaci major outer membrane protein
 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE
 38; Mismatches
 Kousoulas KG,
 Disclosure; Page 56-57; 72pp; English.
 Pred.
 AAW98187 standard; Protein; 402 AA
 TAEARLINERAAHVSGOFRF 367
 vaccine; genetic immunisation
 98WO-US17943
 97US-0057147
 Baghian A, Chouljenko VN,
 (first entry)
 Conservative
 Major outer membrane
 WPI; 1999-254214/21
 Similarity
 Chlamydia psittaci
 N-PSDB; AAX25046
 05-JUL-1999
 28-AUG-1998;
 28-AUG-1997;
 Best Local Sim
 04-MAR-1999
 AAW98187;
 348
 146
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 291
 AAW981.87
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 to a promoter, a nucleotide sequence that encodes a region containing at protein of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly callular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Th1-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAY56757-71 represent MOMP sequences from a variety of servoars of C. trachomatis.
 Major outer membrane protein; MOMP; Chlamydia; vaccine; immune response; cellular response; immunogen; Thl-like CD4 response; mucosal immunity.
 outer membrane protein
 invention provides a non-replicating vector that comprises, linked
 62 SMGAKPTGSAAANYTTA---VDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS 238
 Gaps
 23 lpvgnpaepsimidgilwegfggdpcdpcttwcdaislrlgyygdfvfdrvlktdvnkqf 82
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 239 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL
 299 LGNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLIAEARLINERA
 7;
 Length 387;
 Indels
 DB 20;
 Chlamydia, useful in vaccines and as immunogen
 :99
 Non-replicating vector encoding fragments of the
 69.5%; Score 1356.5; DB 2
66.4%; Pred. No. 5.1e-126;
 51; Mismatches
 C. trachomatis serovar SFPD MOMP sequence
 52pp; English.
 AAY56768 standard; Protein; 404 AA.
 (first entry)
 Best Local Similarity 66.4
Matches 245; Conservative
 Disclosure; Fig 10 A-F;
 Chlamydia trachomatis.
 359 AHVSGOFRF 367
 379 ahvnaqfrf 387
 387 AA;
 W09951745-A2
 22-FEB-2000
 14-OCT-1999
 Sequence
 Query Match
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against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Thi-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAY56757-71 represent MOMP sequences from a variety of serovars of C. trachomatis.
 at
 The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly cellular)
 Non-replicating vector encoding fragments of the outer membrane protein
 SMGAKPTGS---AAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFGVKG------TTVNANELPNVSLSNGVVELYTDTSFSWSV 170
 GARGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGV 230
 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN 290
 LTAWNPSLLGNAT-----ALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADK 344
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 23 lpvgnpaepsimidgilwegfggdpcdpcttwcdaislrlgyygdfvfdrvlktdvnkqf
 Length 404;
 C. trachomatis JM109 pCT33-H major outer membrane protein.
 3e-125;
66;
 Chlamydia, useful in vaccines and as immunogen
 DB 20;
 69.1%; Score 1349; D
64.8%; Pred. No. 3e-1
ive 51; Mismatches
 Disclosure; Fig 10 A-F; 52pp; English.
 AA.
 WSLTAEARLINERAAHVSGQFRF 367
 AAW76366 standard; protein; 376
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yavtvetrlideraahvnagfrf
99WO-CA00292
 98US-0055765
 Conservative
 MANITOBA
 WPI; 1999-620205/53.
 Best Local Similarity
Matches 248; Conserv
 404 AA;
 (UYMA-) UNIV
07-APR-1999;
 07-APR-1998;
 03-DEC-1998
 Bruhnam RC;
 Sequence
 Query Match
 10
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 AAW76366
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to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Thi-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAX5675771 represent MOMP sequences from a variety of sercvars of C. trachomatis.
 Major outer membrane protein; MOMP; Chlamydia; vaccine; immune response; cellular response; immunogen; Th1-like CD4 response; mucosal immunity.
 outer membrane protein
 The invention provides a non-replicating vector that comprises, linked
 ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT 234
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 SMGAKPTGSAAANY - - - - TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG
 DB 20; Length 397;
 Query Match 68.6%; Score 1338.5; DB 20; Lengt Best Local Similarity 64.8%; Pred. No. 3.3e-124; Matches 243; Conservative 52; Mismatches 71; Indels
 Non-replicating vector encoding fragments of the of Chlamydia, useful in vaccines and as immunogen
 Disclosure; Fig 10 A-F; 52pp; English.
 98US-0055765.
 LINERAHVSGOFRF 367
 Chlamydia trachomatis
 (UYMA-) UNIV MANITOBA
 WPI; 1999-620205/53.
 ¥
 W09951745-A2
 07-APR-1999;
 07-APR-1998;
 14-OCT-1999
 Bruhnam RC;
 Sequence
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 3;
 AAW76362-w76366 are major outer membrane proteins isolated from Chlamydia trachomatis which are used for the measurement of an antibody against Chlamydia trachomatis, by using it as an antigen in the form of a reagent. The method can give a diagnostic method for Chlamydia trachomatis-infected diseases with high specificity.
 FSMGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 | ||| || : ||:
61 fqmgaapttndaadlqndpktnvarpnpaygkhmqdaemftnaaymalniwdrfdvfctl 120
 GASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGAR 173
 TGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTA 293
 WNPSLLGNAT -- ALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEA 351
 Gaps
 9
 1 MLPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKT 60
 trachomatis
Major outer membrane protein; antibody; antigen; diagnosis; disease
 GALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATA
 DB 19; Length 376;
 6
 Chlamydia 1
gene, for 1
 68.9%; Score 1345.5; DB 19; Lengu.
65.2%; Pred. No. 6.1e-125;
wismatches 71; Indels
 Preparation of major outer membrane protein of - by cloning and recombinant expression of the diagnostic of Chlamydia infections
 C. trachomatis serovar H MOMP sequence
 Claim 2; Page 15-16; 19pp; Japanese
 ₹
 AAY56766 standard; Protein; 397
 (ELED) DENKI KAGAKU KOGYO KK
 97JP-0040780.
 97JP-0040780
 (first entry)
 |||:|||||||
rlideraahvnaqfrf 376
 Best Local Similarity 65.2
Matches 245; Conservative
 RLINERAAHVSGQFRF 367
 Chlamydia trachomatis.
 WPI; 1998-535045/46.
 376 AA
 JP10234395-A
 25-FEB-1997;
 25-FEB-1997;
 22-FEB-2000
 08-SEP-1998
 Sequence
 AAY56766;
 Query Match
 61
 117
 174
 234
 294
 352
 361
 RESULT 1
AAY56766
ID AAX5
XX
AC AAX5
XX
DT 22-F
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295 NPSLL--GNATALSTIDSFSDFMQIVSCQINKFKSRKACGVIVGAILVDADKWSLIAEAR 352
 07-APR-1999;
 07-APR-1998;
 22-FEB-2000
 14-0CT-1999.
 Bruhnam RC;
 Sequence
 AAY56764;
 Query Match
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 AAY56764
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 The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassage. Immunisation with the vector induces a broad spectrum of immune responses, including Th1-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences ANYSO(577-71 represent MOMP sequences from a variety
 MOMP; Chlamydia; vaccine; immune response; Th1-like CD4 response; mucosal immunity.
 outer membrane protein
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 SMGAKPTGSAAANY ----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
 118 ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
 Gaps
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 23 lpvgnpaepsimidgilwegfggdpcdpcttwcdaismrvgyygdfvfdrvlktdvnkef 82
 175 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
 DB 20; Length 397;
 6
 Indels
 Non-replicating vector encoding fragments of the of Chlamydia, useful in vaccines and as immunogen
 ; Score 1336.5; DB 20; Pred. No. 5.1e-124; 50; Mismatches 73;
 C. trachomatis serovar L3 MOMP sequence.
 Disclosure; Fig 10 A-F; 52pp; English.
 AAY56763 standard; Protein; 397 AA
 of serovars of C. trachomatis
 protein;
 cellular response; immunogen;
 68.5%;
64.8%;
 98US-0055765.
 99WO-CA00292
 (first entry)
 Ouery Match
Best Local Similarity 64.8
Matches 243; Conservative
 Chlamydia trachomatis.
 (UYMA-) UNIV MANITOBA
 membrane
 WPI; 1999-620205/53
 397 AA;
 WO9951745-A2
 07-APR-1998;
 07-APR-1999;
 22-FEB-2000
 outer
 14-0CT-1999
 Bruhnam RC;
 Sequence
 AAY56763
 62
 Major
 235
 AAY56763
 RESULT
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vaccines to generate a protective immune response (mainly cellular) against MOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including Thi-like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAV56757-71 represent MOMP sequences from a variety
 MOMP; Chlamydia; vaccine; immune response; Th1-like CD4 response; mucosal immunity.
 The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2, 3 and 5 of a major outer membrane protein (MOMP) of a Chlamydia strain. The vector is used: (a) in
 Non-replicating vector encoding fragments of the outer membrane protein of Chlamydia, useful in vaccines and as immunogen
 118 ASNGYIRGNSTAFNLVGLFGVKGTTV---NANELPNVSLSNGVVELYTDTSFSWSVGARG 174
 62 SMGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
82
 61
 23 lpvgnpaepsimidg1lwegfggdpcdpcttwcdaismrmgyygdfvfdrvlktdvnkef
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 .
m
 Length 396;
 Indels
 67.9%; Score 1326; DB 20;
64.7%; Pred. No. 5.6e-123;
iive 48; Mismatches 76;
 C. trachomatis serovar A MOMP sequence.
 Disclosure; Fig 10 A-F; 52pp; English.
 AAY56764 standard; Protein; 396 AA
 C. trachomatis.
 protein;
 cellular response; immunogen;
 99WO-CA00292
 98US-0055765
 (first entry)
 Conservative
 367
 397
 Chlamydia trachomatis
 MANITOBA
 ||:||||||: ||||| 383 lideraahvnaqfrf
 outer membrane
 353 LINERAAHVSGQFRF
 WPI; 1999-620205/53.
 Local Similarity
les 242; Conserv
 AA;
 serovars of
 (UYMA-) UNIV
 WO9951745-A2
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The invention provides a non-replicating vector that comprises, linked to a promoter, a nucleotide sequence that encodes a region containing at least one of the conserved domains 2. 3 and 5 of a major outer membrane protein (WOMP) of a Chlamydia strain. The vector is used: (a) in vectores to generate a protective immune response (mainly cellular) against WOMP, and (b) as immunogens to raise anti-MOMP antibodies, useful in standard immunoassays. Immunization with the vector induces a broad spectrum of immune responses, including fih.like CD4 responses and mucosal immunity, providing significant protection against subsequent challenge. Sequences AAX56757-71 represent MOMP sequences from a variety
 Major outer membrane protein; MOMP; Chlamydia; vaccine; immune response; cellular response; immunogen; Th1-like CD4 response; mucosal immunity.
 encoding fragments of the outer membrane protein
 234
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
 Chlamydia, useful in vaccines and as immunogen
 sedneuce
 52pp; English.
 Ş
 AAY56765 standard; Protein; 397
 serovars of C. trachomatis.
 C. trachomatis serovar C MOMP
 99WO-CA00292
 98US-0055765
 (first entry)
 Disclosure; Fig 10 A-F;
 354 INERAAHVSGQFRF 367
 |:|||||||
|ideraahvnaqfrf 396
 Non-replicating vector
 Chlamydia trachomatis.
 (UYMA-) UNIV MANITOBA
 WPI; 1999-620205/53.
 397 AA;
 W09951745-A2
 07-APR-1999;
 07-APR-1998;
 22-FEB-2000
 14-0CT-1999
 Bruhnam RC;
 AAY56765;
 Seguence
 383
175
 235
```

protein; antibody; antigen; diagnosis;

Chlamydia trachomatis

Major outer

JP10234395-A.

97JP-0040780. 97JP-0040780

25-FEB-1997; 25-FEB-1997; KAGAKU KOGYO

(ELED ) DENKI

C. trachomatis JM109 pCT33-C major outer membrane protein.

(first entry)

03-DEC-1998

AAW76363; AAW76363

15

AAW76363 RESULT

standard; protein; 376 AA.

NPSLLGNATALS -- TIDSFSDFMQIVSCOINKFKSRKACGVTVGATLVDADKWSLTAEAR 352

LINERAAHVSGQFRF 367 1::||||||: ||||| 383 lideraahvnaqfrf 397

353

295

GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW

118

62 SMGAKPTGSAAANY ----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG

23 lpvgnpaepsimidgilwegfggdpcdpcttwcdaismrvgyygdfvfdrvlktdvnkef

```
AAW76362-W76366 are major outer membrane proteins isolated from Chlamydia trachomatis which are used for the measurement of an antibody against Chlamydia trachomatis, by using it as an antigen in the form of a reagent. The method can give a diagnostic method for Chlamydia trachomatis-infected diseases with high specificity.
 Preparation of major outer membrane protein of Chlamydia trachomatis by cloning and recombinant expression of the gene, for use as a diagnostic of Chlamydia infections
 67.6%; Score 1320.5; DB 19; Length 376; 64.4%; Pred. No. 1.8e-122; Live, 49; Mismatches 76; Indels 9;
 Claim 2; Page 12; 19pp; Japanese.
 Conservative,
 WPI; 1598-535045/46.
 Similarity
 376 AA;
 Local Simines 242;
 Query Match
Best Local S
Matches 242
 Sequence
```

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Gaps

1 MIPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKT 60

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DB 20; Length 397;

67.7%; Score 1321.5; DB 20 64.0%; Pred. No. 1.6e-122; iive 51; Mismatches 75;

Conservative

Local Similarity ses 240; Conserv

Best Loca Matches

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Query Match

LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61

us-09-391-606-16.rag

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TGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTA 293
|||:||||||||
rlideraahvnaqfrf 376
 RLINERAAHVSGQFRF 367
 234
 352
 361
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 Qγ
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Search completed: February 7, 2002, 21:34:40 Job time: 20759 sec

Fri

Scoring table:

Searched:

Database

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Perfect score:

Sequence:

OM protein

on:

115 97.5 90.5 87.5 87.5 87.5

qq δλ g

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APPLICANT: Ladd, Anna
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Jamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
 Length 25;
 Indels
 CUDULAL.

CIP: 10154-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995
 Query Match 6.4%; Score 124; DB 1; L. Best Local Similarity 84.0%; Pred. No. 1.6e-06; Matches 21; Conservative 3; Mismatches 1;
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERNCE/DOCKET NUMBER: 1151-4146 UT
TELEPHONE: (212)415-8745
TELEPHONE: (212)415-8745
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
 US 08/057,166
 Sequence 45, Application US/08488351A Patent No. 5843446 GENERAL INFORMATION:
 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polosimis
 103 ALNIWDRFDVFCTLGASNGYIRGNS 127
 1 ALNIWDRFDVFCTLGATTGYLKGNS 25
 ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
 APPLICATION NUMBER: US 08
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
 FILING DATE: 7-JUN-19
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
 ; MOLECULE TYPE: peptide US-08-446-692-45
COMPUTER READABLE FORM:
 amino acid
 ns
 US-08-488-351A-45
 TOPOLOGY:
 COUNTRY:
 STATE:
 òy
 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
 APPLICANT: The Government of the United States of America
APPLICANT: as represented
APPLICANT: as represented
APPLICANT: by the Secretary of the Department of Health and Human Services
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINE FOR
TITLE OF INVENTION: CHLAMYDIA
FITLE OF INVENTION: TRACHOMATIS
NUMBER OF SEQUENCES: 3
 269 RATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALSTTD-SFSDFMQIVSCQINKFKS 327
 Gaps
 10;
 Query Match 6.4%; Score 125; DB 5; Length 42; Best Local Similarity 61.9%; Pred. No. 2.8e-06; Matches 26; Conservative 4; Mismatches 2; Indels
 103 ALNIWDRFDVFCTLGASNGYIRGNSTAFNLVGLFGVKGTTVN 144
 1 ALNIWDRFDVFCTLGATTGYLKGNS-----FDV--TTLN 32
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US93/08739
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,671 US
FILING DATE: 18 SEP 93
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
 Sequence 3, Application PC/TUS9308739 GENERAL INFORMATION:
 Sequence 45, Application US/08446692
Patent No. 575951
GENERAL INPORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
 N-terminal
 TYPE: amino acid
STRANDEDNESS: single
 MOLECULE TYPE: peptide HYPOTHETICAL: NO
 linear
 10154-0053
 CLASSIFICATION:
 ; FRAGMENT TYPE:
PCT-US93-08739-3
 HYPOTHETICAL:
 FILING DATE
 RESULT 3
US-08-446-692-45
 RESULT 2
PCT-US93-08739-3
 COUNTRY:
ZIP: 101
 328 R 328
 CITY: STATE:
 61
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Immunogenic LHRH peptide constructs and synthetic universal immune stimulators for vaccines
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
 ö
 Length 25;
 6.4%; Score 124; DB 5;
84.0%; Pred. No. 1.6e-06;
 3; Mismatches
 JMBER: PCT/US95/13841
25-OCT-1995
 103 ALNIWDRFDVFCTLGASNGYIRGNS 127
 Sequence 24, Application US/08446692
Patent No. 575951
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
 08/328,519
 1 ALNIWDRFDVFCTLGATTGYLKGNS 25
 REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326
FILING DATE: 25-0CT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
 ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
 E: Maria C.H. Lin
345 Park Avenue
 SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/U
 Floppy disk
 25 amino acids
 Best Local Similarity 84.0
Matches 21; Conservative
 SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO:
 Lin, Maria C.H.
 NUMBER OF SEQUENCES: 3
 MOLECULE TYPE: peptide
 ZIP: 10154-0053
COMPUTER READABLE FORM:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 amino acid
 OPERATING SYSTEM:
 New York
 New York
 FILING DATE:
 10154
 ADDRESSEE:
 PCT-US95-13641-17
 TOPOLOGY:
 STATE: N'COUNTRY:
 US-08-446-692-24
 COUNTRY:
 Query Match
 STATE:
 RESULT
 APPLICANT: The Government of the United States of America
APPLICANT: as represented
APPLICANT: by the Secretary of the Department of Health and Human Services
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINE FOR
TITLE OF INVENTION: CHLAMFOLA
TITLE OF INVENTION: TRACHOMATIS
 ö
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 ;
0
 Length 25;
 Length 25;
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08739
 ; DB 5;
1.6e-06;
 6.4%; Score 124; DB 2;
84.0%; Pred. No. 1.6e-06;
 Pred. No. 1.66
3; Mismatches
 3; Mismatches
 1151-4146 US2
 6.4%; Score 124;
84.0%; Pred. No. 1
 Sequence 17, Application PC/TUS9513841 GENERAL INFORMATION:
 Sequence 1, Application PC/TUS9308739 GENERAL INFORMATION:
 PC-DOS/MS-DOS
 103 ALNIWDRFDVFCTLGASNGYIRGNS 127
 103 ALNIWDRFDVFCTLGASNGYIRGNS 127
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/947,671
FILLING DATE: 18 SEP 93
INFORMATION FOR SEQ ID NO: 1:
 1 ALNIWDREDVECTLGATTGYLKGNS 25
 1 ALNIWDRFDVFCTLGATTGYLKGNS 25
 REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEPHONE: (516)751-6849
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
 REGISTRATION NUMBER: 29,323
 25 amino acids
 SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
 Query Match 6.4
Best Local Similarity 84.0
Matches 21; Conservative
 Query Match 6.4
Best Local Similarity 84.0
Matches 21; Conservative
 internal
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
 LENGTH: 25 amm.
 amino acid
 CLASSIFICATION:
 ; FRAGMENT TYPE:
PCT-US93-08739-1
 RESULT 6
PCT-US95-13841-17
 US-08-488-351A-45
 ANTI-SENSE:
 RESULT 5
PCT-US93-08739-1
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Gaps
 GENERAL INFORMATION:
APPLICANT: DeMars, Robert I.
APPLICANT: Ortiz, Linette (n.m.i.)
TILLE OF INVENTION: Antigenic Peptides Of Chlamydia trachomatis
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
 ö
 ;
 Length 31;
 Length 37;
 Indels
 1; Indels
 COMPTIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,385B
 Score 119; DB 3; I
Pred. No. 7.5e-06;
5; Mismatches 6;
 Score 124; DB 2;
Pred. No. 3e-06;
3; Mismatches 1;
 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SCHWARTZ, CAT1 R.
REGISTRATION NUMBER: 29, 437
REFERENCE/DOCKET NUMBER: 960296.93456
TELECOMMUNICATION:
 STREET: 411 East Wisconsin Avenue
 Chlamydia trachomatis
 103 ALNIWDRFDVFCTLGASNGYIRGNS 127
 FRAGMENT TYPE: internal fragment ORIGINAL SOURCE:
 Sequence 1, Application US/08519385B Patent No. 6001372
 1 ALNIWDRFDVFCTLGATTGYLKGNS 25
TELECOMMUNICATION INFORMATION:
 Quarles & Brady
 TELEPHONE: (414) 277-5715
TELEFAX: (414) 277-5715
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 Query Match 6.1%;
Best Local Similarity 64.5%;
Matches 20; Conservative
 6.48;
84.08;
 TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
 31 amino acids
 Query Match 6.4
Best Local Similarity 84.0
Matches 21; Conservative
 TYPE: amino acid
STRANDEDNESS: single
 MOLECULE TYPE: peptide HYPOTHETICAL: no
 TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-24
 STRAIN: Serovar E
INDIVIDUAL ISOLATE:
 linear
 amino acid
3Y: linear
 STATE: WI
COUNTRY: U.S.A.
ZIP: 53202-4497
 ou
 FILING DATE:
 ADDRESSEE:
 ORGANISM:
 TOPOLOGY:
 US-08-519-385B-1
 ANTI-SENSE:
 US-08-519-385B-1
 LENGTH:
 RESULT
 δy
 GENERAL INCORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Anna
APPLICANT: Zamb, Timothy
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 Gaps
 ;
0
 6.4%; Score 124; DB 1; Length 37;
84.0%; Pred. No. 3e-06;
tive 3; Mismatches 1; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
 ATTORNEY AGENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-UNN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14 APR-1994
CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
 US-08-488-351A-24; Sequence 24, Application US/08488351A; Patent No. 5843446
 103 ALNIWDRFDVFCTLGASNGYIRGNS 127
 1 ALNIWDRFDVFCTLGATTGYLKGNS 25
 SSEE: Maria C.H. Lin
: 345 Park Avenue
New York
 Query Match 6.4 Best Local Similarity 84.0 Matches 21; Conservative
 LENGTH: 37 amino acids
 MOLECULE TYPE: peptide US-08-446-692-24
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 CLASSIFICATION: 424
 TYPE: amino acid
TOPOLOGY: linear
 COUNTRY: US
ZIP: 10154-0053
 CLASSIFICATION:
 ADDRESSEE:
 STREET:
 RESULT
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118 GTAYNSLAPKGAPNASEWSDNAKLNTFAQAPYLSDTITAADGIK---VGTDTAQAGAAVY 174
 175 ANKTYQPEP----QVGPSEWNTSIENVKAGGRALKQTTAMQPCYGSYARPTNEHGGQSKD 230
 231 DNIELKFFDSANNAANTAQVVFYTEDVNLEMPDTHLVFKPTVTNGTIASESLLGQQAAPN 290
 RCNSTAF -- NLVGLFGVKGT -- -- TVNANELPNVSLSNGVVELY -- - TDTSFSWSVGA 172
 RG-----ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPT 226
 345 LGDRTRYFSLWNSAVDSYDPDVRVIENHGVEDELPNYC-FPLSAVGEIKNYKGIK-PDNG 402
 403 GGGGWTADNTVSEANHIGIGNIAAMEINLQANLWRSFLYSNVGLYLPDDLKYTPGNIKLP 462
 WSRATFDADNIRIAQPKLPTAVLNLTA-WNPSLLGNATALSTTDSFSDFMQIVSCQINKF 325
 ---VNPF 502
 16 GTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTFSMGAKPTGSAAANY 75
 Indels 145;
 Length 919;
 ; Score 101.5; DB 2;
; Pred. No. 0.11;
45; Mismatches 158;
 predicted hexon protein sequence for human Adenovirus 12
 463 DNKNTYEYMNGRVTAPGLVDTYVNIGARWSPDVMDN---
 76 TTAVDRPNPAYNKHLHDAEWFTN----AGFIAL---
 ----DVFCT-----
 271010-363
 JAHER: US/08/788,674
24-JAN-1997
 inch diskette
 24,025
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
 SYSTEM: MS-DOS
Word Perfect 5.1
 5.2%;
 NAME: Olstein, Elliot M. REGISTRATION NUMBER: 24, REFERENCE/DOCKET NUMBER:
 ATTORNEY/AGENT INFORMATION:
 Ouery Match
Best Local Similarity 20.03
Matches 87; Conservative
 CURRENT APPLICATION DATA:
 TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS
 326 KSRKACGVTVGATLV 340
 NHHRNAGLRYRSMLL 517
 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
 TOPOLOGY: linear
MOLECULE TYPE: protein
 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
 IBM PS/2
 APPLICATION NUMBER:
 105 -NIWDRF----
 OPERATING SYSTEM:
SOFTWARE: Word Pe
 amino acid
 DAGVATATGTKS-
 CLASSIFICATION:
 STRANDEDNESS
 FILING DATE:
 NAME, KEY:
NAME, KEY:
 COMPUTER:
 12
 173
 227
 267
 124
 :
RESULT
 Gaps
 Sequence 51, Application US/09100409A
Patent No. 6090388
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: PREPIDE COMPOSITION FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
TITLE OF INVENTION: IMMUNE DISORDERS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
 DB 3; Length 25;
1.4e-05;
 Having Altered
 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
 Carella, Byrne, Bain,
Gilfillan, Cecchi, Stewart &
 Mismatches
240 TINYHEWQVGASLSYRLNSLVPYIGVQWSRA 270
 5.9%; Score 115;
80.0%; Pred. No. 1
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,409A
 1151-4154
 APPLICANT: ROY, Soumitra
TITLE OF INVENTION: Adenoviruses HE
TITLE OF INVENTION: Hexon Proteins
 103 ALNIWDRFDVFCTLGASNGYIRGNS 127
 Sequence 4, Application US/08788674 Patent No. 5922315 GENERAL INFORMATION:
 MORGAN & FINNEGAN
 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS
 REFERENCE/DOCKET NUMBER: 11
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
 6 Becker Farm Road
 Floppy disk
 ATTORNEY/AGENT INFORMATION:
 345 Park Avenue
 25 amino acids
 Conservative
 212-751-6849
 COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
 INFORMATION FOR SEQ ID NO.
 peptide
 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, 1
 REGISTRATION NUMBER:
 Olstein
 amino acid
 Query Match
Best Local Similarity
Matches 20; Conserv
 linea
 STREET: b Decreter:
 CLASSIFICATION:
 New York
 MEDIUM TYPE:
 FILING DATE
 ADDRESSEE:
 ADDRESSEE:
 RESULT 10
US-09-100-409A-51
 US-09-100-409A-51
 SOFTWARE:
 SOFTWARE:
 TOPOLOGY:
 RESULT 11
US-08-788-674-4
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```
STREET: 7 Skyline Drive CITY: Hawthorne
 // ORGANISM: Peptide sequence
US-09-371-913A-7
 Conservative
 COMPUTER READABLE FORM:
 PatentIn Ver.
 Query Match
Best Local Similarity
Matches 75; Conserva
NUMBER OF SEQ ID NOS:
 USA
 MEDIUM TYPE:
 10532
 ADDRESSEE:
 RESULT 14
US-08-471-033-21
 SOFTWARE: Pat
SEQ ID NO 7
LENGTH: 784
 STATE: N
COUNTRY:
 TYPE: PRT
 382
 143
 g
 ŏ
 16;
 APPLICANT: Sturgis, Blake
TITLE OF INVENTION: Pesticidal Toxins and Genes from Bacillus laterosporus
TITLE OF INVENTION: Strains
FILE REFERENCE: MA-194C2 US
CURRENT APPLICATION NUMBER: US/09/371,913A
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,955
PRIOR FILING DATE: 1998-08-10
 282 WSANLSPAAQLFATVYKNASAPASLRGLATNVANYNAWSISSPPSYTSGDSNYDEKLYIN 341
 342 ALSPLITSNGWPNAHFIMDTSRNGVQP----TKQQAWGDWCNVIGTGFGVQPTINTGD 395
 --SLSNGVVE 159
 185 --- DCAAAASNGEYTVANNGVANYKAY--IDSIVAQLKAYPDVHTILIIEPDSLAN---- 235
 160 LYTDTSFSWSVGARGALWECGCATLGAEFQYAQSKPYVEELNVICNVSQFSVNKPKGYKG 219
 258 SLVPYIGVQ-WSRATFDADNIRI-AQPKLPTAVLNLTAWNP--SLLGNATALSTTDSFSD 313
 -----FIALNIWDR 109
 GENERAL INCORMATION:
APPLICANT: YAMANOBE, Takashi
APPLICANT: WATANNBE, Manabu
APPLICANT: WATANNBE, Manabu
APPLICANT: SUMIDA, Naomi
APPLICANT: SUMIDA, Naomi
APPLICANT: AOYAGI, Kaoru
APPLICANT: MOVAKANI, Takeshi
TITLE OF INVENTION: PROPUCING THE SAME
 220 VAFPLPTDAGV-----ATATGTKSATINYHEWQVGASLSYR-----LN
 Length 457;
 68 TGSAAANYTTAVDRPN-------PAYNKHLHDAEWFTNAG---
 110 FDVFCTLGASNG-YIRGNSTAFNLVGLFGVKGTTVNANELPNV-
 5.0%; Score 97.5; DB 3;
22.3%; Pred. No. 0.097;
Live 36; Mismatches 114;
 CURRENT APPLICATION NUMBER: US/09/142,759A CURRENT PAPLICATION NUMBER: US/09/142,759A CURRENT FILING DATE: 1998-09-14 EARLIER APPLICATION NUMBER: PCT/JP97/00824 EARLIER FILING DATE: 1997-03-14 EARLIER FILING DATE: 1996-03-14 NUMBER: OF SEQ ID NOS: 30
 APPLICATION NUMBER: 60/138,251
FILING DATE: 1999-06-08
 ; ORGANISM: Acremonium cellulolyticus US-09-142-759-1
 Sequence 7, Application US/09371913A
Patent No. 6297369
 Sequence 1, Application US/09142759A Patent No. 6127160
 Narva, Kenneth E.
Stockhoff, Brian A.
 Finstad Lee, Stacey
Walz, Mikki
 Schnepf, H. Ernest
 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
 Best_Local Similarity 22.3
Matches 67; Conservative
 GENERAL INFORMATION:
 RESULT 13
US-09-371-913A-7
 APPLICANT:
APPLICANT:
APPLICANT:
 Query Match
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18;
 FDSHTVGDPYTDYEKAARDLDLANAKETFNPLVAAFPSVNVNLEKVILSPNEDLSNS-VE 326
 SHSSINWSYT-NTEGVSIEAGSGPLGISYGVSANYQHSETVAK-EWGTSTGNTSQFN--- 381
 273
 414
 -- PNVSLSNGVVE 159
 274 ADNIRIAQPKLPTAVLNLTAWN--PSLLGNATALSTTDSFS------DFMQIVSCQI 322
 415 NDTVATITAKSNSTALSISPGESYPKKGONGIAINTMDDFNSHPITLNKQQLDQIFNNKP 474
 208 ASKINLFIQNMKRDEDATDIDGDSIPDLWEENGYTIQNKVAVKWDDSFAAKGYIKFVSNP 267
 160 LYTDTSFSWSVGARGALWECGCATLG-----AEFQYAQSKPKVEELNVICNVSQFSVNK 213
 APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
 214 PKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFD
 ------TASAGYLNANVRYN--NVGTGAIYEVKPTTGFV------LD
 DYVFDRILKVDAP - - - - - KTFSMGAKPTGSAAANYTTAVDR - PNPAYNKHLHDAEWF -
Score 90.5; DB 4; Length 784;
Pred. No. 1.2;
49; Mismatches 137; Indels 127;
 -TNAGFIALNIWDRFDVFCTLGAS-----NGYIRGNSTAFNLVGLFGVKGTT---
 PatentIn Release #1.0, Version #1.30B
 323 NKFKSRKACGV----TVGATLVDADKWS 346
 475 LMLETNQADGVYKIKDTSGNIVTGGEWN 502
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
FILING DATE:
 CIBA-GEIGY Corporation
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 --VNANEL--
 Sequence 21, Application US/08471033 Patent No. 5770696
 APPLICANT: Millins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
 4.6%;
 'Alcent MC.GENERAL INFORMATION:
APPLICANT: Warren, Gregory
APPTICANT: Koziel, Michael
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46 DYVFDRILKVDAPKTFSMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIAL- 104
 ----NIWDRFDVFCTLGASNGYIRGNSTAFNLVGLFGVKGTT-- 142
 212 KOKMKRDIDEDTDTDGDSIPDLWE-----ENGYTIONKVAVKWDDSLASKGYTKF 261
 ----PNVSLSN 155
 262 VSNPLDSHTVGDPYTDYEKAARDLDLSNAKETFNPLVAAFPSVNVSMEKVILSPNENLSN 321
 156 GUVELYTDTSFSWSVGARGALWECGCATLGAEF ---- QYAQSKPKVEELNVIC - NVSQFS 210
 S-VESHSSTNWSYT-NTEGASIEAGGGPLGLSFGVSVTYQHSETVAQEWGTSTGNTSQFN 379
 211 VNKPKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRA 270
 271 TEDADNIRIAQPKLPTAVLNLTAWN-----PSLLGNATALSTTDSFSDF-MQIVSCQI 322
 No. 5840868el Pesticidal Proteins and Strains 50\,
 -----TASAGYLNANVRYN--NVGTGAIYDVKPTTSFV-----
 Indels 133;
 Length 834;
 PatentIn Release #1.0, Version #1.30B
 Ouery Match 4.5%; Score 87.5; DB 2; Best Local Similarity 20.2%; Pred. No. 2.8; Matches 74; Conservative 38; Mismatches 122;
 TYCKNET CASH, AMERICA GATY M. REGISTRATION NUMBER: 40,403
REGISTRATION NUMBER: CGC 1695/CIP3/DIV6

 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SED-1994
 Corporation
 APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
 US 08/218,018
 FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
 COMPUTER: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release. 1
 REFERENCE/DOCKET NUMBER: CCTELECOMMUNICATION INFORMATION:
 FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
 : CIBA-GEIGY Co
 TELEPHONE: 919-541-8582
 CURRENT APPLICATION DATA:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 FILING DATE: 09-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
 919-541-8689
 ; MOLECULE TYPE: protein US-08-471-044-21
 CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
 amino acid
 linea
 Hawthorne
 USA
 10532
 ADDRESSEE:
 TOPOLOGY:
 STATE: N
COUNTRY:
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 155 EYQSDTKFNIDS-KTFK-ELKLFKIDSQNQSQQVQLRNPEFNKK-ESQEFLAKASKTNLF 211
 ----NIWDRFDVFCTLGASNGYIRGNSTAFNLVGLFGVKGTT-- 142
 ---PNVSLSN 155
 262 VSNPLDSHTVGDPYTDYEKAARDLDLSNAKETFNPLVAAFPSVNVSMEKVILSPNENLSN 321
 156 GVVELYTDTSFSWSVGARGALWECGCATLGAEF----QYAQSKPKVEELNVIC-NVSQFS 210
 322 S-VESHSSTNWSYT-NTEGASIEAGGGPLGLSFGVSVTYQHSETVAQEWGTSTGNTSQFN 379
 211 VNKPKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRA 270
 46 DYVFDRILKVDAPKTFSMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIAL- 104
 212 KOKMKRDIDEDTDTDGDSIPDLWE------ENGYTIQNKVAVKWDDSLASKGYTKF 261
 271 TFDADNIRIAQPKLPTAVLNLTAWN-----PSLLGNATALSTTDSFSDF-MQIVSCQI 322
 Gaps
 ----TASAGYLNANVRYN--NVGTGAIYDVKPTTSFV----
 Indels 133;
 Length 834;
 - SQLv3
 ; Score 87.5; DB 1;
; Pred. No. 2.8;
38; Mismatches 122;
 REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
 143 -----VNANEL-----
 APPLICATION NUMBER: US 08/218,018 FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/037,057 FILING DATE: 25-MAR-1993
ATTOMNEY/AGENT INFORMATION: NAME: Pace, Gary M.
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
 Sequence 21, Application US/08471044
Patent No. 5840868
 Desai, Nalini M
Kostichka, N. Kristy
Duck, Nicholas B
 Warren, Gregory W
Koziel, Michael G
Mullins, Martha A
Nye, Gordon J
 INFORMATION FOR SEQ ID NO: 21:
 Estruch, Juan J
 LENGTH: 834 amino acids TYPE: amino acid
 Query Match
Best Local Similarity 20.28
Matches 74; Conservative
 919-541-8689
 SEQUENCE CHARACTERISTICS
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Carr, Brian
 GENERAL INFORMATION:
APPLICANT: Warren,
APPLICANT: Wallins,
APPLICANT: Mullins,
APPLICANT: Nye, Gor
APPLICANT: Carr, Br
APPLICANT: Carr, Br
APPLICANT: Catch,
APPLICANT: Catch,
APPLICANT: Estruch,
 |: : |
NQLINNK 471
 323 NKFKSRK 329
 105 -----
 US-08-471-033-21
 RESULT 15
US-08-471-044-21
 TELEFAX:
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Gaps

323 NKFKSRK 329 |: : | 465 NQLINNK 471 Qy

Search completed: February 7, 2002, 21:36:26 Job time: 20495 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 7, 2002, 21:38:10 ; Search time 96.2 Seconds
(without alignments)
290.604 Million cell updates/sec

US-09-391-606-16 1952 1 MLPVGNPSDPSLLIDGTIWE.....TAEARLINERAAHVSGQFRF 367 Title: Perfect score: Sequence:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES |               | A43587 major outer membra | major outer | 4 major outer | I40739 major outer membra |        | -      |      | I40740 major outer membra | MMCWPM major outer membra |      |      | major outer | major outer |        | S16034 major outer membra |        |        |        |      | S12799 major outer membra | MMCWTE membra | MMCWTC membra |        |        | H71484 probable major out |        | JC1432 major outer membra | 40.4 | SIIU12 MEMDIA |
|-----------|---------------|---------------------------|-------------|---------------|---------------------------|--------|--------|------|---------------------------|---------------------------|------|------|-------------|-------------|--------|---------------------------|--------|--------|--------|------|---------------------------|---------------|---------------|--------|--------|---------------------------|--------|---------------------------|------|---------------|
|           | DB            | . ~                       | ~           | ~             | 7                         | -      | 7      | 7    | 7                         | Н                         | ~    | N    | 7           | 7           | 7      | Ç                         | П      | 7      | 7      | 7    | 7                         | Н             | П             | 7      | ~      | ~                         | Н      | 7                         | ~    | 1             |
|           | Length        | 389                       | 389         | 389           | 389                       | 389    | 389    | 392  | 402                       | 402                       | 402  | 402  | 387         | 404         | 387    | 387                       | 397    | 397    | 375    | 374  | 396                       | 393           | 397           | 393    | 393    | 393                       | 395    | 393                       | 394  |               |
| d         | Query         | 99.7                      | 99.7        | 97.8          | 96.4                      | 78.6   | 76.7   | 75.7 | 72.7                      | 72.5                      | 72.2 | 72.1 | 69.3        | 69.5        | 69.1   | 69.1                      | 68.7   | 9.89   | 68.3   | 68.0 | 67.9                      | 67.4          | 67.4          | 67.3   | 67.1   | 67.0                      | 67.0   | 8.99                      | 66.3 |               |
|           | Score         | 1947                      | 1947        | 1910          | 1882                      | 1534.5 | 1496.5 | 1477 | 1419                      | 1415                      | 1410 | 1408 | 1351.5      | 1351        | 1349.5 | 1349.5                    | 1340.5 | 1338.5 | 1333.5 | 1328 | 1325                      | 1315.5        | 1315.5        | 1313.5 | 1310.5 | 1308.5                    | 1307.5 | 1303.5                    | 1295 |               |
|           | Result<br>No. | -                         | 7           | m             | 7                         | 2      |        | 7    |                           |                           |      |      |             |             | 14     | 15                        | 16     | 17     | 18     | 19   | 20                        | 21            | 22            | 23     | 24     | 25                        | 56     | 27                        | 28   |               |

| major outer membra | major outer membra | outer membrane pro | probable outer mem | outer membrane pro | major outer membra | outer membrane pro |  | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 600                | ATB                | 333                | 333                | 333                | 593                |                    | 593                | 593                | 587                | 593                | 593                | 179                | 587                | 742                | 587                |  |
| S11(               | MMC                | A603               | B60                | C603               | F30                | C30                | D30                | B30593             | 1305               | E30                | A305               | H714               | G30E               | H817               | H30                |  |
| 2                  | _                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  |  |
| 372                | 394                | 158                | 156                | 155                | 136                | 135                | 136                | 136                | 136                | 136                | 136                | 340                | 134                | 340                | 134                |  |
| 65.8               | 65.3               | 19.1               | 18.5               | 18.2               | 11.0               | 11.0               | 10.9               | 10.7               | 10.6               | 10.6               | 10.4               | 6.7                | 6.7                | 9.3                | 9.5                |  |
| 1285               | 1275               | 373                | 361                | 355.5              | 215.5              | 215                | 212.5              | 208.5              | 206.5              | 206.5              | 203.5              | 1.89               | 186.5              | 1.82               | 179.5              |  |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 36                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |  |
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    | •                  | ٠,                 |                    |                    |  |

## ALIGNMENTS

|         | RESULT 1<br>A43587                                                                                                                                                            |                                              |
|---------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|
|         | major outer membrane protein, porin CP0051 precursor [imported]                                                                                                               | ported] - Chlamydophila pneu                 |
|         | C:Species: Chlamydophila pheumoniae. Chlamydia pheumoniae                                                                                                                     | a                                            |
| · · · , | C; Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 11-May-2000                                                                                                  | _change 11-May-2000                          |
|         | ; c;Accession: A4328/; A49/21; A49216; G/2044; F81619<br>R;Perez Melgosa, M.; Kuo, C.C.; Campbell, L.A.                                                                       |                                              |
|         | Infect. Immun. 59, 2195-2199, 1991                                                                                                                                            | 7                                            |
|         | A. Tefe- Seguence analysis of the major outer membrane protein gene of thiammydia A. Reference number: A43867; MUID:9124474                                                   | rocein gene di chiamydia phe                 |
|         | A; Accession: A43587                                                                                                                                                          |                                              |
|         | A; Molecule type: DNA A; Residues: 1-389 < PER>                                                                                                                               |                                              |
|         | A;Cross-references: GB:M69230; NID:9144540; PIDN:AAA73071.1; PID:9144541                                                                                                      |                                              |
|         | R; Carter, M.W.; Al-Mahdawi, S.A.H.; Giles, I.G.; Treharne, J. Gen. Microbiol, 137, 465-475, 1991                                                                             | e, J.D.; Ward, M.E.; Clarke,                 |
|         | A; Title: Nucleotide sequence and taxonomic value of the major outer membrane                                                                                                 | major outer membrane protein                 |
|         | A; Reference number: A49751; MUID:91237311                                                                                                                                    |                                              |
|         | A:Status: proliminary                                                                                                                                                         |                                              |
|         | A; Molecule type: DNA                                                                                                                                                         |                                              |
|         | A; Residues: 1-389 <car></car>                                                                                                                                                |                                              |
|         | A; Cross-references: GB:M64064; GB:M34942; NID:g144534; PII                                                                                                                   | PIDN:AAA23143.1; PID:g144535                 |
|         | A; Note: 1solate IOL-207                                                                                                                                                      |                                              |
|         | Infect. Immun. 60, 5319-5323. 1992                                                                                                                                            |                                              |
|         | A; Title: Similarity of Chlamydia pneumoniae strains in the                                                                                                                   | strains in the variable domain IV region     |
|         | A; Reference number: A49216; MUID:93084388                                                                                                                                    | •                                            |
|         | A; Accession: A49216                                                                                                                                                          |                                              |
|         | A; Status: preliminary A:Molecule from: DNA                                                                                                                                   |                                              |
|         | A; Residues: 297-352 <gay></gay>                                                                                                                                              |                                              |
|         | A; Cross-references: GB:S50607; NID:9260972; PIDN:AAB24363.1; PID:9260973                                                                                                     | 3.1; PID:9260973                             |
|         | A; Note: sequence extracted from NCBI backbone (NCBIN:120604, NCBIP:120605)                                                                                                   |                                              |
|         | K.Kalman, S.; MitChell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Nature Genet 21 285-289 1000                                                                       | , J.; Olinger, L.; Grimwood,                 |
|         | A,Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis                                                                                                        | C. trachomatis.                              |
|         | A: Reference number: A72000; MUID: 99206606                                                                                                                                   |                                              |
|         | A; Accession: G72044                                                                                                                                                          |                                              |
|         | A; Molecule type: DNA                                                                                                                                                         |                                              |
|         | A:Cross-references: GB-AE001652: GB-AE001363: NID-04276997: PIDN-AAD16834 1: PID-043<br>A:Cross-references: GB-AE001652: GB-AE001363: NID-04276997: PIDN-043018834 1: PID-043 | 97: PIDN:AAD18834 1: PID:043                 |
|         | A) Experimental source: strain CWL029                                                                                                                                         | C. E. C. |
|         | R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;                                                                                              | lberg, J.F.; White, O.; Hick                 |
| ***     | ; , C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolona<br>Nucleic Acids Res 28 1307-1406 2000                                                                           | nay, J.; McClarty, G.; Salzb                 |
|         | A:Title: Genome Sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR3                                                                                          | and Chlamydia pheumoniae AB3                 |
|         | A; Reference number: A81500; MUID: 20150255                                                                                                                                   | } 3                                          |
|         | A) ACCESSION: RSIDIA                                                                                                                                                          |                                              |
|         | A:Molecule type: DNA                                                                                                                                                          |                                              |
|         |                                                                                                                                                                               |                                              |

Query Match

ŏ g Qγ g QΥ g Qγ q ά Q

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outer
 major outer membrane protein - Chlamydophila psittaci
C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
C;Accession: I40864; S3465
R;Girjes, A.A.; Carrick, F.N.; Lavin, M.F. &
Gene 138, 139-142, 1994
A;Title: Remarkable sequence relatedness in the DNA encoding the major outer
A;Reference number: 140864; MUID:94171025
 383
 361
 143
 241
 263
 301
 361
 A, Residues: 1-389 <RES>
A, Cross-references: EMBL:X72023; NID:g313844; PIDN:CAA50906.1; PID:g313845
C;Superfamily: Chlamydia major outer membrane protein
 121
 181
 203
 241
 301
 TILLATSDSFSDFWQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARRLINERAAHV 383
 181
 83
 61
 24 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDKILKVDAPKTF
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG
 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC
 ATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN
 ATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 ATLGAEFOYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATI
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN
 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC
 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATI
 Length 389
 Indels
 Query Match 97.8%; Score 1910; DB 2; Best Local Similarity 97.5%; Pred. No. 2.2e-147; Matches 357; Conservative 5; Mismatches 4;
 A; Accession: I40864
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA_
 SGQFRF 367
 SCOFRF 367
 SGOFRE
 m
 362
 ~
 62
 122
 204
 264
 324
 182
 242
 264
 302
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 182
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 302
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 GB:AE002168; GB:AE002161; NID:g7188982; PIDN:AAF37944.1; PID:g718899
ce: strain AR39, HL cells
 ₽.;
 RESULT 2
D86577
major outer membrane protein [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Species: D86577
R;Shirai, M.; Hitakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Accession: D86577
A;Accession: D86577
A;Accession: D86577
A;Molecule type: DNA
A;Residues: 1-389 <STO>
A;Residues: 1-389 <STO>
A;Experimental source: strain J138
C;Genetics:
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Chlamydia major outer membrane protein
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0
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 301
 361
 121
 122 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
 Gaps
 Gaps
 83
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
A, Residues: 1-389 <REA>
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A; Genetics:
C; Superfamily: Chlamydia major outer membrane protein
C; Superfamily: Chlamydia major outer membrane protein
C; Keywords: membrane protein
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 84 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG
 242 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN
 62 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFINAGFIALNIWDRFDVFCTLGASNG
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0
 389;
 Length 389;
 Indels
 0; Indels
 Length.
 99.7%; Score 1947; DB 2; L
100.0%; Pred. No. 2.2e-150;
ive 0; Mismatches 0;
 Score 1947; DB 2; I
Pred. No. 2.2e-150;
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0
 Mismatches
 99.7%; Scilarity 100.0%; P
 Best Local Simitarity 100.
Matches 366; Conservative
 Similarity
 SGQFRF 389
 362 SGQFRF 367
 Query Match
Best Local Simi
Matches 366;
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PID:940601

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A;Title: Cloning and sequence analysis of the major outer membrane protein genes of A;Title: Cloning and sequence analysis of the major outer membrane protein genes of A;Teference number: A60109, MUID:89212917
A;Reference number: A60109
A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-389 <ZHA>
C;Superfamily: Chlamydia major outer membrane protein
C;Superfamily: Chlamydia major outer membrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-389/Product: major outer membrane protein #status predicted <MAT>
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C;Species: Chlamydophila psittaci, Chlamydia psittaci
C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Mar-2000
 62 S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
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 A;Cross-references: EMBL:X51859; NID:g40600; PIDN:CAA36152.1;
C;Superfamily: Chlamydia major outer membrane protein
F:1-22/Domain: signal sequence #status predicted <SIG.
F;23:389/Product: major outer membrane protein #status predict
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llarity 75.7%; Prèd. No. 6.5e-117;
Conservative 39; Mismatches 49;
 51;
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R;Zhang, Y.X.; Morrison, S.G.; Caldwell, H.D.; Baehr,
Infect. Immun. 57, 1621-1625, 1989
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 Conservative
 Query Match
Best Local Similarity
Matches 278; Conserv
 Local Similarity
les 272; Conserv
 type: DNA
1-389 <HER>
 383 MNAQFRF 389
 Query Match
 Best Loca
Matches
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major outer membrane protein precursor - Chlamydophila pneumoniae (strain equine/N16)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
A;Variety: strain equine/N16
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Apr-2000
C;Accession: 140739
B;Storey, C; Lusher, M; Yates, P; Richmond, S.
J; Gen. Microbiol. 139, 2621-2626, 1993
A;Ritle: Evidence for Chlamydia pneumoniae of non-human origin.
A;Reference number: 140739; MUID:94103736
A;Reference number: 140739
A;Reference number: 140739
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A;Residues: 1-389 <STO>
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C;Comment: On the basis of the major outer membrane protein the authors classified the chomestic.
 an ovine abortion
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 - Chlamydophila psittaci (strain S26/3)
 MACWP3
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major outer membrane protein precursor - Chlamydophila psittaci (strain S26/C;Species: Chlamydophila psittaci, Chlamydia psittaci
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Mar-2000
C;Accession, A.J; Tan, T.W.; Baxter, S.; Inglis, N.F.; Dunbar, S.
FERS Microbiol. Lett. 65, 153-158, 1989
A;Title: Sequence analysis of the major outer membrane protein gene of an ov A;Reference number: S08770
A;Reference number: S08770
 241
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN 301
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 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
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C;Superfamily: Chlamydia major outer membrane protein
C;Keywords: membrane protein
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 389;
 Indels
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 Score 1882; DB 2;
Pred. No. 4.2e-145;
5; Mismatches 5;
 15; Mismatches
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 Best Local Similarity 94.5
Matches 346; Conservative
 SGOFRE 389
 SCOFRE 367
 384 SGQFRF
 Query Match
 362
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A; Title: Evidence for Chlamydia pneumoniae of non-human origin.
A; Reference number: 140739; MUID:94103736
A; Recession: 140740
A; Status: nucleic acid sequence not shown; translation not shown; translated from GBA; Residues: 1-402 <RES>
 nucleotide sequence of
 9
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J. Gen. Microbiol. 139, 2621-2626, 1993
 S-MGAKP---TGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
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 LTAWNPSLLGNATALSTT---DSFSDFMQIVSCQINKFKSRKACGVTVGATLVDANKWSL 347
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ITTWNPSLLGSTTALPNNAGKDVLSDVLQIASIQINKWKSRKACGVAVGATLIDADKWSI 382
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70.5%; Pred. No. 1.6e-107;
ive 37; Mismatches 61;
 - Chlamydophila
ttaci, Chlamydia
 TAEARLINERAAHVSGQFRF 367
 al Similarity 70.59
268; Conservative
RAAHVSGQFRF
 Query Match
Best Local Si
Matches 268;
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 143
 62
 83
 117
 203
 231
 291
 323
 348
 382
 173
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major outer membrane protein precursor - Chlamydophila psittaci (strain Fpn/pring)
C; Species: Chlamydophila psittaci, Chlamydia psittaci
C; Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 31-Mar-2000
C; Accession: 140859; A60371; S16137
R; StCorey, C: Lusher, M.; Yates, P.; Richmond, S.
J. Gen. Microbiol. 139, 2621-2626, 1993
A; Title: Evidence for Clamydia pneumoniae of non-human origin.
A; Reference number: 140739; MUID:94103736
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A; Reference number: 140739; MUID:94103736
A; Reference for Sequence not shown; translation not shown; translated from GB/EME
A; Residues: 1-392 < RES.
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A; Residues: 1-392 < RES.
A; Reperimental source: strain Fpn
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C; Genetics:
C; Superfamily: Chlamydia major outer membrane protein
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 Gaps
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9
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HVNAQFRF 389
 360 HVSGQFRF 367
 Query Match
 300
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 Matches
 237
 83
 62
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| Qy         173 RGALWECGCATLGAEFQYAQSKPKVEELAVICHVSQFSVNKPKGYKGVAFPLPTDAGY 230           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII                                                                                                                                                                                                                                                     | Qy 348 TAEARLINERAAHVSGQFRF 367                                  | submitted to the EMBL Data Library, December 1990 A; Reference number: A44565 A; Accession: A44565 A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-402 <-EVE> A; Torss references: GB:X56980; NID:g40568; PIDN:CAA40300.1; PID:g40569 B; Everett, K.D.E.; Andersen, A.A.; Plaunt, M.; Hatch, T.P. Infect. Immun. 59, 2853-2855, 1991 A; Title: Cloning and sequence analysis of the major outer membrane protein gens A; Reference number: A60341; MUID:91310346 A; Reference number: A60341; MUID:91310346 A; Residues: 23-35 <-EVE> A; Residues: 23-35 <-EVE> A; Residues: 23-35 <-EVE> A; Residues: 23-35 <-EVE> A; Residues: B0341 A; Rolecule type: DNA A; Rolecule type: DNA A; Residues: Latra nucleic acid sequence not shown A; Molecule type: DNA A; Residues: Latra nucleic acid sequence not shown | C; Superfamily: Chlamydia major outer membrane protein C; Keywords: membrane protein F;1-22/Domain: signal sequence #status predicted <sig> F;23-402/Product: major outer membrane protein #status experimental <mat> Cuery Match  Query Match Matches 267; Conservative 38; Mismatches 61; Indels 14; Gaps 6 Matches 267; Conservative 38; Mismatches 61; Indels 14; Gaps 6 Qy 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVEDRILKVDAPKTF 61                                       </mat></sig> | 0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5   0.5 |
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Gaps

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50; Mismatches

Length 404; Indels

PID:9410147

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 231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTĄVLN 290
 LTAWNPSLLGNAT-----ALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADK 344
 322 VTTWNPTIAGAGTIADGTGAAATANGLADTLQIVSLQLNKMKSRKSCGLAIGTTIVDADK 381
 SMGAKPTGS --- AAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISLRIGYYGDFVFDRVLKTDVNKQF
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A;Cross-references: GB:L19221; NID:g410146; PIDN:AAA16615.1;
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Best Local Similarity 65.09
Matches 249; Conservative
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A; Status: preliminary;
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 Query Match
Best Local Si
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 :Genetics:
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 C; Genetics
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 140741
major outer membrane protein - Chlamydia trachomatis
c.Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Aug-1999
C;Accession: 140741
R;Zhang, Y.X.; Fox, J.G.; Ho, Y.; Zhang, L.; Stills, H.F.; Smith, T.F.
R;Zhang, Y.X.; Fox, J. 1993
A;Zitle: Comparison of the major outer-membrane protein (MOMP) gene of mouse pneumonitis
A;Reference number: A49379; MUID:94104488
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A; Residues: 1-387 <TET>
A; Cross-references: GB:AE002272; GB:AE002160; NID:g7190083; PIDN:AAF38941.1; PID:g719009
A; Cross-references: strain Nigg (MoPn)
C; Genetics:
A; Gene: TC0052
C; Superfamily: Chlamydia major outer membrane protein
 RESULT 12
(281747
major outer membrane protein, porin TCO052 [imported] - Chlamydia muridarum (strain Nigg C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C;Accession: C81747
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
A;Accession: C81747
A;Status: preliminary
A;Molecule type: DNA
 3;
 323 ITTWNPSLIGSTTALPNNSGKDVLSDVLQIASIQINKMKSRKACGVAVGATLIDADKWSI 382
 119 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 179 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS 238
 239 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL 298
 Gaps
 82
 61
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISLRLGYYGDFVFDRVLKTDVNKQF
 101 CGCATLGASFQYAQSKPKVEELNVLCNAAEFTINKPKGYVGQEFPLNIKAGTVSATDTKD
 299 LGNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLIAEARLINERA
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 SMGAKPTGSAAANYTTA----VDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA
 1;
 Length 387;
 Indels
 69.2%; Score 1351.5; DB 2; 66.4%; Pred. No. 4.5e-102; ive 50; Mismatches 67; :
 383 TGEARLINERAAHMNAQFRF 402
 348 TAEARLINERAAHVSGQFRF
 245; Conservative
 Query Match
Best Local Similarity
Matches 245; Conserv
 359 AHVSGQFRF 367
 387
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379 AHVNAQERE
 RESULT 13
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C;Accession: JT0947
R;Fielder, T.J.; Pal, S.; Peterson, E.M.; de la Maza, L.M.
Gene 106, 137-138, 1991
A;Title: Sequence of the gene encoding the major outer membrane protein of the mouse A;Reference number: JT0947; MUID:92039057
A;Accession: JT0947
A;Molecule type: DNA
 A;Cross-references: GB:M64171; NID:g144536; PIDN:AAA23144.1; PID:g144537 C;Comment: C. trachomatrs are Gram negative bacteria that cause a variety of infectio C;Comment: This protein is strongly antigenic and elicits neutralizing antibodies an
 3;
mouse pneumonitis major outer membrane protein - Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999
 Gaps
 61
 82
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 DB 2; Length 387;
 69.1%; Score 1349.5; DB 2;
66.1%; Pred. No. 6.6e-102;
ive 50; Mismatches 68;
 Chlamydia major outer membrane protein
 Conservative
 A,Gene: omlMoPn
C,Superfamily: Chlamydia majo
C,Keywords: membrane protein
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239 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL 298
 LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA
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AHVNAQFRF 387
 AHVSGQFRF 367
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major outer membrane protein - Chlamydia trachomatis
C:Species: Chlamydia trachomatis
C:Species: Chlamydia trachomatis
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1996
C;Accession: S16034; A43875
R;Zhang, Y.X.; Zhang, L.
R;Zhang, Y.X.; Zhang, L.
A;Description: The nucleotide sequence of major outer membrane protein gene of mouse bid A;Reference number: S16034
A;Reference number: S16034
A;Reference preliminary
A;Relevant Special minary
A;Residues: 1-387 < ZHA>
A;Residues: 1-387 < ZHA>
A;Residues: 1-387 < ZHA>
 A; Residues: 1730 < CLAA>
A; Cross references: EMBL:X60678
A; Cross references: EMBL:X60678
A; Cross references: EMBL:X60678
A; Cross references: EMBL:X60678
Infect: Immun. 59, 4147-4153, 1991
A; Title: Functional and structural mapping of Chlamydia trachomatis species-specific majargerene number: A43875; MUID:92040090
A; Reference number: A43875; MUID:92040090
A; Accession: A3875
A; Accession: A3875
A; Molecule type: nucleic acid
A; Molecule type: nucleic acid
A; Residues: 314-312 < PET>
A; Molecule type: nucleic acid
A; Residues: 314-312 < PET>
C; Superimental source: mouse pneumonitis strain
A; Note: sequence extracted from NCBI backbone (NCBIP:62877)
C; Superfamily: Chlamydia major outer membrane protein
 3;
 179 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS 238
 201 CGCPTLGASFQYAQSKPKVEELNVLCNAAEFTINKPKGYVGQEFPLNIKAGTVSATDTKD 260
 299 IGNATALSTIDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA 358
 119 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL 298
 62 SMGAKPTGSAAANYTTA----VDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS 238
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 7;
 Length 387;
 Indels
 DB 2;
 68;
 69.1%; Score 1349.5; DB 366.1%; Pred. No. 6.6e-102.tive 50; Mismatches 68.
 Best Local Similarity 66.1
Matches 244; Conservative
 359 AHVSGQFRF 367
 111: 1111
379 AHVNAQFRF 387
 Query Match
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February 7, 2002, 21:42:47; Search time 76.51 Seconds (without alignments) 175.872 Million cell updates/sec
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1952
1 MLPVGNPSDPSLLIDGTIWE......TABARLINERAAHVSGQFRF 367
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
 OM protein - protein search, using sw model
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Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, 100059 Total number of hits satisfying chosen parameters: 100059 segs, 36664827 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 200000000 SwissProt\_39:\* Title: Perfect score: Sequence: Scoring table: Database : Searched:

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|---------------------|-----------|-----------|-----------|-----------|-------------|------|-------------|--------------------|--------|--------------------|--------|--------|--------------------|--------|--------|------|--------------------|-----|-----|-------|--------------------|------------|-----------|--------------------|------------|--------------|------|------|-------|------|-------|------|--------------------|
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| Lenath DB           |           |           |           |           |             |      |             |                    |        |                    |        |        |                    |        |        |      | 394 1              |     |     |       | 919 1              | 1848 1     | 556 1     | 3421 1             | 864 1      | 2021 1       |      | 2292 | ٠.    |      | m     | œ    | 1086               |
| %<br>Query<br>Match | 7.66      | 96.4      | 88.7      | 78.6      | 75.7        | 72.5 | 9.69        | 68.7               | 68.6   | 67.9               | 67.4   | 67.4   | 67.3               | 67.0   | 67.0   | 66.3 |                    | 6.7 | ٠   | ٠     | 5.1                |            |           |                    |            |              |      | 4.8  |       | 4.7  | 4.7   | 4.7  | 4.6                |
| Score               | 1947      | 1882      | 1732      | 1534.5    | 1477        | 1415 | 1358.5      | 1340.5             | 1338.5 | 1325               | 1315.5 | 1315.5 | 1313.5             | 1308.5 | 1307.5 | 1295 | 1275               | 189 | 182 | 147.5 | 100.5              | 86         | 96        | 96                 | 95.5       | 93.5         | 93.5 | 93.5 | 92.5  | 92.5 | 91.5  | 91   | 90.5               |
| Result<br>No.       | ·         | 7         | æ         | ₹         | Ŋ           | 9    | 7           | 80                 | 6      | 10                 | 11     | 12     | 13                 | 14     | 12     | 16   | 17                 | 18  | 19  | 20    | 21                 | 22         | 23        | 24                 | 25         | 56           | 27   | 28   | 29    | 30   | 31    | 32   | 33                 |

| P37650 escherichia | P11461 vibrio angu<br>P77468 escherichia |                          | P43319 escherichia<br>P16465 proteus mir | P23176 aspergillus<br>Q05911 saccharomyc | Q9jib6 mus musculu<br>P39105 saccharomyc |
|--------------------|------------------------------------------|--------------------------|------------------------------------------|------------------------------------------|------------------------------------------|
| YHJL_ECOLI         | FATA_VIBAN<br>SFMD_ECOLI                 | POLG_ENMG3<br>Y396_RICPR | YRAK_ECOLI<br>HLYB_PROMI                 | AMYG_ASPAK<br>PUR8_YEAST                 | BIRF_MOUSE                               |
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| 1140               | 726                                      | 901<br>208               | 363<br>561                               | 639<br>482                               | 1403<br>664                              |
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| ALIGNMENTS                                                            |                                                              |
|                                                                       |                                                              |
| STANDARD: 389 AA                                                      |                                                              |
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| 1. 23, Created)                                                       |                                                              |
| 1. 23, Last sequence update)                                          |                                                              |
| I. 40, Last annotation update)                                        |                                                              |
| CONDESS OF CHOSE (MOMP).                                              |                                                              |
| CENOGES OR CEOUSI.                                                    |                                                              |
| Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila                  |                                                              |
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| .A.                                                                   |                                                              |
| STKAIN=IUL-ZU/;<br>MFDT.INF=01037311. DubMod=0033374.                 |                                                              |
| r, rubmed-2000074,<br>-Mahdawi S.A.H., Giles I.G., Trebarne           | - C                                                          |
| ke I.N.;                                                              | )<br>;                                                       |
| uence and taxonomic value of the major                                | or outer membrane                                            |
| Chlamydia pneumoniae IOL-207.";                                       |                                                              |
| 01. 137:465-475(1991).                                                |                                                              |
|                                                                       |                                                              |
| ·A·                                                                   |                                                              |
| 4. PuhMed=1840574.                                                    |                                                              |
| Perez Melgosa M., Kuo CC., Campbell L.A.:                             |                                                              |
| sis of the major outer membrane protein                               | ein gene of                                                  |
| oniae.";                                                              |                                                              |
| 59:2195-2199(1991).                                                   |                                                              |
|                                                                       |                                                              |
| .A.                                                                   |                                                              |
| Mitchell W.M., Tharp A.C., Stratton C.W., Sriram S.                   |                                                              |
| 1999) to the EMBL/GenBank/DDBJ databases                              | ases.                                                        |
|                                                                       |                                                              |
| .A.                                                                   |                                                              |
|                                                                       |                                                              |
| 6; PubMed=10192388;                                                   |                                                              |
| Kalman S., Mitchell W., Marathe R., Lammel C., Fan J                  | Fan J., Hyman R.W.,                                          |
| mwood J., Davis K.w., Stephens K.S.;                                  | 4000                                                         |
| nomes of chiamydia pheumoniae and c.                                  | rracnomatis.";                                               |
| . ( 6661 ) 606 606                                                    |                                                              |
| , A                                                                   |                                                              |
|                                                                       |                                                              |
| 5; PubMed=10684935;                                                   |                                                              |
| ham R.C., Shen C., Gill S.R., Heidel                                  |                                                              |
| y E.K., Peterson J., Utterback T., Berry                              | erry K., Bass S.,                                            |
| man J., Khouri H., Craven B., Bowman                                  | Dodson R.,                                                   |
| N GWIND M., Nelson W., DeBoy R., Kolonay J., McClarty G.,             | Salzberg                                                     |
| r C.M.,<br>es of Chlamvdia trachomatis MoPn and                       | Chlamydia                                                    |
|                                                                       | nan Impano                                                   |
| Res. 28:1397-1406(2000).                                              |                                                              |
|                                                                       |                                                              |
| SEQUENCE FROM N.A.                                                    |                                                              |
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NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN 301
 389 AA
 BY SIMILARITY.
 PRT;
 MEDLINE=94103736; PubMed=8277245;
 41628 MW;
 346; Conservative
 STANDARD;
 389
 24 3
389 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=83558;
 SGQFRF 367
 384 SGQFRF 389
 OMPA OR OMP1
 OMIN_CHLPN
 STRAIN=N16
 SEQUENCE
 SIGNAL
 RESULT 2
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 Matches
 242
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 OLIGOMERS.
 84 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIMDRFDVFCTLGASNG 143
 241
 263
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG 121
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 24 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 83
 Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
 122 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC
 182 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATI
 membrane; Transmembrane; Porin; Signal; Complete proteome.
 ;
0
 99.7%; Score 1947; DB 1; Length 389; 100.0%; Pred. No. 6.1e-154; Live 0; Mismatches 0; Indels
 MAJOR OUTER MEMBRANE PROTEIN
 15D984151E41F8F2 CRC64;
 Nucleic Acids Res. 28:2311-2314(2000).
 InterPro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia OMP: 1
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ProDom; PD001717; Chlamydia_OMP; 1.
MEDLINE=20330349; PubMed=10871362;
 MEDLINE=20298986; PubMed=10839753;
 EMBL; AF131889; AAD22492.1; EMBL; AE001652; AAD18834.1; EMBL; AE002167; AAF37944.1; EMBL; AP002247; BAA98902.1; EMBL; AB033787; BAA85940.1; PIR; A49751; A49751.
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 EMBL; M64064; AAA23143.1; -. EMBL; M69230; AAA73071.1; -.
 Local Similaricy res 366; Conservative
 SEQUENCE FROM N.A.
 SEQUENCE
 Query Match
 SIGNAL
 Best Loca
Matches
 Outer
 62
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 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 -i- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULER WEIGHT OLIGOMERS.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-i- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 Storey C., Lusher M., Yates P., Richmond S.; "Evidence for Chlamydia pneumoniae of non-human origin."; J. Gen. Microbiol. 139:2621-2626(1993).
-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.
121
 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
 Gaps
 83
 61
 24 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKIDAPKTF
 ATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINEFAAHV
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 SMGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNG
 ;
0
 Length 389;
 MAJOR OUTER MEMBRANE PROTEIN.
801622F05D841967 CRC64;
 Indels
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 96.4%; Score 1882; DB 1;
94.5%; Pred. No: 1.5e-148;
iive 15; Mismatches 5;
 Chlamydia pneumoniae (Chlamydophila pneumoniae)
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP).
 EMBL; L04982; AAA17397.1; -.
InterPro; IPR000604; Chlamydia_OMP.
Prfan; PF01308; Chlamydia_OMP; 1.
ProDom; P0001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
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OMPA OR OMP1
 OM1A_CHLPS
 P16567
 OM1A_CHLPS
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 143
 323
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 Kaltenboeck B., Kousoulas K.G., Storz J.;

Kaltenboeck B., Kousoulas K.G., Storz J.;

"Structures of and allelic diversity and relationships among the major outer membrane protein (omph) genes of the four chlamydial species.";

J. Bacteriol. 175:487-502(1933).

-! FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH

-!- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS PORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- SIBLEARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATI 241
 NYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGN 301
 NPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNGYIRGNSTAFNLVGLFGVKGTT 142
 AGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTFSMGAKPTGSAAANYTTAVDRP
 ;
0
 Length 333;
 5; Indels
 35811 MW; 204604512C4C3B3F CRC64;
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 Score 1732; DB 1;
Pred. No. 3.2e-136;
 20-AUG-2001 (Rel. 40, Last annotation update) MAJOR OUTER MEMBRANE PROTEIN (MOMP) (FRAGMENT).
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 (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
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 (Chlamydophila
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 InterPro; IPR000604; Chlamydia_OMP.
 Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
 STRAIN-KOALA TYPE I;
MEDLINE-93123168; Pubmed-8419295;
 88.7%;
97.3%;
 EMBL; M73038; AAD38210.1;
 Matches 324; Conservative
 STANDARD;
 Chlamydia pneumoniae
 333 AA;
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=83558;
 384 SGQFRF 389
 362 SGQFRF 367
 OMPA OR OMP1
 30-MAY-2000
30-MAY-2000
 OM1K_CHLPN
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 modified and this statement is not removed: Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 STRAIN-BOVINE ABORTION ISOLATE BA1;
X MEDLINE-96189655; Pubmed-8605581;
A Griffiths P.C., Plater J.M., Martin T.C., Hughes S.L.,
Bughes K.J., Hewinson R.G., Dawson M.;
T "Epizocitic bovine abortion in a dairy herd: characterization of a
T Chlamydia psittaci isolate and antibody response.";
Br. Vet. J. 131:683-693(1995).
C -!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTRY
EDIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
THE INTRACELLULAR RETICULATE BODY WEMBRANE.
C -ISUBURIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP
MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
C -ISUBCLULAR LOCATION: INTERGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
C -IS SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 322
240
 SEQUENCE FROM N.A.
STRAIN=OVINE ENZOOTIC ABORTION ISOLATE S26/3;
MEDLINE=90128177; PubMed=2612883;
Herring A.J., Tan T.W., Baxter S., Inglis N.F., Dunbar S.;
"Sequence analysis of the major outer membrane protein gene of an ovine abortion strain of Chlamydia psittaci.";
FEMS Microbiol. Lett. 53:153-158(1989).
 121 VAANELPHVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQSKPKVEELNV
 VNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQSKPKVEELNV
 IGVOWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLGNATALSTTDSFSDFMQIVSCQI
 ICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSYRLNSLVPY
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
WCBL_TaxID=83554;
 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP)
 membrane; Transmembrane; Porin; Signal.
 Chlamydia psittaci (Chlamydophila psittaci).
 389 AA
 331 NKFKSRKACGVTVGATLVDADKWSLTAEARLIN 333
 NKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 Interpro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
 ProDom; PD001717; Chlamydia_OMP; 1
 EMBL; X51859; CAA36152.1; -.
 L39020; AAB02850.1; -.
 STANDARD;
 PIR; S08770; MMCWP3
 SEQUENCE FROM N.A.
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A40371; A40371.
S16137; S16137.
 SEQUENCE
 SIGNAL
 RESULT 6
OM1E_CHLPS
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PIR;
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 STRAIN=FPN/PRING;
STRAIN=FPN/PRING;
MEDLINE-9410736; pubMed-8277245;
MEDLINE-9410736; pubMed-8277245;
MEDLINE-9410736; pubMed-8277245;
MEDLINE-9410736; pubMed-Res P., Richmond S.;
Fordence for Chlamydia pneumoniae of non-human origin.";
J. Gen. Microbiol. 139:2621-2626(1993).
J. Gen. Microbiol. 149:2621-2626(1993).
J. Gen. M
 240
 300
 382
 121 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG 180
 S-MGAKPIGSAAANYTTAVDRPNPAYNKHLHDAEWFINAGFIALNIWDRFDVFCTLGASN 120
 NATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAH 360
 Gaps
 23 LPVGNPAEPSLLIDGTMWEGASGDPCDPCSTWCDAISIRAGYYGDYVFDRVLKVDVNKTI 82
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 323 EATALDTSNKFADFLQIASIQINKMKSRKACGVAVGATLIDADKWSITGEARLINERAAH
 181 CATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKSAT
 INYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLLG
 1;
 Length 389;
MAJOR OUTER MEMBRANE PROTEIN
 Indels
 741B5A23ACDBB447 CRC64
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 DB 1;
 49:
 ; Score 1534.5; DB 1
; Pred. No. 8.8e-120;
39; Mismatches 49;
 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
02-UG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP)
 392 AA
 (Rel. 24, Created)
(Rel. 24, Last sequ
(Rel. 40, Last ann
 41883 MW;
 78.6%;
75.7%;
 EMBL; X61096; CAA43409.1; -
 Query Match
Best Local Similarity 75.73
Matches 278; Conservative
 STANDARD;
 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=83554;
 :: ||||
MNAQFRF 389
 VSGQFRF 367
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389 A
 OWID_CHLPS

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TO OWID_CHLPS

DT 01-DEC-1992

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STRAIN=FRU/P

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 -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 of the major outer membrane protein gene.";
FEMS Microbiol. Lett. 55:229-234(1988).
-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.
-!- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 201
 236
 261
 296
 321
 SLLGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINE 356
 61
 Pickett M.A., Everson S.J., Clarke I.N.; "Chlamydia psittaci ewe abortion agent: complete nucleotide sequence
 62 S-MGAKPIGSA--AANYTIAVDRPNPAYNKHLHDAEWFINAGFIALNIWDRFDVFCTLGA
 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATGT
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP
 ; 9
 Length 392;
 MAJOR OUTER MEMBRANE PROTEIN
88B3C5D90BBA26DB CRC64;
 Indels
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 75.7%; Score 1477; DB 1;
74.1%; Pred. No. 5.1e-115;
iive 38; Mismatches 52;
 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP).
Interpro; IPR000664; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 402 AA.
 42069 MW;
 Conservative
 STANDARD;
 RAAHVSGQFRF 367
 392 AA;
 Query Match
Best Local Similarity
Matches 275; Conserv
 SEQUENCE FROM N.A.
STRAIN-EAE A22/M;
 |||||: |||||
RAAHINAQFRE
 NCBI_TaxID=83554;
 OMPA OR OMP1
 OM1E_CHLPS
P10332;
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STRAIN=MOPN;
MEDLINE=94104488; PubMed=8277858;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 membrane;
 STRAIN=MOPN
 CONFLICT
CONFLICT
CONFLICT
 CONFLICT
 SIGNAL
 gene.
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 9
 MEDLINE-92039057; PubMed-1937036;
Fielder T.J., Pal S., Peterson E.M., la Maza L.M.;
"Sequence of the gene encoding the major outer membrane protein of the
mouse pneumonitis blovar of Chlamydia trachomatis.";
Gene 106:137-138(1991).
 GASNGYIRGNSTAFNLVGLFGVKGTTVNANE----LPNVSLSNGVVELYTDTSFSWSVGA 172
 290
 323 ITTWNPSLLGSTTTLPNNGGKDVLSDVLQIASIQINKMKSRKACGVAVGATLIDADKWSI 382
 S-MGAKP----IGSAA-ANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTL 116
 LTAWNPSLLGNATALSTT --- DSFSDFWQIVSCQINKFKSRKACGVTVGATLVDADKWSL 347
 61
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 23 LPVGNPAEPSLLIDGTMWEGASGDPCDPCATWCDAISIRAGYYGDYVFDRVLKVDVNKTF
 RGALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGV
 231 ATATGTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLN
 14;
 72.5%; Score 1415; DB 1; Length 402; 70.3%; Pred. No. 7.2e-110;
 MAJOR OUTER MEMBRANE PROTEIN.
 Indels
 43277 MW; E6CF00D9DF1EE87A CRC64;
 62;
 OMPA OR OMPI OR TC0052.
Chlamydia muridarum.
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
 OMPI_CHLMU STANDARD; PRT; 387 AA. P75024; Q04063; Q9X718; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 40, Last annotation update) MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (MOMP)
 InterPro; IPR000664; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 37; Mismatches
 TAEARLINERAAHVSGQFRF 367
 EMBL; X12647; CAA31177.1; -. EMBL; M36703; AAA23146.1; -.
 Best Local Similarity 70.3
Matches 267; Conservative
 PIR; S05954; MMCWPM.
 23 4
402 AA;
 SEQUENCE FROM N.A.
 SECUENCE FROM N.A
 STRAIN-MOPN
 SEQUENCE
 Query Match
 RESULT 7
OMP1_CHIMU
D OMP1_CHIMU
DT 30-MAY
DT 30-MAY
DT 30-MAY
DT 20-AUG
DE MAJOR
GN OMPA 0
OS Chlamy
OC Bacter
OX Chlamy
CR RELEATE
RP SEQUEN
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 Kaltenboeck B., Kousoulas K.G., Storz J.;

"Structures of and allelic diversity and relationships among the major outer membrane protein (ompa) genes of the four chlamydial species.";
J. Bacteriol. 175:487-502(1993).

"FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.

"SUBJUNIT: DISULIEDE BOND INTRARACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULEN-WEIGHT OLIGOMERS.
"SUBCELLULAR LOCATION: CELL WALL SURFACE.
"HE SUBCELLULAR INTEGRING PROMINED FOR THE STRUCTURAL INTEGRITY OF THE EXTRA-CELLULAR INFECTIOUS ELEMENTARY BODY & THE DEVELOPMENTAL CONVERSION TO THE PLASTIC AND FRAGILE INTRACELLULAR RETICULATE
Zhang Y.X., Fox J.G., Ho Y., Zhang L., Stills H.F., Smith T.F.; "Comparison of the major outer-membrane protein (MOMP) gene of mouse pneumonitis (MOPN) and hamster SFPD strains of Chlamydia trachomatis with other Chlamydia strains."; Mol. Biol. Evol. 10:1327-1342(1993).
 (In) Mardh P.A., la Placa M., Ward M. (eds.);
Proceedings of the european society for chlamydia research and the
second international symposium of Uppsala university centre for std
research, pp.38-38, University of Uppsala, Uppsala (1992).
 .;
G.,
 Carter M.W., Giles I., Everson J.S., Clarke I.N.; "Chlamydia trachomatis mouse blovar: major outer membrane protein
 Transmembrane; Porin; Signal; Complete proteome.
 STRAIN-MOPN / NIGG;
MEDLINE-20150255; PubMed=10684935;
Read T.D. Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K.,
Bass S., Linher K., Meidman J., Khouri H., Craven B., Bowman C.
Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty (
Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 BY SIMILARITY.
MAJOR OUTER MEMBRANE PROTEIN.
 SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 F -> Y (IN REF. 5
Y -> F (IN REF. 5
L -> F (IN REF. 1
A -> P (IN REF. 1
 pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000)
 InterPro; IPR000604; Chlamydia_OMP. Pfam; PF01308; Chlamydia_OMP; 1. ProDom; PD001717; Chlamydia_OMP; 1.
 MEDLINE-93123168; PubMed-8419295;
 EMBL; N64171; AAA23144.1; -.
EMBL; U60196; AAB07068.1; -.
EMBL; X63409; CAA45006.1; -.
EMBL; AE002272; AAF38941.1; -.
EMBL; M73044; AAD29101.1; -.
TIGR; TC0052;
 STRAIN=SSP.BV.MOUSE / NIGG II;
 [5]
SEQUENCE OF 37-375 FROM N.A.
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Matches 244; Conservative
 LINERAHVSGQFRF 367
 STANDARD;
 PIR; S06589; MMCWTH.
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=813;
 OMPA OR OMP1L3
 OMIN_CHLTR
P23114;
 SEQUENCE
 SIGNAL
 OMIN_CHLTR
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 amydia trachomatis.",

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mitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY

BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH

THE INTRACELLULAR RETICULATE BODY MEMBRANE.

SUBBUNT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP

MOLECULAR LOCATION: INTEGRAL MEMBRANE PROFIEIN.

SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 oţ
 62 SMCAKPTGSAAANYTTA---VDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 83 EMCAAPTGD--ADLTTAPTPASRENPAYGKHMQDAEMFTNAAYMALNIWDRFDVFCTLGA 140
 SNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWE 178
 Gaps
 61
 82
 Hamilton P.T., Malinowski D.P., "Nucleotide sequence of the major outer membrane protein gene from
 'Sequence analysis of the major outer membrane protein gene (ompA)
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDFTTWCDAISLRLGYYGDFVFDVKVFTDVNKQF
 179 CGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGTKS
 201 CGCATLGASFQYAQSKPKVEELNVLCNAAEFTINKPKGYVGQEFPLNIKAGTVSATDTKD
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 ATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSL
 7;
 Length 387;
 01-07N-1990 (Rel. 13, Created)
01-FED-1991 (Rel. 17, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR H PRECURSOR (MOMP).
 Indels
42009 MW; 4FD6FDC23248E0A2 CRC64;
 ; Score 1358.5; DB 1;
; Pred. No. 3.3e-105;
50; Mismatches 66; 1
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 397 AA
 Chlamydia trachomatis serovar H.";
Nucleic Acids Res. 17:8366-8366(1989).
 STRAIN=SEROVAR H;
MEDLINE=90045958; Pubmed=2813066;
 69.68;
 Local Similarity 60.7
es 246; Conservative
 STANDARD;
 Chlamydia trachomatis."
Submitted (SEP-2000) to
 AA;
 379 AHVNAOFRF 387
 SEQUENCE FROM N.A.
 Similarity
 359 AHVSGQFRF 367
 SEQUENCE FROM N.A.
 NCBI_TaxID=813;
 STRAIN-H/UW-4;
387
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 Fielder T.J., Peterson E.M., de la Maza L.M.;
"Nucleotide sequence of DNA encoding the major outer membrane protein of Chlamydia trachomatis serovar L3.";
of Chlamydia trachomatis serovar L3.";
ene 101:159-160(1991).
-! FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
 234
 117
 ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 NPSLLGNAT -- ALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEAR 352
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR H. 478ACE3808BF37BA CRC64;
 Gaps
 61
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCATWCDAISMRVGYYGDFVFDRVLKTDVNKEF
 SMGAKPTGSAAANY - - - - TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG
 5
 Length 397;
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR L3 PRECURSOR (MOMP).
 68.7%; Score 1340.5; DB 1; Length
65.1%; Pred. No. 1e-103;
iive 51; Mismatches 71; Indels
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
 Outer membrane; Transmembrane; Porin; Signal.
 AA
 397
 entities requires a license agreement (sor send an email to license@isb-sib.ch)
 InterPro; IPR000604; Chlamydia_OMP. Pfam; PF01308; Chlamydia_OMP; 1. ProDom; PD001717; Chlamydia_OMP; 1.
 STRAIN=404 / SEROVAR L3;
MEDLINE=91285429; Pubmed=2060793;
 23 397 M
397 AA; 42946 MW;
 EMBL; X16007; CAA34145.1; -. EMBL; AF304857; AAG41415.1;
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PubMed=2235504;

us-09-391-606-16.rsp

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01-AUG-1990
 OM1E_CHLTR
 CHAIN
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Э
 OLIGOMERS.
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR L3
: F1DDCF09535C2595 CRC64;
 ASNGYIRGNSTAFNLVGLFGVKGTTVNANE---LPNVSLSNGVVELYTDTSFSWSVGARG 174
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 Gaps
 SMGAKPTGSAAANY ----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISMRVGYYGDFVFDRVLKTDVNKEF 82
 61
 SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPINENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMEN SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE. SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 203 ALWECGCATLGASFQYAQSKPKVEELNVLCDASEFTINKPKGYVGAEFPLDITAGTEAAT
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT
 6
 DB 1; Length 397;
 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR A PRECURSOR (MOMP).
 Indels
 73;
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 5e-103;
INTRACELLULAR RETICULATE BODY MEMBRANE
 membrane; Transmembrane; Porin; Signal.
 396 AA
 ; Score 1338.5;
; Pred. No. 1.5e
49; Mismatches
 or send an email to license@isb-sib.ch)
 EMBL; X55700; CAA39226.1; -.
PIR; JE0413; JE0413.
InterPro; IPR006604; Chlamydia_OMP.
 Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
 PRT;
 42885 MW;
 68.68;
 Ouery Match 68.6%;
Best Local Similarity 65.1%;
Matches 244; Conservative 4
 Ä
 ||:|||||||
383 LIDERAAHVNAQFRF 397
 STANDARD;
 LINERAAHVSGQFRF 367
 SEQUENCE FROM N.A.
STRAIN-SAI/OT / SEROVAR
 Chlamydia trachomatis.
 397 AA;
 NCBI_TaxID=813;
 OMPA OR OMP1A
 OMIA_CHLTR
P23732;
 SEQUENCE
 SIGNAL
 RESULT 10
001A_CHLTR
10 MAA_C
AC P23732
DT 01-NOV
DT 20-AUG
DE MAJOR
GN 0MPA OR
CO BACLER
OX BACLER
OX CALAMY
OX BACLER
OX CALAMY
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 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 'Chlamydia trachomatis strain A/SA1/OT.";
Nucleif Acids Res. 18:6136-61365(1990).
- I- FÜRCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY
- BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
 OLIGOMERS
 SWGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
 ASNGYIRGNSTAFNLVGLFGVKGTTV---NANELPNVSLSNGVVELYTDTSFSWSVGARG 174
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT 234
 GTKSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAW 294
 Gaps
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR A. 2F9D3B0CE2D08162 CRC64;
 23 LFVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISWRMGYYGDFVFDRVLKTDVNKEF 82
 61
 THE INTRACELULAR RETICULATE BODY MEMBRANE.
--- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMER-
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
--- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 NPSLLGNATALSTTDS-FSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARL
 membrane protein gene of
 .;
80
 Length 396;
 Indels
 Query Match 67.9%; Score 1325; DB 1; Best Local Similarity 64.7%; Pred. No. 2e-102; Matches 242; Conservative 47; Mismatches' 77;
 Created)
Last sequence update)
Last annotation update)
 Outer membrane; Transmembrane; Porin; Signal.
 393 AA
Hayes L.J., Clarke I.N.; "Nucleotide sequence of the major outer
 or send an email to license@isb-sib.ch)
 InterPro; IPR000604; Chlamydia_OMP. Pfam; PF01308; Chlamydia_OMP; 1. ProDom; PD001717; Chlamydia_OMP; 1.
 PRT;
 42877 MW;
 EMBL; M33635; AAA92785.1;
PIR; S12799; S12799.
 EMBL; N58938; AAA23141.1;
 STANDARD:
 IDERAAHVNAQFRF 396
 354 INERAAHVSGQFRF 367
 396
 396 AA;
 01-AUG-1990
20-AUG-2001
 ESULT 11
OM1E_CHLTR
D OM1E_CI
D OM1E_CI
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DT 01-AUG
DT 20-AUG
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 4;
 trachomatis, serovar E.";
Nucleic Acids Res. 18:3414-3414(1990).
-!- FOUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE. OF ELEMENTARY
BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
THE INTRACELLULAR RETICULATE BODY MEMBRANE.
-!- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP
MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
-!- SIBILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 62 SMGAKP---TGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFG - - VKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 177 WECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGT 236
 237 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP 296
 SLIGNATALSTID-SFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISMRMGYYGDFVFDRVLKTDVNKEF 82
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR
 STRAIN=BOUR / SEROVAR E;

BUDILNE-BOUR 7731;

PRETERSON E.M., Markoff B.A., de la Maza L.M.;

"The major outer membrane protein nucleotide sequence of Chlamydia
 202 WECGCATLGASFQYAQSKPKVEELNVLCNAAEFTINKPKGYVGQEFPLALIAGTDAATGT
 7;
 DB 1; Length 393;
 Match 67.4%; Score 1315.5; DB 1; Length Local Similarity 65.3%; Pred. No. 1.2e-101; les 243; Conservative 46; Mismatches 76; Indels
OUTER MEMBRANE PROTEIN, SEROVAR E PRECURSOR (MOMP).
 42424 MW; AB2B82D16027B361 CRC64;
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
 Outer membrane; Transmembrane; Porin; Signal.
 PIR; S10201; MMCWTE.
InterPro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
ProDom; PE001717; Chlamydia_OMP; 1.
 EMBL; X52557; CAA36791.1; -.
 ERAAHVSGQFRF 367
 ERAAHVNAQFRF 393
 23 3
393 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=813;
 OR OMP1E
 SEQUENCE
 Query Match
 SIGNAL
 119
 297
 356
 Matches
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 Stephens R.S., Sanchez-Pescador R., Wagar E.A., Inouye C., Urdea M.S., "Diversity of Chlamydia trachomatis major outer membrane protein
 Dean D., Suchland R.J., Stamm W.E.; "Evidence for long-term cervical persistence of Chlamydia trachomatis
 J. Infect. Dis. 182:909-916(2000).
-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
 OLIGOMERS
 62 SMGAKPTGSAAANY----TTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLG 117
 ALWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATAT 234
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR C. 0047BCDB108E5309 CRC64;
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 -i- SUBUNIT: DISULFIDE BOND INTERACTIONS WITHIN AND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMER SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN. OUTER MEMBRANE.-i- SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 67.4%; Score 1315.5; DB 1; Length 397;
 01-NOV-1988 (Rel. 09, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR C PRECURSOR (MOMP).
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
 ; Pred. No. 1.2e-101; 49; Mismatches 76;
 THE INTRACELLULAR RETICULATE BODY MEMBRANE.
 PIR; S11011; MMCWTC.
InterPro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP; 1.
Propom; P0001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 AA.
 397
 STRAIN=C/TW3;
MEDLINE=20407420; Pubmed=10950788;
 Bacteriol. 169:3879-3885(1987).
 SEQUENCE FROM N.A.
MEDLINE=87307955; Pubmed=3040664;
 01-NOV-1988 (Rel. 09, Created)
 42892 MW;
 EMBL; M17343; AAA23156.1; -. EMBL; AF202455; AAG09443.1;
 64.3%;
 Matches 241; Conservative
 STANDARD;
 OMPA OR OMP1 OR OMP1C.
 397 AA;
 by ompl genotyping.
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=813;
 OMIC_CHLTR
P08780;
 SEQUENCE
 Query Match
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 Science 282.754-759(1998).

-!- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH THE INTRACELLULAR RETICULATE BODY MEMBRANE.

-!- SUBMINI: DISQLEIDE BOND INTEREXCITONS WITHIN UND BETWEEN MOMP MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 SELGNATALSTTD-SFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 Sayada C., Denamur E., Elion J.; "Complete sequence of the major outer membrane protein-encoding gene of Chlamydia trachomatis serovar Da."; Gene 120:129-130(1992).
 MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP
 WECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGT
 an obligate intracellular pathogen of humans:
 Stothard D.R., Boguslawski G., Jones R.B.; "Phylogenetic analysis of the Chlamydia trachomatis major outer membrane protein and examination of potential pathogenic
 30-MXY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR CUTER MEMBRANE PROTEIN, SEROVAR D PRECURSOR (MOMP).
 SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY.
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 393 AA.
 [2]
SEQUENCE FROM N.A.
STRAIN=D/IU-71960;
MEDLINE=98339860; PubMed=9673241;
 Infect. Immun. 66:3618-3625(1998).
 STRAIN=D/B-120;
MEDLINE=93013014; PubMed=1398119;
 30-MAY-2000 (Rel. 39, Created)
 STANDARD;
 OMPA OR OMP1 OR CT681.
 382 EFAAHVNAQFRF 393
 "Genome sequence of an
Chlamydia trachomatis
 EFAAHVSGQFRF 367
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN-D/UW-3/CX;
 determinants.";
 NCBI_TaxID=813;
 Davis R.W.;
 CHLTR
 046409;
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 4;
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR L1.; 7A952839408EE2DF CRC64;
 203 ALWECGCATLGASFQYAQSKPKVEELNVLCNASEFTINKPKGYVGAEFPLNITAGTEAAT 262
 SNGYIRGNSTAFNLVGLFG--VKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 SMGAKP----TGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 Gaps
 82
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 NPSLLGNATALS - - TTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEAR
 DB 1; Length 393;
 01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR L1 PRECURSOR (MOMP).
 74; Indels
 Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 67.3%; Score 1313.5; DB 64.5%; Pred. No. 1.8e-101
 Outer membrane; Transmembrane; Porin; Signal.
 393 A.A.
 51; Mismatches
 PIR; S06299; S06259.
Interpro; IPR000604; Chlamydia_OMP.
Pfam; PF01108; Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
 PRT;
 (Rel. 17, Created)
(Rel. 17, Last seq
 42543 MW;
 EMBL; M36533; AAA23142.1; -.
 Best Local Similarity 64.5
Matches 240; Conservative
 ||:||||||: |||||
383 LIDERAAHVNAQFRF 397
 353 LINERAAHVSGQFRF 367
 STANDARD;
 393 AA;
 NCBI_TaxID-813
 OMPA OR OMPILI
 01-FEB-1991
 OMIL_CHLTR
P19542;
 SEQUENCE
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 SITEMATE CONTROL OF STATEMENT O
 SLLGNATALSTTD-SFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLIN 355
 SMGAKP---TGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 SNGYIRGNSTAFNLVGLFG--VKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 321
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 BY SIMILARITY.
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR, 8CD692FD3EFF21D6 CRC64;
 WECGCATLGAEFQYAQSKPKVEÉLNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGT
 WECGCATLGASFQYAQSKPKVEELNVLCNAAEFTINKPKGYVGKEFPLDLTAGTDAATGT
 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP
 membrane; Transmembrane; Porin; Signal; Complete proteome.
 7;
 DB 1; Length 393;
 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN, SEROVAR F PRECURSOR (MOMP).
 76; Indels
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
 67.0%; Score 1308.5; DB 1
64.8%; Pred. No. 4.6e-101;
ive 48; Mismatches 76;
 395 AA
send an email to license@isb-sib.ch)
 EMBL; X62918; CAA44701:1; -.
EMBL; AF063195; AAC31436.2; -.
EMBL; AE001338; AAC68276.1; -.
Interpro; IPR000604; Chlamydia_OMP.
Pfam; PF01308; Chlamydia_OMP.
ProDom; PD001717; Chlamydia_OMP; 1.
 PRT;
 393 AA; 42438 MW;
 SEQUENCE FROM N.A.
STRAIN=IC-CAL3 / SEROVAR F;
 Query Match 67.0
Best Local Similarity 64.8
Matches 241; Conservative
 STANDARD;
 Chlamydia trachomatis.
 356 ERAAHVSGQFRF 367
 NCBI_TaxID=813;
 OMPA OR OMPLE
 OM1F_CHLTR
P16155;
 SEQUENCE
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OM1F_CHLTR
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 236
 296
 62 SMG---AKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 83 EMGEALAGASGNTTSTLSKLVERTNPAYGKHMODAEMFTNAACMTLNIWDRFDVFCTLGA 142
 119 SNGYIRGNSTAFNLVGLF--GVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGAL 176
 262
 SL--LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLI 354
 MAJOR OUTER MEMBRANE PROTEIN, SEROVAR F. 7F90FFDEEC264ACF CRC64;
 Gaps
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
 23 LPVGNPAEPSLMIDGILWEGFGGDPCDPCTTWCDAISMRMGYYGDFVFDRVLKTDVNKEF
 WECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVAFPLPTDAGVATATGT
 237 KSATINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNP
 ۲;
 Length 395;
 76; Indels
SIMILARITY: BELONGS TO THE CHLAMYDIAL OMP FAMILY
 DB 1;
 67.0%; Score 1307.5; DB 1
63.5%; Pred. No. 5.6e-101;
ive 53; Mismatches 76;
 InterForm, A. S. Chlamydia_OMP; 1.
ProDom; PD001717; Chlamydia_OMP; 1.
Outer membrane; Transmembrane; Porin; Signal.
 7, 2002, 21:42:47
 PIR; S08463; MMCWTF.
InterPro; IPR000604; Chlamydia_OMP.
 42586 MW;
 EMBL; X52080; CAA36299.1; -.
 Query Match
Best Local Similarity 63.5'
Matches 237; Conservative
 395
 355 NERAAHVSGQFRF 367
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DERAAHVNAQFRF 395
 Search completed: February
 23
395 AA;
 Job time: 601 sec
 SEQUENCE
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RESULT
 February 7, 2002, 21:41:21 ; Search time 172 Seconds
 (without alignments)
312.104 Million cell updates/sec
 1 MLPVGNPSDPSLLIDGTIWE......TAEARLINERAAHVSGQFRF 367
 473505
GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 473505 seqs, 146272329 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
 US-09-391-606-16
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 seq length: 0 seq length: 2000000000
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 Title:
Perfect score:
Sequence:
 Scoring table:
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 Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_vertebrate:

sp\_rodent:\*

sp\_plant:\* sp\_virus:\*

sp\_phage:\*

sp\_organelle:\*

sp\_mammal:\* sp\_mhc:\*

## SUMMARIES

| Description   |                                   | _                                                                                                      | _                                                                                                                                                                                                                                       | •                                                                                      | _                                                                                                                                                                                                                                                                                                                                         | •                                                                                                                                                                                          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        2 09AIM         09aik1           1477         75.7         392         2 09ABM         09aik1           1469.5         75.3         380         2 09AIM         09aik1           1469.5         75.3         380         2 09AIM         09aik1           1420.5         72.8         341         2 09AIM         09aik1           1419         72.7         402         2 046193         046193           1419         72.7         4046193         046193         046193 | Query         Query           Score         Match Length DB         ID           1910         97.8         389         2         008085         008085           1531.5         78.5         389         2         008085         008085         008086           1501.5         78.4         389         2         008084         008086         008086           1501.5         76.9         391         2         008081         009aik         009aik           1497.5         76.7         389         2         09AIH9         009aik         09aik           1480         75.8         381         2         09AIH9         09aik         09aik           1477         75.7         392         2         09AIH9         09aik         09aik           1477         75.7         392         2         09AIL1         09aik         09aik           1420.5         75.3         380         2         09AIL1         09aik           1420.5         72.8         341         2         09AIL1         09aik           1415         72.5         382         2         09AIL9         09aik           1415         72.5 | Score Match Length DB ID  1910 97.8 389 2 008085 1531.5 78.5 389 2 09APM4 1529.5 78.4 388 2 09APM4 1501.5 76.9 391 2 046235 1497.5 76.7 389 2 09AIM9 1487 76.2 392 2 09AIM9 1480 75.8 381 2 09AIM9 1480 75.8 381 2 09AIM3 1473 75.3 380 2 09AIM3 1473 75.3 380 2 09AIM3 1481 75.3 380 2 09AIM3 1483 72.9 391 2 09AIM3 1419 72.7 402 2 09AIM3 1415 72.5 382 2 09AIM3 1415 72.5 387 2 09AIM3 | Score         Query           1910         97.8         389         2 008085         008085           1531.5         78.5         389         2 09APM4         098081           1529.5         78.4         388         2 09APM4         098081           1501.5         76.9         381         2 09APM4         09apM4           1501.5         76.9         381         2 09APM4         09apM4           1497.5         76.7         389         2 09APM4         09apM6           1497.5         76.7         389         2 09AIM4         09aik0           1480         75.8         390         2 09AIM4         09aik1           1470         75.7         390         2 09AIM5         09aik2           1469.5         75.3         380         2 09AIM1         09aik1           1469.5         75.3         381         2 09AIM1         09aik1           1420.5         72.8         341         2 09AIM7         09aik1           1415         72.5         395         2 09AIM7         09aik1           1415         72.5         395         2 09AIM7         09aik1           1415     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| chlamydia<br>chlamydia<br>chlamydia<br>chlamydia | 009307 chlamydia p<br>069307 chlamydia p<br>069306 chlamydia p<br>Qyxbf6 chlamydophi<br>Qyxbf5 chlamydophi<br>069305 chlamydia p | Q9ai18 chlamydia s<br>Q46407 chlamydia t<br>Q9ai14 chlamydia s<br>O69093 chlamydia t<br>Q9ai15 chlamydia t | chlamydia<br>chlamydia<br>chlamydia<br>chlamydia | Q9aiji chlamydia s<br>Q9f950 chlamydia t<br>Q9aii6 chlamydia s<br>Q46406 chlamydia t<br>Q9aii7 chlamydia s<br>O52924 chlamydia s |
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| ·                                                |                                                                                                                                  |                                                                                                            |                                                  |                                                                                                                                  |
| Q46203<br>Q46236<br>Q9AIJ3<br>O70085             | 069307<br>069306<br>09XBF6<br>09XBF5<br>069305                                                                                   | Q9AII8<br>Q46407<br>Q9AII4<br>Q69093<br>Q9AII5                                                             | 069094<br>069095<br>09AIJ0<br>09F951             | 09A1J1<br>09F950<br>09AII6<br>046406<br>09AII7                                                                                   |
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| 7777                                             | 363                                                                                                                              | 4444                                                                                                       | mmmn                                             | 1331.5<br>1331.5<br>1330.5<br>1327.5<br>1326                                                                                     |
| 222<br>222<br>4                                  | 228782                                                                                                                           | 30<br>33<br>34<br>34                                                                                       | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~           | 0 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5                                                                                          |
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## ALIGNMENTS

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SEQUENCE FROM N.A.
STRAIN=KOALA TYPE 1;
MEDLINE-94171025; PubMed-8125292;
GLITJES A.A., Carrick F.N., Lavin M.F.;
Remarkable sequence relatedness in the DNA encoding the major outer membrane protein of Chlamydia psittaci (koala type I) and Chlamydia
 MULL X72023; CAA50906.1; --

R EMBL; X72023; CAA50906.1; --

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DR PFOM; PF01308; Chlamydia_OMP; 1.

DR PRINTS; PR01334; CHLAMIDIAOWP; 1.

RW Outer membrane; Transmembrane; Porin; Signal.

KW Outer membrane; Transmembrane; Porin; Signal.

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Bacteria: Chlamydiales: Chlamydiales: Chlamydiaeee; Chlamydophila.
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97.8%; Score 1910; DB 2;
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Matches 357; Conservative 5; Mismatches 4;
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 pneumoniae.
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 62 S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 83 TGMGAVPTGTAAADYKTPTDRPNIAYGKHLQDAEWFTNAAFLALNIWDRFDIFCTLGASN 142
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 "Identification of protective epitopes by sequencing of the major outer membrane protein gene of a variant strain of Chlamydia psittaci
 23 LPVGNPAEPSLLIDGTMWEGASGDPCDPCSTWCDAISIRAGYYGDYVFDKVLKVDVNKTI 82
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 324 TTTLATSDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERAAHV
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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Infect. Immun. 69:607-612(2001).
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 23 3
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384 SGQFRF 389
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 01-JUN-2001
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01-JUN-2001
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 Q9APM4;
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S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
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 Gaps
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8E232D22C9B9948D CRC64;
 Indels
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL, AF269259; AAK00240.1; .
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383 MNAQFRF 389
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01-JUN-2001
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 299 LGNATALSTTDSFSDFMQIVSCQINKFKSRKACGVTVGATLVDADKWSLTAEARLINERA 358
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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STRAIN-CALLPORNIA TURKEY 1, CT1;
MEDLINE-21078680; PubMed=11211261;
Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae";
"Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
"EMBL; AF269260; AAK00241.1;
 Query Match 76.7%; Score 1497.5;
Best Local Similarity 72.9%; Pred. No. 1.3e-
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 359 AHVSGQFRF 367
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 62 S-MGAKPTGSAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
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D98A8F5E76362A00 CRC64;
 48; Indels.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Last annotation update)
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL; L55436; AAA23147.1;
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01-NOY-1996 (TYEMBLFEL. 01, Created)
01-NOY-1996 (TYEMBLFEL. 01, Last sequen
01-JUN-2001 (TYEMBLFEL. 17, Last annotea
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR.
 POTENTIAL.
 STRAIN-GERMAN DUCK;
MEDLINE-21078680; PubMed-11211261;
 22 PC
391 MA
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Submitted (MAR-1994) to
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STRAIN-AVIAN TYPE C;
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23
391 AA;
380 AHMNAQFRF 388
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 AHVSGQFRF 367
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383 AHMNAQFRF 391
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EMBL; AF269267; AAK00248.1;
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 SEQUENCE FROM N.A.
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 STRAIN=1710S;
 Bacteria;
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 182 ATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATGTKSA 239
 122 YIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGC 181
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SEQUENCE FROM N.A. STAIN-GUIDE ON JUNCTIVITIS, GPIC, ATCC VR813; STAIN-GUIDEA PIG INCLUSION CONJUNCTIVITIS, GPIC, ATCC VR813; MEDIINE-89212917; Pubmed-2707861; Zhang Y.X., Morrison S.G., Caldwell H.D., Baehr W.; Cloning and Sequence analysis of the major outer membrane protein genes of two Chlamydia psittaci strains."; infect. Immun. 57:1621-1625(1989).
 240 TINYHEWQVGASLSYRLNSLVPYIGVQWSRATFDADNIRIAQPKLPTAVLNLTAWNPSLL
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Chlamydiales; Chlamydiales; Chlamydiales: Chlamydiales; Chlamydiales: Chlamydial
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Bush R.M., Everett K.D.;
"Modecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
 76.7%; Score 1497.5; DB 2
73.9%; Pred. No. 1.3e-113;
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001)
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 Kaltenboeck B., Kousoulas K.G., Storz J.;
"Structures of and allelic diversity and relationships among the maj
outer membrane protein (ompA) genes of the four chlamydial species.
J. Bacteriol. 175:487-502(1993).
 ASNGYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALW
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 Length 392;
 MAJOR OUTER MEMBRANE PROTEIN.
FC31FC051955246C CRC64;
 Everett K.D.E., Hambly W.A., Andersen A.A.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF269279; AAK00260.1; -
 Chlamydiales; Chlamydiaceae; Chlamydophila
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN PRECURSOR (FRAGMENT).
 . 49;
 76.2%; Score 1487; DB 2; 74.2%; Pred. No. 9.4e-113; iive 39; Mismatches 49;
 Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
 381 AA
POTENTIAL
 PRT;
 MEDLINE=21078680; PubMed=11211261;
 MEDLINE=93123168; PubMed=8419295;
22 PC
392 MJ
42293 MW;
 SEQUENCE OF 34-369 FROM N.A.
 Local Similarity 74.2
nes 276; Conservative
 PRELIMINARY;
 Chlamydophila pecorum
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ERAAHMNAQFRF 392
 356 ERAAHVSGOFRF 367
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. 140 ASNGYFKASSAAFNLVGLIGLKGTDFN-NQLPNVAITQGVVEFYTDTTFSWSVGARGALW 198
 ECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATATG 235
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 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
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 23 LPVGNPAEPSLLIDGTWWEGASGDPCDPCATWCDAISIRAGFYGDYVFDRILKVDVNKTI
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88B3C09C1FEE26DB CRC64;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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(TrEMBLrel. 17, Last annotation update)
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MEDLINE-21078680; PubMed-11211261;
Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL; AF269257; AAK00238.1;
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 22 PC
392 MJ
42051 MW;
 Query Match 75.78
Best Local Similarity 74.18
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23
392 AA;
 0990B0;
01-JUN-2001
 SEQUENCE
 SIGNAL
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 SMGAKPTG-SAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG 180
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 Gaps
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 Length 381;
 POTENTIAL.
MAJOR OUTER MEMBRANE PROTEIN.
29406725CF9D3512 CRC64;
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B62858403DBFA4E6 CRC64;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83554;
 | STRAIN-NEW JERSEY 1, NJ1;
| STRAIN-NEW JERSEY 1, NJ1;
| X MEDLINE-11078680; PubMed-11211261;
| A Bush R.M., Everett K.D.;
| T Molecular evolution of the Chlamydiaceae.";
| RL Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
| DR EMBL; AF269266; AAK00247.1; -...
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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3.3e-112;
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73.7%; Pred. No. 4.2e-112;
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tive 47; Mismatches
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15
381
41332 MW;
 42042 MW;
 Best Local Similarity 72.8 Matches 267; Conservative
 Best Local Similarity 73.79
Matches 274; Conservative
 390 AA;
 361 VSGQFRF 367
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LSAQCRF 381
 CHAIN
SEQUENCE
 Query Match
 SEQUENCE
 Query Match
Signal.
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SIGNAL
 Q9AIJ5
 375
 62
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 136
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RESULT Q9AIJ5

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Gaps

Indels ' 6; Length 392;

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INERAAHMNAQFRF 391
 354 INERAAHVSGQFRF 367
 391 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=83554;
 361 VSGQFRF 367
 LSAQCRF 380
 18 V 1
 STRAIN=WC;
 Signal.
NON_TER
SIGNAL
CHAIN
 SEQUENCE
 Q9AIJ2
 176
 RESULT 12
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 3;
 Kaltenboeck B., Kousoulas K.G., Storz J.; "Studtures of and allelic diversity and relationships among the major outer membrane protein (ompA) genes of the four chlamydial species."; J. Bacteriol. 175:487-502(1993).
 SMGAKPTG-SAAANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASN 120
 GYIRGNSTAFNLVGLFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECG 180
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 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF 61
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 DB 2; Length 380;
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829A18D3C5A85008 CRC64;
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 Everett K.D.E., Hambly W.A., Andersen A.A.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF269280; AAK00261.1;
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=85991;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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71.4%; Pred. No. 2.4e-111;
tive 54; Mismatches 48;
 MEDILINE=210/8680; PubMed=11211261;
Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
 380 AA
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 MEDLINE=93123168; PubMed=8419295;
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Best Local Similarity 71.4%
Matches 262; Conservative
 PRELIMINARY;
 \begin{array}{c} 1 \\ 15 \\ 380 \end{array}
 Chlamydophila pecorum
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RAAHINAQFRF 392
 357 RAAHVSGQFRF 367
 380 AA;
 [3]
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SEQUENCE FROM N.A.
 16 11
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SEQUENCE
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DT 094111
DT 01-JUN-
DT 01-JUN-
DT 01-JUN-
DE MAJOR 01
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 RESULT 11
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62 S-MGAKPTGSA--AANYTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGA 118
 119 SNGYIRGNSTAFNLVGLFGVKGTT-VNA--NELPNVSLSNGVVELYTDTSFSWSVGARGA 175
 LWECGCATLGAEFQYAQSKPKVEELNVICNVSQFSVNKPKGYKGVA--FPLPTDAGVATA 233
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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 MEDILINE=21078680; PubMed=11211261;
Bush R.M., Everett K.D.;
"Molecular evolution of the Chlamydiaceae.";
Int. J. Syst. Evol. Microbiol. 51:203-220(2001).
EMBL; AF269269; AAK00250.1;
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Gaps.

us-09-391-606-16.rspt

Q9X717

RESULT 13

29X717

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 323 ITTWNPSLLGSTTALPNNAGKDVLQIASIQINKMKSRKACGVAVGATLIDADKWSI 382
 2 LPVGNPSDPSLLIDGTIWEGAAGDPCDPCATWCDAISLRAGFYGDYVFDRILKVDAPKTF
 14;
 Length 402;
 Storey C., Lusher M., Yates P., Richmond S.;
Evidence for Chlamydia pneumoniae of non-human origin.";
J. Gen. Microbiol. 139-2621-2626(1993).
EMBL. L04980; AAA17396.1;
InterPro. IPR000604. Chlamydia_OMP.
InterPro. IPR000604. Chlamydia_OMP.
PFM.: PF01308; Chlamydia_OMP.
PRINTS; PR01334; CHLAMIDIAOMP.
 MAJOR OUTER MEMBRANE PROTEIN.
E36ABCB5AF04820A CRC64;
 Indels
 MAJOR OUTER MEMBRANE PROTI
 Chlamydia psittaci (Chlamydophila psittaci).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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 STRAIN+MENINGOPNEUMONITIS, MN, ATCC VR122; MEDLINE-21078680; Pubmed-11211261; Bush R.M., Everett K.D.; "Molecular evolution of the Chlamydiaceae."; Int. J. Syst. Evol. Microbiol. 51:203-220(2001). EMBL; AF269262; AAK00243.1;
 72.7%; Score 1419; DB 2; 70.5%; Pred. No. 3.2e-107
 382 AA
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 22 PO
402 MA
43261 MW;
 41231 MW;
 348 TAEARLINERAAHVSGQFRF 367
 PRELIMINARY;
 382
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402 AA;
 382 AA;
 SEQUENÇE FROM N.A.
 NCBI_TaxID=83554;
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SEQUENCE
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 Query Match
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Q9AIJ9
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 LFGVKGTTVNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQSK 194
 YTTAVDRPNPAYNKHLHDAEWFTNAGFIALNIWDRFDVFCTLGASNGYIRGNSTAFNLVG 134
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last annotation update)
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 341 AA.
 35; Mismatches
 402
 01-NOV-1996 (TrEMBLrel. 01, Last sequer 01-JUN-2001 (TrEMBLrel. 17, Last annota MAJOR OUTER MEMBRANE PROTEIN PRECURSOR. MOMP.
 Created)
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 NCBI_TaxID=83554;
 046193;
01-NOV-1996
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 Query Match
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Matches

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RESULT 14
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DT 01-NOV
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CN MOMP.
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CS Bacter
CX NCBL
RR ILL
RP SEQUEN

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9
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 348 TAEARLINERAAHVSGQFRF 367
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Search completed: February 7, 2002, 21:41:22 Job time: 4651 sec

Arabidopsis thalia Human LYST1 longer Human bg protein a Human bg protein a Bacillus subtilis F. heparinum NR-19 Flavobacterium hep

AAW23596 AAW31950

Neisseria meningit Chlamydia pneumoni Neisseria meningit

AAW53957 AAW94087 AAY58457 AAY38832 AAY35534 AAY38831

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117.311 Million cell updates/sec
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1 MTKKHYAWVVEGILNRLPKQ......DKLGSDFTFRKFDLGIISAF
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Streptococcus pneu Streptococcus pneu Human TANGO 265 ex Human PRO1317 prot Human PRO1317 prot Human PRO1317 (UN Human TANGO 265. Protein of the inv Transposase from 9 Streptococcus pneu Arabidopsis thalia Protein involved 1 Rabbit complement

AAW55085 AAB66046 AAB66045 AAB24084 AAY99418

AAB66043 AAB66167 AAR24302

AAG30604 AAY36942 AAY81576

AAW18313 AAB37984

## ALIGNMENTS

RESULT

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A\_Geneseq\_1101:\*

Database

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Lorf2; vaccine; antibacterial; antigen. Ä 7]16 AAY92716 standard; Protein; 422 98US-0106037.99US-0154658.99US-0427501. 99WO-GB03565 Chlamydia pneumoniae lorf2 Chlamydia pneumoniae WO200024901-A1. 28-OCT-1999; 29-AUG-2000 28-OCT-1998; 20-SEP-1999; 04-MAY-2000 26-OCT-1999; AAY92716; 

Dunn PL; (CONN-) CONNAUGHT LAB LTD. RP, MPI; 2000-350742/30. Oomen Murdin AD,

N-PSDB; AAA28411

Isolated polynucleotide encoding a Chlamydia polypeptide useful to treat, diagnose and prevent disease caused by Chlamydia infection

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:\*

|   | Description                 |   | Chlamydia pneumoni | Chlamydia pneumoni | Chlamydia trachoma | Porphorymonas ging | Porphorymonas ging | Streptococcus pneu | Streptococcus pneu | Amino acid sequenc | S. epidermidis ope | S. epidermidis ope | H. pylori outer me |
|---|-----------------------------|---|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|   | ID                          |   | AAY92716           | AAY35359           | AAX37570           | AAY34536           | AAY34403           | AAW55103           | AAY81502           | AAY43631           | AAG82023           | AAG82824           | AAY17217           |
|   | DB                          | : | 21                 | 20                 | 20                 | 20                 | 20                 | 19                 | 21                 | 21                 | 22                 | 22                 | 20                 |
|   | Query<br>Match Length DB ID |   | 422                | 438                | 372                | 951                | 953                | 711                | 2234               | 1091               | 303                | 359                | 327                |
| æ | Query<br>Match              |   | 99.7               | 99.7               | 65.7               | 7.5                | 7.5                | 7.1                | 7.1                | 6.9                | 6.9                | 6.9                | 6.8                |
|   | Score                       |   | 1162               | 1162               | 765.5              | 88                 | 88                 | 83                 | 83                 | 81                 | 80                 | 80                 | 79                 |
|   | Result<br>No.               |   | 1                  | 7                  | e                  | 4                  | S                  | Q                  | 7                  | ω                  | თ                  | 10                 | 11                 |

Page 1157; Disclosure; 1912pp; English.

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 This is the lorf2 protein of a strain of Chlamydia pneumoniae. Comparison of this sequence as to the recently published genome sequence of C. pneumoniae reveals that the sequence actually contains at least two open reading frames, a first one in the 5' portion and a second one in the 3' portion of the sequence. Despite the presence of the stop codon at the end of this sequence, c. pneumoniae does make a 76 kba product. It appears possible that C. pneumoniae is able to read through this stop codon and produce a full-length product terminated by the stop codon at the end of the second open reading frame. There is at least one in-frame ATG upstream of the start codon. This suggests that the first open reading frame may form part of one or more larger open reading frames when lotted to the start codon. This suggests that the first open reading frame way form part of one or more larger open reading frames. The lorfz protein or DNA can be used as a vacche for humans to treat or prevent disease caused by Chlamydia infection. The sequences or an antibody to lorfz can be used to diagnose a Chlamydial infection.
 Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
 206 mtkkhyawvvegilnrlpkqffvkcsvvdwntfvpsetsttekaatnamkykycvwqwlv 265
 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSA 120
 121 TVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGI 180
 Gaps
 1 MTKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLV 60
 .;
0
 Length 422;
 Indels
 Chlamydia pneumoniae transmembrane protein sequence
 Score 1162; DB 21;
Pred. No. 4.8e-119;
0; Mismatches 1;
 tdslsfraygayskpandklgsdftfrkfdlglisaf 422
 181 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 217
 Genome sequence of Chlamydia pneumoniae
 AA
 6; Fig 1A-C; 88pp; English.
 AAY35359 standard; Protein; 438
 99.7%;
 98WO-IB01890
 98US-0107078.
97FR-0014673.
 (first entry)
 Best Local Similarity 99.5
Matches 216; Conservative
 Chlamydia pneumoniae
 WPI; 1999-357842/30.
 422 AA;
 (GEST) GENSET
 13-SEP-1999
 W09927105-A2
 20-NOV-1998;
 04-NOV-1998;
21-NOV-1997;
 03-JUN-1999.
 Griffais R;
 AAY35359;
 Sednence
 Query Match
 Claim
 386
 61
 AAY353
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 Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachomą; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or phermofits. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
 121 TVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGI 180
 342 tvryeyvealsvpeidvsgigrgnllkfwfagaiaanydpkeangftnykgfsalymygi 401
 61 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSA 120
 Gaps
 1 MTKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLV 60
 0
 Length 438;
 Indels
 99.7%; Score 1162; DB 20;
99.5%; Pred. No. 5.1e-119;
iive 0; Mismatches 1;
 Chlamydia trachomatis cellular envelope protein.
 tdslsfraygayskpandklgsdftfrkfdlgiisaf 438
 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 217
 Genome sequence of Chlamydia trachomatis
 AAY37570 standard; Protein; 372 AA
 97FR-0015041.
97FR-0016034.
 98WO-IB01939.
 98US-0107077
 (first entry)
 Matches 216; Conservative
 Chlamydia trachomatis
 WPI; 1999-371125/31.
 Best Local Similarity
 438 AA;
 (GEST) GENSET
 W09928475-A2
 27-NOV-1998;
 17-DEC-1997;
 04-NOV-1998;
 38-NOV-1997;
 07-OCT-1999
 10-JUN-1999
 Griffais R;
 AAY37570;
 Sequence
 Query Match
 402
 AAY37570
 RESULT
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Porphorymonas gingivalis (PC) polypeptide sequences given in AAY34318 to NAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
 117 DWSATVRYEYVEALSVPEIDVSGIGRG-NLLKFWFAQAIAANYDPKEAN---SFTNYKGF 172
 AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine; antigenic.
 Antigenic Porphorymonas gingivalis peptides for preventing
 Score 88; DB 20;
Pred. No. 1.4;
 Margetts MB,
 Margetts MB,
 17; Mismatches
 Claim 1; Page 526-527; 588pp; English.
 Porphorymonas gingivalis protein PG67
 AAY34403 standard; Protein; 953 AA
 Hocking DM,
Webb EA;
 DW,
 173 SALYMYGITDSLSFRAYGAYSKP 195
 Hocking DN
Webb EA;
 7.5%;
 98AU-0005028.
97AU-0000839.
97AU-0001182.
98AU-0001546.
 98AU-0002264.
98AU-0002911.
98AU-0003128.
98AU-0003338.
 98WO-AU01023
 98AU-0003654
 98AU-0004917
 (first entry)
 Best Local Similarity 30.1 Matches 25; Conservative
 Porphorymonas gingivalis
 Barr IG,
Rothel LJ,
 Barr IG,
Rothel LJ,
 WPI; 1999-385613/32
N-PSDB; AAX91754.
 951 AA;
 CSLC-) CSL LTD.
 WO9929870-A1
 22-MAY-1998;
29-JUL-1998;
 10-DEC-1998;
 . 8661
 25-AUG-1999
 04-AUG-1998;
 30-JAN-1998;
 05-MAY-1998;
 17-JUN-1999
 766
 10-MAR-1998,
 gingivitis
 Agius CT,
Ross BC,
 Agius CT,
Ross BC,
 Sequence
 AAY34403;
 Query Match
 31-DEC-1
 09-APR-1
 23-APR-1
 - DEC-
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 AAY34403
 RESULT
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 4;
 AAX36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. This polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholnitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
 318
 Gaps
 MIKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFV----PSETSTTEKAATNAMKYKYCV 55
 WQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAK------ATKTTLNGKENLAW
 104 FIGGTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEA
 19;
 164 NSFTNYKGFSALYMYGITDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 217
 Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
 DB 20; Length 372;
 ; Score 765.5; DB 20; Length
; Pred. No. 1.4e-75;
27; Mismatches 41; Indels
 Disclosure; Page 1226; 1755pp; English
 Porphorymonas gingivalis protein PG67
 AAY34536 standard; Protein; 951 AA
 65.78;
62.88;
 98AU-0002911
98AU-0003128.
98AU-0003338.
98AU-0003654.
 98AU-0005028
97AU-0000839
 98AU-0001546
98AU-0002264
 98WO-AU01023
 97AU-0001182
 (first entry)
 Ouery Match 65.7%
Best Local Similarity 62.8%
Matches 147; Conservative
 Porphorymonas gingivalis.
 vaccine; antiqenic
 372 AA;
 (CSTC-) CST TLD
 W09929870-A1
 09-APR-1998;
23-APR-1998;
05-MAY-1998;
 10-DEC-1998;
 25-AUG-1999
 17-JUN-1999
 04-AUG-1998
 30-JAN-1998
10-MAR-1998
 22-MAY-1998
29-JUL-1998
 10-DEC-1997
 31-DEC-1997
 AAY34536;
 Sequence
 99
 AAY34536
 RESULT
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Patterson MA;

4

Gaps

9

Indels

35;

Length 951;

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The present sequence represents a protein from Streptococcus pneumoniae.

The nucleic acid sequence encoding the Streptococcus pneumoniae protein

The nucleic acid sequence encoding the Streptococcus pneumoniae.

Streptococcus pneumoniae, for inducing protective antibodies against

Streptococcus pneumoniae, for treatment or prevention of infection e.g.

pneumonia, otitis media or meningitis, probes based on the nucleic acid

are used to detect Streptococcus infection (by usual hybridisation or

amplification methods), also for isolating Streptococcus genes or their

antibodies in standard immunoassays, especially for diagnosing or

monitoring infections. Antibodies which bind the protein are used to

detect corresponding antigans, to purify the protein and for passive

detect corresponding antigans, to purify the protein and for passive

immunisation (optionally coupled to a toxin). Vaccines are administered,

e.g. by injection, orally or through the skin, typically at 0.01-1000
 492 arkgekwsdídlrtmvergknipalífmvsignelgeangdahslatvk-rlvkv--ikdv 548
 DVSGIGRGNLLKFWFA-----MY 178
 549 dktryvtmgadkfrfgngsgghekiadeldavgfny----sednykalrakhpkwliy 602
 AKA-----TKTTL-NGKENLA---WFIGGTLGGLRKAGDWSATVRYEYVEALSVPEI 135
 TFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYLYGAFL----MNPL 87
 Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antinflammatory; meningitis; infection; diagnosis; pneumococcal disease.
 179 GITDSLSFRAYGAYSKP-----SDFTFRKFDLGI
 7.1%; Score 83; DB 19; Length 711; 23.4%; Pred. No. 3.2;
 Streptococcus pneumoniae type 4 protein sequence #2.
 Mismatches
 Pred. No.
 AAY81502 standard; Protein; 2234 AA.
 Claim 11; Page 66; 118pp; English.
 (MICR-) MICROBIAL TECHNICS LTD
 98GB-0016337.
99US-0125164.
 (first entry)
 Streptococcus pneumoniae.
 Conservative
 Similarity
 WO200006737-A2.
 214 ISAF 217
 27-JUL-1999;
 24 - MAY - 2000
 19-MAR-1999;
 10-FEB-2000
 Query Match
Best Local S:
Matches 57;
 AAY81502;
 Sequence
 32
 88
 AAY81502
 RESULT
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4,
 Porphorymonas gingivalis (PG) polypeptide sequences given in AAV34318 to AAV34583. AAX91802 to AAX91809 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines sepecially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
 117 DWSATVRYEYVEALSVPEIDVSGIGRG-NLLKFWFAQAIAANYDPKEAN---SFINYKGF 172
 Gaps
 Streptococcus pneumoniae, antigen, vaccine; infection; diagnosis; detection; pneumonia; otitis media; meningitis.
 to AAX91801 encode two hundred and sixty six antigenic
 . 9
 Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
 Query Match
7.5%; Score 88; DB 20; Length 953;
Best Local Similarity 30.1%; Pred. No. 1.4;
Matches 25; Conservative 17; Mismatches 35; Indels
 Antigenic Porphorymonas gingivalis peptides for preventing
 Johnson LS, . Kunsch CA;
 Streptococcus pneumoniae SP0051 protein.
 /label= unknown
/note= "encoded by NAG"
 Claim 1; Page 373-375; 588pp; English
 Location/Qualifiers
 AAW55103 standard; Protein; 711 AA.
 173 SALYMYGITDSLSFRAYGAYSKP 195
 || | | : || || : || 556 rrlydyslsaglsttlygmf-kp 577
 (HUMA-) HUMAN GENOME SCI INC.
 97WO-US19422.
 96US-0029960
 (first entry)
 Streptococcus pneumoniae.
 WPI; 1998-272224/24.
N-PSDB; AAV27364.
 1999-385613/32.
 953 AA;
 Misc-difference
 31-OCT-1996;
 WO9818930-A2
 30-OCT-1997;
 07-MAY-1998.
 gingivitis
 AAW55103;
 Sequence
 AAW55103
 RESULT
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14;

81; Indels

99EP-0107413

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26-APR-1999;
 09-NOV-1.999;
 Matches
 AAG82023
 RESULT
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 14;
 AAV81501 to AAV81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antibilammatory properties.

The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosts of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
 New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
 642
 88 AKA-----TKTTL-NGKENLA---WFIGGTLGGLRKAGDWSATVRYEYVEALSVPEI 135
 136 DVSGIGRGNLLKFWFA------MY 178
 -----ANDKLG-----SDFTFRKFDLGI 213
 483 thnpaseqtlqiaaelgl-----lvqeeafdtwygg-kkp-ydygrffekdathpe 531
 643 gsetssatrtrgsyyrperelkhsngpernyeqsdygndrvgwgktataswtfdrdnagy 702
 Gaps
 32 TFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYLYGAFL----MNPL 87
 hmc gene; 3-hydroxy-3-methylglutaryl-CoA synthase; HMG-CoA synthase; mevalonate pathway; carotenogenic yeast; isopentenyl pyrophosphate; farnesyl pyrophosphate; isoprenoid; carotenoid; astaxanthin; cancer; antioxidant; colouring reagent; farmed fish industry.
 589 dktryvtmgadkfrfgngsgghekiadeldavgfny----sednykalrakhpkwliy
 78;
 7.1%; Score 83; DB 21; Length 2234; 23.4%; Pred. No. 16;
 81; Indels
 Amino acid sequence of the HMG-CoA synthase enzyme.
 28; Mismatches
 AAY43631 standard; Protein; 1091 AA
 Page 72; 108pp; English
 179 GITDSLSFRAYGAYSKP-----
 11-FEB-2000 (first entry)
 Best Local Similarity 23.49
Matches 57; Conservative
Hansbro PM;
 2234 AA;
 Phaffia rhodozyma
 214 ISAF 217
 703 agqf 706
Gilbert CFG,
 EP955363-A2
 10-NOV-1999
 Claim 1;
 AAY43631;
 Sequence
 Query Match
 AAY43631
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synthase (HMG-CoA synthase) enzyme, and is encoded by the hmc gene. The enzyme is involved in the mevalonate pathway in the carotenogenic yeast Phaffia rhodozyma. The specification also describes enzymes that are involved in the pathway from isopententy pyrophosphate to farnesyl pyrophosphate. The enzymes of the invention are used in the production of isoprenoids and carotenoids, especially astaxanthin. Astaxanthin is useful for the pharmaceutical industry, to protect cells against cancer as it has a strong antioxidation property. Astaxanthin is also useful as a colouring reagent in the farmed fish industry, e.g. salmon.
 756 wldsvegmevmaasfnstsrfarlgsikcgmagrslyirlatstgdamgmnmagkgteka 815
 :| : | | : | | : | | 816 letlseyfpsmqilalsgnycidk----kpsainwiegrgksvvaesvipgaivksvl-- 869
 -----KAGDWSATV 122
 Isolated DNA sequences encoding enzymes, useful for the production of
 Gaps
 The present sequence is represents a 3-hydroxy-3-methylglutary1-CoA

 S. epidėrmidis open reading frame protein sequence SEQ ID NO:1140.

 45 ATNAMKY-----YLYGVWQWLVGKHSQVPWINGQKKPL----YLYGAFLMNPLAK
 Length 1091;
 SR1 strain; infection; diagnosis;
 8 WV--VEGI-----LNRLPKOFFVKCSVVDWNTFVPSETST
 50;
 DB 21;
 90 ATXTT-----LNGKENLAWFIG----GTLGGLR-----
 6.9%; Score 81; DB 22.4%; Pred. No. 9.8;
 123 RYÉYVEAL-----SVPEIDVSGIGRGNLL 146
 Mismatches
 925 cmtlmeavndgkdllitcsmpaiecgtvgggtfl
 Claim 3; Page 37-40; 58pp; English.
 A
 Setoguchi Y;
 (HOFF) HOFFMANN LA ROCHE & CO AG
 AAG82023 standard; Protein; 303
 30;
 09-NOV-2000; 2000WO-US30782.
98EP-0108210
 isoprenoids and carotenoids
 Staphylococcus epidermidis
 Staphylococcus epidermidis
 (first entry)
 Conservative
 Hoshino T, Ojima K,
 WPI; 2000-001086/01.
 1091 AA;
 Query Match
Best Local Similarity
 N-PSDB; AAZ30171
 WO200134809-A2
06-MAY-1998;
 48;
 03-SEP-2001
 Sequence
 AAG82023;
```

12;

09-NOV-2000; 2000WO-US30782

WO200134809-A2

17-MAY-2001

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Annology to Tepreson uncertain activity and therefore epidermidis.

(II), given in AAG81454 to AAG8120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used to accination. The nucleic acids (I) may be used to produce the sepidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the AH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AH455091 to AH55090 represent olygonacleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequences are given in the disclosure for SEQ ID NO:4454 so even though sequences are present for SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472,
 12;
 to AAH53970 represent nucleic acids (I) encoding polypeptides
 67 PWINGOKKPLY-----AWFIG 106
 141 pwvieesktvfesrvlplllddnnhyrlygifllh------qlngkeilmtediwsi- 191
 107 GILGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRG-----NLLKF-------WFAQ 152
 153 A---IAANYDPKEANSFINYKGFSALYMYGITDSLSFRAYGAYSKPANDK-LGSDFIFRK 208
 245 aemiiaenvdlvdvdryv----aafvy----lsyr---rssqpltkrqlmddfnvsr 290
 Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
 S. epidermidis open reading frame protein sequence SEQ ID NO:2742.
 68;
 Staphylococcus epidermidis SR1 strain; infection; diagnosis;
 6.9%; Score 80; DB 22; Length 303; 24.6%; Pred. No. 2.1; ive 22; Mismatches 48; Indels
 Claim 18; Page 330; 2188pp; English
 AAG82824 standard; Protein; 359 AA.
 Staphylococcus epidermidis
 (first entry)
 vaccination; endocarditis.
 Conservative
(GLAX) GLAXO GROUP LTD
 2001-316495/33.
 Best Local Similarity
 303 AA;
 N-PSDB; AAH52873
 209 FDL 211
 291 yki 293
 03-SEP-2001
 Kimmerly WJ;
 45;
 AAG82824;
 Sequence
 Query Match
 10
 Matches
 AAG82824
 RESULT
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AAH55304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polyuncleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used to be accounted to the present invention.
 N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SBQ ID NO:4454 so even though sequences are given in the disclosure for SBQ ID NO:4465 to 4472, no sequences are present for SBQ ID NO:4455 to 4464.
 | |: |: |: |: |: |: |: |----lesmndyeklyltylvggltlnkldf--ihrgmgrlynfkkfkyntslftdwlng 300
 153 A---IAANYDPKEANSFTNYKGFSALYMYGITDSLSFRAYGAYSKPANDK-LGSDFTFRK 208
 67 PWINGQKKPLY-----AWFIG 106
 197 pwvieesktvfesrvlplllddnnhyrlygifllh-----qlngkeilmtediwsi- 247
 Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis "
 48; Indels
 107 GTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRG-----NLLKF----
 6.9%; Score 80; DB 22;
24.6%; Pred. No. 2.7;
tive 22; Mismatches 48
 AAY17217 standard; Protein; 327 AA.
 Claim 18; Page 714; 2188pp; English.
 99US-0164258
 (first entry)
 Conservative
 GLAX) GLAXO GROUP LTD
 Query Match
Best Local Similarity
Matches 45; Conserva
 WPI; 2001-316495/33
 N-PSDB; AAH53674
 209 FDL 211
 ykl 349
 09-NOV-1999;
 03-AUG-1999
 Kimmerly WJ;
 AAY17217;
 Sequence
 248
 347
 RESULT 11
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Dp
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12;

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STSMOGLEKAATTVAVPODKSEEEKVKERLITKRELITCEDLKDNGYTVWFEDISILELL

QFVSKISGTNEVFDSNDLQFNVT1VSHDPTSVDDLSTILLQVLKMHDLKVVEGONNVL

TYRDPHLSKLSTVVTDSSLEKTCCEAVVTRVFRLYSVSPSAAVN110PLLSHDA1VSA

SEATRHYISDTAGNVDKVSDLLAALDCPGTSVDMTEVEVKTANPAALVSYCQDVLGT

LAEDDAFQMFIQPGTNKIFVVSSPRLANKAEQLLKSLDVPEMAHTLDDPASTALALGG

TGTSPKSLENTKLKYONGEVIANALQDIGVINYTYTAMBDEPINTNSIQMLEVN

NSIVIIGNOGNVDRAYJGLLAGLDLPPRQVYTEVLLLDTSLEKSWDFGVQWVALGDEQS

KVAXASGLLNNTGIATPTKATVPPGTPNPGSIPLPPPQQLTGFSOMLNSSSAFGLGI
 /protein_id="AAD18840.1"

Aboutein_id="AAD18840.1"

Aboutein_id="1377004"

/translation="WILPNDILETUNKRESPQANKVWPVTTFSLARNLSVSKFLPCL
SKEOKLEILOFITSHFNHIEGFGFFIVLPLKDTPDLWOLDSYLLHSLLPYDLVGNDFGGE
SKEOKLEILOFITSHFNHIEGFGFFIVLPLKDTPDLWOLDSYLHSKLSFAFSSEFG
FLTTNRKNCGTGLLAGOTELLAGALLYSKEFTNLIDEPVEITTSSLLAGVTGFPGNIVV
ISNRCSLGLTEELLSSLRITASKLSVAEVARKRLSEENSGDLKNLILRSLGLTHV
 FLSLVPERISKILAKALQPSPNNRYSSTREFIQDIHHYRMSGDMQEDLRIKDHTVALY
EQLQTQRFWILAPETLERPDFISGVLYHQGYPLYPHAYDTLEGDYFNIMLGYSPISNA
TIALSVVKSLVCQQDLQRPFLDRVCETNECLIRMKIPIDEMGISILCLEISKENKELS
WIAGGKTVFWIKRQGRVVQDFESFSPGLGKTTSLQIRFTKVAMEIGDBAVVCTLELEE
SVASLKTLSLAELQDRRQKAIFCPIESIHGGIQSRQHGSNSPSTLISLKRIR"
 COLELKETLDALSWIOLGIDLGLIKVTENHPLWNPLFWQIRRAHLALOKOAEDSRDLO
KDTISHLRASVLKELTKGLSPESF"
 /Translation="MKTVILNIGRKILGGIKKKKKKIGILSGLFFLDLVLLGVSSQRP
TETSANVKHULRDEKLAACPKNSAASLSAKKSHTKKTPGESIPSKVFSKDATQDKTF
OKTSGSAFPAKPTILKELEVEKRPREPRRTAADVKRSPRFLPYÖGVEBEVPAASKEOL
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Direct Submission

Submitted (01-MAR-2000) The Institute for Genomic Research, 9715

Medical Center Dr. Rockville, MD 20850, USA

On Jun 1, 2000 this sequence version replaced gi:7188982
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Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, B.K., Peterson, J., Omayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J. McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
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Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA
Nucleic Acids Res. 28 (12), 2311-2314 (2000)
Direct Submission
Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.
Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.
Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microblology; 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8505, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp,
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| 179525<br>183<br>179585<br>243<br>179645<br>303<br>179705                                                                                                                    | L 4 L 8 L 4 L                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 603<br>180005<br>663<br>180065<br>723<br>180125<br>783                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 180185<br>843<br>180245<br>903<br>180305<br>180365 | 1023<br>180425<br>1083<br>180485                             |
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 Nucleotide sequence and taxonomic value of the major cuter membrane protein gene of Chlamydia pneumoniae IOL-207 J. Gen. Microbiol. 137, 465-475 (1991) 91237311
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 Direct Submission
Submitted (12-JUN-1993) M. Lavin, Professor of Molecular C
Queensland Institute of Medical Res, The Bancroft Centre,
Herston Road, Brisbane QLD 4029, AUSTRALIA
 Lavin, M.

Direct Submission
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 major outer membrane protein.
Chlamydophila pneumoniae.
Chlamydophila pneumoniae.
Chlamydophila pneumoniae.
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Chlamydophila pneumoniae
Bacteria: Chlamydiales: Chlamydiaceae; Chlamydophila.
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 gtatctggtcagttcagattc 1101
 င္ပ
 607
 1021
 1087
 1081
 187
 184
 241
 307
 301
 367
 361
 427
 421
 487
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 601
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 661
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outer membrane protein

07-MAY-1999

BCI

CHTOMPAAD 1261 bp DNA Chlamydophila abortus strain B577 major precursor (ompA) gene, complete cds.

RESULT 15 CHTOMPAAD LOCUS DEFINITION

```
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KGSSTAAODLBVWGTAAFTALTUNDRFDIFCTGASGALWEGGCATLGAEFOYAGSNP
IEMLNVVSSPAOFVVHKPRGYKGTAFPLPLTAGTDQATDTKSATIKYHEWQVGLALSY
RLNMLVPXISVNWSRATFDADAIRIAQPKLAAAVLNLTTWNFTLGERTALDTSNKFA
DFLQTASIQINKMKSRRATEDADAIRIAQPKLAAAVLNLTTWNFTLGERTALDTSNKFA

277 9 350 4
277 9 350
 ä
 among the chlamydial
 240
 205
 385
 agacctaacccggcctacaataagcatttacacgatgcagagtggttcactaatgcaggc 300
 360
 505
 ggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagttaaaggt 420
 actactgtaaatgcaaatgaactaccaaacgtttctttaagtaacggagttgttgaactt 480
 63
 4 ttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggt
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 precursor"
 Length 1261;
 Chiamydophila abortus
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
I (bases 1 to 1261)
Kaltenboeck, B., Kousoulas, K.G. and Storz, J.
Structures of and allelic diversity and relationships
major outer membrane protein (ompA) genes of the four
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/db_xref="GI:4757612"
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ilarity 72.2%;
Conservative
 GI:144564
 Similarity
 M73036
M73036.1
 species
 359
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Best Local Simil
Matches 795; (
 source
 BASE COUNT
ORIGIN
 ORGANISM
 REFERENCE
AUTHORS
TITLE
ACCESSION
VERSION
 124
 266
 386
 301
 446.
 184
 241
 361
 506
 421
 MEDLINE
 gene
 KEYWÓRDS
SOURCE
 JOURNAL
 CDS
 FEATURES
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1021 gatgetgataaatggteacttactgeagaagetegtttaattaacgagagagetgeteec 1080
 901 aatgocacagcattgtctactactgattcgttctcagacttcatgcaaattgtttcctgt 960
 ccatacattggagtacaatggtctcgagcaacttttgatgctgataacatccgcattgct 840
 566 TCCTCCATAGCAGCTGATCAGCTTCCCAATGTAGGCATCACTCAAGGAATCGTTGAATTT 625
 ATGAATGCTCAATTCAGATTC 1246
 1081 gtatctggtcagttcagattc 1101
 481
 601
 781
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Search completed: February 7, 2002, 19:39:47 Job time: 13901 sec

C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM C. trachomatis MOM Sequence encoding Paraphany of trachomatic MOM A encoding Chlamy Clamy Coligonucleotide D1 Oligonucleotide D1 Oligonucleotide D2 Oligonucleotide D3 Oligonucleotide D

```
MOMP; psittacosis; infection;
 Chlamydia psittaci major outer membrane protein DNA
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AAX25044
AAA08122
AAA081230
AAA08123
AAA08123
AAA08123
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 Major outer membrane protein; MOME
Vaccine; genetic immunisation; ss
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 98WO-US17943
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 Chlamydia psittaci
 WO9910005-A1
 28-AUG-1998;
 28-AUG-1997;
 05-JUL-1999
 04-MAR-1999
328.8
321.8
287.4
287.4
287.4
287.4
 140
 AAX25047;
 Key
 AAX25047
 RESULT
 chlamydia psittaci
chlamydia psittaci
chlamydia psittaci
C. pneumoniae sero
chlamydia trachoma
chlamydia trachoma
DNA encoding chlam
chlamydia trachoma
 Search time 685.35 Seconds
(without alignments)
1377.275 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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1 atgitgccigtagggaaccc......talciggicagitcagatic 1101
 Description
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| SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn/Na1997.DAT:
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 /SIDS2/gcgdata/geneseq/geneseqn/NA1999.
 IDS2/gcgdata/geneseg/genesegn/NA1998.
 4.5
Compugen Ltd.
 hits satisfying chosen parameters:
 930621 seqs, 428662619 residues
 ٠.
 GenCore version
Copyright (c) 1993 - 2000
 20:17:12
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - nucleic search, using sw model
 AAX25048
AAX25046
 AAA64764
AAH56267
 AAX25047
 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
 7, 2002,
 seq length: 0 seq length: 2000000000
 US-09-391-606-14
 N_Geneseq_1101:*
 DB
 Length
 February
 Query
Match
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Potal number of

Searched:

Minimum DB s Maximum DB s

Database

Perfect score:

Title:

Sequence:

OM nucleic

.. 0

Scoring table:

Major outer membra MOMP containing fu Chlamydia trachoma C. trachomatis maj

Tully TN;

Kousoulas KG,

Chouljenko VN,

Baghian A,

WPI; 1999-254214/21 P-PSDB; AAW98188.

Sequence encoding Complete genome s Chlamydia psittaci

AAV62447 AAZ92753 AAV40646 AAN60007 0 AAZ01425 AAX25045

446.7 443.5 443.4 343.1 320.1

5523.2 5514.6 5514.6 4479.4 4477.8 397.2 352.2

Score

Result No.

20

(LOUU ) UNIV LOUISIANA & AGRIC & MECH COLLEGE.

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ï
 360
 480
 625
 685
 009
 745
 146 ttgcctgtagggaacccagctgaaccaagtttattaatcgatggcactatgtgggaaggt 205
 getgeaggagateettgegáteettgegetaettggtgegaegetattagettaegtget 123
 ggattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaaacattt 183
 Gaps
 63
 protein (MOMP
 tacacagacacctctttctcttggagcgtaggcgctcgtggagccttatgggaatgcggt
 tgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaagttgaagaactt
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 agacctaacccggcctacaataagcatttacacgatgcagagtggttcactaatgcaggc
 tcctccatagcagctgatcagcttcccaatgtaggcatcactcaaggaatcgttgaattt
 This DNA sequence codes for the major outer membrane protein (WOMI see AAW98187) of Chlamydia psittaci strain B577. A claimed MOMP polypeptide (see AAW98184) comprises regions VD3 and VD4 of MOMP i.e. it lacks regions VD1 and VD2. A claimed vaccine composition includes the MOMP polypeptide, optionally fused to a maltose binding protein.
 encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking the regions VDI and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in birds.
 4 ttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatagggaaggt
 tc---tatgggagccaagcctactggatccgctgctgcaaactatactactgccgtagat
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 tatacagatacaacattctcttggagtgtaggtgcacgcggagctttatgggagtgtggt
 3;
 Length 1261;
 Score 600.2; DB 20; Length
Pred. No. 6.1e-173;
0; Mismatches 303; Indels
 Sequence 1261 BP; 359 A; 275 C; 277 G; 350 T; 0 other;
for Chlamydia psittaci infections
 Disclosure; Page 57-60; 72pp; English
 54.5%;
72.2%;
 Local Similarity 72.2
nes 795; Conservative
 new vaccine
 Query Match
 Best Loca
Matches
 184
 386
 446
 909
 999
 979
 541
 241
 301
 361
 421
 481
 601
 64
 124
```

οy a à g Q g οy Op δý q οŽ g

q

Qγ

g οy a δŽ g à

Ω

atcaattatcatgaatggcaagtaggagcctctctatcttacagactaaactctttagtg 780

720

gettteeeettgecaacagaegetggegtagcaacagetactggaacaaagtetgegaee

746

q

661 908 721

ò

Q

ŏ

gcatttcctttacctctaacagctggtactgatcaggcaactgacactaagtcggctaca

```
This DNA sequence codes for the major outer membrane protein (MOMP, see AAW98187) of Chlamydla psittaci strain 6BC. Claimed MOMP polypeptides (see AAW98183 and AAW98184) comprise regions VD3 and VD4 of an MOMP, i.e. they lack regions VD1 and VD2. Claimed vaccine compositions include such MOMP polypeptides, optionally fused to a maltose binding protein. Also claimed are isolated nucleic acids encoding the polypeptide, a vector, and a method of preventing C.
 901 aatgccacagcattgtctactactgattcgttctcagacttcatgcaaattgtttcctgt 960
cagecaaaactacctacagetgttttaaacttaactgcatggaaccettetttactagga 900
 ccttacattagcgtaaactggtcacgagcaacttttgatgctgacgctatccgcatcgct
 ccatacattggagtacaatggtctcgagcaacttttgatgctgataacatccgcattgct
 MOMP; psittacosis; infection;
 Tully
 Chlamydia psittaci major outer membrane protein
 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE.
 KG,
 Kousoulas
 Disclosure; Page 62-65; 72pp; English.
 Location/Qualifiers
364..1572
/*tag= a
 genetic immunisation; ss.
 BP
 1226 atgaatgctcaattcagattc 1246
 1081 gtatctggtcagttcagattc 1101
 standard; DNA; 1660
 98WO-US17943
 97US-0057147
 ΛN,
 (first entry)
 Chouljenko
 WPI; 1999-254214/21.
 Chlamydia psittaci
 P-PSDB; AAW98189
 WO9910005-A1
 28-AUG-1997;
 28-AUG-1998;
 05-JUL-1999
 outer
 04-MAR-1999
 Baghian A,
 AAX25048
 AAX25048;
 vaccine;
 Major
 1021
 998
 781
 926
 841
 961
 Key
 AAX25048
 RESULT
 g
 δλ
 g
 Ω
 qq
 δy
 oy
Oy
 Db
 ò
 Ωp
 Qy
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us-09-391-606-14.rng

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4;
 cgtggagctttatgggaatgtggttgtgcaactttaggagctgagttccaatacgctcaa 1029
 cgtggagccttatgggaatgcggttgtgcactttgggagctgaattccaatatgcacag 576
 069
 750
 810
 989
 430 ttgcctgtagggaacccagctgaaccaagtttattaatcgatggcactatgtgggaaggt 489
 231
 699
 849
 gotgoaggagatcottgogatcottgogotacttggtgogacgotattagottacgtgot 123
 ggattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaaacattt 183
 670 gaagcaaatggcagaccgaacatcgcttacggaaggcatatgcaagatgcagagtggttt 729
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 ---actactgtaaatgcaaatgaactaccaaacgtttct 456
 Gaps
 63
 ttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggt
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 ttaagtaacggagttgttgaactttacacagacacctctttctcttggagcgtaggcgct
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 tccaaacctaaagttgaagaacttaatgtgatctgtaacgtatcgcaattctctgtaaac
 ijμ
 184 tctatgggagccaagcctactggatccgctgctgcaaactatactact-------
 aaacccaagggctataaaggcgtt-----gctttccccttgccaacagacgctggcgta
psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially
 42;
 Length 1660;
 Indels
 other
 Score 526.4; DB 20;
Pred. No. 2.3e-150;
0; Mismatches 306;
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 G; 488
 0; Mismatches
 492 A; 342 C; 338
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 Conservative
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 792;
 Best Loca
Matches
 850
 970
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 1030
 490
 550
 610
 637
 691
 124
 349
 409
 457
 751
 811
 64
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This DNA sequence codes for the major outer membrane protein (MOMP, see AAM98187) of Chlamydia psittaci strain LSUWTCK, a cockatiel isolate (the MOMP gene sequence of this isolate is identical to that of C. psittaci Avian Type C.). A claimed MOMP polypeptide (see AAM98183) comprises regions VD3 and VD4 of MOMP, i.e. it lacks regions VD1 and VD2. A claimed vaccine composition includes MOMP polypeptide lacking VD1 and VD2. A composition includes MOMP belypeptide lacking VD1 and VD2. Optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acid
 agaaaagcttgtggagttactgtaggagctactttagttgatgctgataaatggtcactt
 1042 actgcagaagctcgtttaattaacgagagagctgctcacgtatctggtcagttcagattc
 ļ
ttaactgcatggaacccttctttactaggaaatgccacagcattgtctactact-----
 ---gattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaagtttaaatct
 encoding the polypeptide, a vector, and a method of preventing psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking
 to prevent C. psittaci infection, especially
 MOMP; psittacosis; infection;
 vaccination.
 other
 Tully TN;
 Chlamydia psittaci major outer membrane protein DNA
 BP; 352 A; 263 C; 260 G; 334 T; 0
 new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE
 genetic
 Kousoulas KG,
 Disclosure; Page 53-55; 72pp; English.
 regions VD1 and VD2 are useful for
 Major cuter membrane protein; MOMI vaccine; genetic immunisation; ss
 ВР
 AAX25046 standard; DNA; 1209
 97US-0057147
 N'N
 entry)
 Chouljenko
 WPI; 1999-254214/21.
P-PSDB; AAW98187.
 (first
 psittaci
 vaccines are used
 Sequence 1209
 WO9910005-A1
 28-AUG-1997;
 28-AUG-1998;
 05-JUL-1999
 04-MAR-1999
 Baghian A,
 Chlamydia
 AAX25046;
 925
 982
 RESULT
ÁAX25046
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4

Gaps

Score 523.2; DB 20; Length 1209; Pred. No. 1.9e-149; 0; Mismatches 308; Indels 42;

;

47.5%; ilarity 69.3%; Conservative

Local Similarity es 790; Conserv

Query Match Best Local S: Matches 790,

```
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 agaaaagcttgtggagttactgtaggagctactttagttgatgctgataaatggtcactt 1041
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 810
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63
 gggttttcagctgcaagctcaatctctaccgatcttccaacgcaacttcctaacgtaggc
 acagaagctacagacaccaaatcagctacaattaaataccatgaatggcaagtaggcctc
 actitigatgcigatactatccgcattgcicaacctaaattaaaatcggagattcttaac
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 q
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 Dp
 QQ
 g
 οy
 Ωp
 Q
 g
 δ
 Q
 οy
 g
 ŏ
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 δ
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 δ
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 ŏ
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 δλ
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 δ
 οŽ
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 QΥ
 δ
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```
infertility;
 pmp gene Ral2 fusion coding sequence
 SS
 Chlamydial infection; sexually transmitted disease; pelvic inflammatory disease; PID; tubal obstruction; inftrachoma; bilindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial;
 BP.
 AAA64764 standard; DNA; 1578
 98US-0208277.
99US-0288594.
99US-0410568.
99US-0426571.
 C. pneumoniae serovar MOMPS
 (first entry)
 Chlamydia pneumoniae.
 (CORI-) CORIXA
 WO200034483-A2
 08-DEC-1999;
 22-OCT-1999;
 08-DEC-1998;
08-APR-1999;
 01-OCT-1999;
 02-FEB-2001
 15-JUN-2000
 AAA64764;
 1147
 AAA64764
 q
```

The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is also coronary heart disease. The present sequence is a nucleic acid sequence isolated in the present invention. thought to play a role in the pathogenesis of atherosclerosis

Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence

Claim 1; Page 205; 256pp; English.

EJ;

Stromberg

s,

Jen

SP, Fling

Skeiky YAW,

Bhatia A,

Probst P,

WPI; 2000-431303/37

Sequence 1578 BP; 414 A; 394 C; 382 G; 388 T; 0 other;

Gaps gttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaagg gctgcctgtggggaatccagctgaaccaagtttattaatcgatggcactatgtgggaagg Length 1578; 42; Indels Score 514.6; DB 21; Pred. No. 9e-147; 0; Mismatches 314; Query Match 46.7%; Best Local Similarity 68.8%; Matches 785; Conservative ( ٣ 435 g δŽ

4;

63

495

g

δ

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RESULT

us-09-391-606-14.rng

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1034
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 1334
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 980
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 924
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182
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 734
 347
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 1035 atctaatcctaagattgagatgctcaacgtcacttcaagcccagcacaatttgtgattca
 caaacccaagggctataaaggcgtt-----gctttccccttgccaacagacgctggcgt
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 c 1575
 1155
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Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease
 The present nucleotide sequence is provided in a specification relating to compounds and methods for the treatment and diagnosis of chiamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of chiamydia antigens and DNA, sequences encoding such polypeptides. They are useful for yeachnating against chiamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections,
 182
 494
 674
 tagoggoatggotgcaactoctacgcaggotataggtaacgcaagtaatactaatcagco
 gttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaagg
 Length 1578;
 Chlamydia; vaccine; infection; fusion protein; antigen; pelvic inflammatory disease; trachoma; atherososlerosis; heart cache respiratory tract infection; Capi; CT529; OMCB; polymorphic membrane protein; pmp; thiol specific antioxidant;
 Indels
 ttctatgggagccaagcctactggatccgctgctgcaaactatactact--
 Scholler
 Sequence 1578 BP; 414 A; 394 C; 382 G; 388 T; 0 other
 22;
 Score 514.6; DB 22;
Pred. No. 9e-147;
0; Mismatches 314;
 SP,
 Fling
 Chlamydia trachomatis pmp gene sequence.
 Skeiky YAW,
 Claim 1; Page 211; 295pp; English.
 atherosclerosis and heart disease
 ВР
 1578
 46.78;
 99US-0454684.
2000US-0556877.
2000US-0598419.
 04-DEC-2000; 2000WO-US32919
 (first entry)
 Best Local Similarity 68.8
Matches 785; Conservative
 Chlamydia trachomatis
 Bhatia A,
 WPI; 2001-374831/39
 (CORI-) CORIXA CORP
 standard;
 WO200140474-A2
 19-APR-2000;
 20-JUN-2000;
 03-DEC-1999;
 07-JUN-2001
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 AAH56267
 Query Match
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AAH56267
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----gccgtagatagacctaacccggcctacaataagcattacacgatgcagagtggtt

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 tagaaaagcttgtggtgtagctgttggtgcaacgttaatcgacgctgacaaatggtcaat 1514
 1155 aacagaagctacagacaccaaatcagctacaattaaataccatgaatggcaagtaggcct 1214
 869
 980
 caaacccaagggctataaaggcgtt-----gctttccccttgccaacagacgctggcgt 689
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 ----gattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaagtttaaatc
 tagaaaagcttgtggagttactgtaggagctactttagttgatgctgataaatggtcact
 agcaacagctactggaacaaagtctgcgaccatcaattatcatgaatggcaagtaggagc
 675 agaagcaaatggcagaccgaacatcgcttacggaaggcatatgcaagatgcagagtggtt
 855 agggttttcagctgcaagctcaatctctaccgatcttccaatgcaacttcctaacgtagg
 tegtggageettatgggaatgeggttgtgeaactttgggagetgaatteeaatatgeaca
 576 gtccaaacctaaagttgaagaacttaatgtgatctgtaacgtatcgcaattctctgtaaa
 aggagettectaatggttacattagaggaaactetacagegtteaatetegttggtttatt
 cggagttaaaggt------actactgtaaatgcaaatgaactaccaaacgtttc
 456 tttaagtaacggagttgttgaactttacacagacacctctttctcttggagcgtaggcgc
 1035 atctaatcctaagattgagatgctcaacgtcacttcaagcccagcacaatttgtgattca
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 cttaactgcatggaaccottctttactaggaaatgccacagcattgtctactact----
 Chlamydia trachomatis major outer membrane protein DNA
 BP.
 AAV62447 standard; DNA; 3133
 (first entry)
 02-FEB-1999
 c 1575
 1101 c 1101
 AAV62447;
 9
 216
 989
 1095
 069
 810
 1275
 1335
 1455
 1575
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 750
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 RESULT
AAV62447
ID AAV6
XX
AC AAV6
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This DNA sequence codes for a 42 kDa major outer membrane protein

(MOMP, see AAW73141) of Chlamydia trachomatis serovar L2. A library

c of chlamydial genomic DNA was produced in the phage lambda 1059

system. A lambda 1059 recombinant having a 9.2 kb insert was shown

to be homologous to lambda gtl1/L2/33 (see AAV62446) by Southern

c analysis and was used for endonuclease digestion mapping and

additional Southern analyses. 2 Contiguous fragments were

identified and these contained sufficient base pairs to encode the

C L2 MOMP gene product. These fragments were cloned into M13 for

DNA sequencing. Novel recombinant DNA constructs are provided for

the expression of a polypeptide having immunological activity

c corresponding to that of a naturally occurring MOMP of C.

trachomatis. Such polypeptides find use as reagents in the

detection of C. trachomatis, or antibodies to C. trachomatis, and

as vaccines against infection by C. trachomatis.
 5 tgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggtg 64
 rrope for detecting Chlamydia trachomatis - comprises polynucleotide fragment that hybridises to major outer membrane protein DNA or RNA
 hosts. A claimed probe for detecting C. trachomatis comprises a polynuclectide fragment that specifically hybridises to a DNA or sequence encoding C. trachomatis 38-45 kDa MOMP. The probe has a sequence which is complementary to at least 12 contiguous bases
 43.5%; Score 479.4; DB 19; Length 3133; 66.5%; Pred. No. 6.9e-136; Indels 13; ive 0; Mismatches 356; Indels 13;
 ф
 diagnosis; vaccine;
 Sequence 3133 BP; 911 A; 667 C; 611 G; 944 T; 0 other;
 ä
 Stephens
 Location/Qualifiers
1288.2472
1288.2472
4*tag= a
1288.1353
/*tag= b
/*tag= c
 Major outer membrane protein; MOMP;
 Mullenbach G,
 of the sequence given in AAV62447
 Claim 5; Fig 2A-E; 15pp; English.
 12
 Chlamydia trachomatis serovar
 85US-0692001.
91US-0691639.
93US-0144095.
95US-0468451.
 WASH-) WASHINGTON RES FOUND
 86US-0818523
 95US-0468451
 Best_Local Similarity 66.5
Matches 741; Conservative
 WPI; 1998-567652/48.
P-PSDB; AAW73141.
 CORP
 Aqabian N, Kuo C,
 (CHIR) CHIRON
 06-JUN-1995;
 14-JAN-1985;
25-APR-1991;
 06-JUN-1995;
 13-JAN-1986;
 28-OCT-1993;
 US5821055-A
 13-OCT-1998
 sig_peptide
 mat_peptide
 Query Match
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19-JUN-2000

AAZ92753;

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2014
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 2135 atatgitcactccctacattggagitaaatggictcgagcaagitttgaigcagacacga
 830 tecgeattgeteagecaaaactacetacagetgttttaaacttaaetgeatggaaeeett
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 1595 caagagagaateetgettaeggeegaeatatgeaggatgetgagatgtttaeaaatgetg
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 1775 agaaccatgctacagtttcagatagtaagcttgtaccaaatatgagcttagatcaatctg
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tgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggtg
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3;

Indels

64

g

AAZ92753 standard; DNA; 3133

AAZ92753 ID AAZ9

RESULT

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The present sequence represents DNA encoding the major outer membrane protein (MOMP) of Chlamydia trachomatis serovar L2. DNA obtained from C. trachomatis serovar L2 was partially digested with DNAse I and C inserted into the bacteriophage vector lambda-gil; a lambda-gil insert c inserted into the bacteriophage vector lambda-gil; a lambda-gil insert (AAA292752; ATCC #40157, referred to as lambda-gill; a lambda-gil insert contained which encodes a protein fragment (AAV81267) reactive with a pool of C. trachomatis-specific monoclonal antibodies. The lambda-gill/L2/33 insert sequence was also used to probe a chamydial genomic DNA phage lambda 1059 library, and the present sequence which encodes the full-length (hamydia trachomatis serovar L2 MOMP was identified. C. trachomatis is a human pathogen responsible for diseases such as trachomatis is a human pathogen responsible for the diseases such as trachomatis. The full-length recombinant MOMP or a fragment thereof is used to elicit the production of antibodies to a MOMP of Chlamydia trachomatis. MOMP proteins are also useful as immunoassay reagents (substitutes for native MOMP) for detecting C. trachomatis or mative MOMP) for detecting C. trachomatis or mative MOMP) for detecting C. trachomatis or mative MOMP) for detecting C. trachomatis or matinodies, for diagnosing infection, or as an immunoassay
 Chlamydia trachomatis major outer membrane protein (MOMP)
 New synthetic or recombinant polypeptide, useful for diagnosing preventing Chlamydia trachomatis infection, is immunologically equivalent to a major outer membrane protein
 antibody production; immunoassay; detection; vaccine; trachoma; inclusion conjunctivitis; pneumonia; lymphogranuloma venereum; mucous membrane genital tract infections; ds.
 DB 21; Length 3133;
 1288..2472
/*tag= a
/product= "Chlamydia trachomatis serovar L2
 BP; 911 A; 670 C; 609 G; 943 T; 0 other;
 Que¹y Match
43.5%; Score 479.4; DB 21;
Best Local Similarity 66.5%; Pred. No. 6.9e-136;
Matches 741; Conservative 0; Mismatches 356;
 Kuo C-C, Mullenbach G;
 Location/Qualifiers
 membrane protein; MOMP;
 Examples; Fig 2; 17pp; English.
 Chlamydia trachomatis serovar
 93US-0144095.
86US-0818523.
91US-0691639.
85US-0692001.
 FOUND
 95US-0466152
 Stephens R,
 (WASH-) WASHINGTON RES
 WPI; 2000-223163/19.
 P-PSDB; AAY81268
 Sequence 3133
 DNA encoding
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14-JAN-1985;
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 28-OCT-1993;
13-JAN-1986;
 29-FEB-2000
 Agabian N,
 vaccines
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ВР

DNA; 3133

standard;

AAV40646

AAV40646

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RESULT

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 gattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaaacatttt 184
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 Score 477.8; DB 19; Length 3133;
Pred. No. 2.1e-135;
0; Mismatches 357; Indels 13;
 The sequence is that encoding a major outer membrane protein (MOMP) of Chlamydia trachomatis. This polypeptide can be used in immunoassays, e.g. to detect Chlamydia trachomatis antibodises in blood, or can be used in vaccines. The polynucleotide can be labelled and used as a diagnostic probe.
 fo:
 immunoassay; diagnosis;
 useful
 Sequence 3133 BP; 909 A; 670 C; 610 G; 944 T; 0 other;
 Chlamydia trachomatis serovar L2 MOMP coding region
 DNA coding for Chlamydia trachomatis polypeptide producing recombinant polypeptide, etc.
 ä
 Stephens
 MOMP; major outer membrane protein; detection; antibody; serovar L2; ds.
 Location/Qualifiers
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 1288..2472
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1287..1353
/*tag= b
 Claim 5; Fig 2; 15pp; English.
 86US-0818523.
85US-0692001.
91US-0691639.
93US-0144095.
95US-0466814.
 WASHINGTON RES FOUND
 43.4%;
ilarity 66.4%;
Conservative
 85US-0692001
 (first entry)
 Chlamydia trachomatis.
 WPI; 1998-376887/32
 Query Match
Best Local Similarity
Matches 740; Conserv
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 4-JAN-1985;
 28-OCT-1993;
06-JUN-1995;
 US5770714-A.
 14-JAN-1985;
 13-JAN-1986;
 27-OCT-1998
 sig_peptide
 23-JUN-1998
 AAV40646
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| 763<br>1030                                                          | 823<br>1090                                                      | 883<br>1150                                                          | 940<br>1210                                                  | 1000                                                                      | 1060<br>1330                                                          |                                                        |
| gaacaaagictgcgaccatcaattatcatgaatggcaagtaggagcctctctatcttaca 763<br> | gactaaactctttagtgccatacattggagtacaatggtctcgagcaacttttgatgctg<br> | 824 ataacatccgcattgctcagccaaaactacctacagctgttttaaacttaactgcatgga<br> | accetecttactaggaaatgecacagcattgtctactactgattcgttctcagact 940 | 941 tcatgcaaattgtttcctgtcagatcaacaagtttaaatctagaaaagcttgtggagtta 1000<br> | ctgtaggagctactttagttgatgctgataaatggtcacttactgcagaagctcgtttaa 1060<br> | 1061 ttaacgagagactgctcacgtatctggtcagttcagattc 1101<br> |
| 704                                                                  | 764                                                              | 1091                                                                 | 884                                                          | 941                                                                       | 1001                                                                  | 1061                                                   |
| oy<br>Ob                                                             | Oy<br>Dp                                                         | Oy<br>Dp                                                             | Qy<br>Dp                                                     | Qy                                                                        | Qy<br>Dp                                                              | oy<br>ea                                               |

Search completed: February 7, 2002, 20:23:45 Job time: 16539 sec

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MOMP; hydrophilic polypeptide; antibody; detection; diagnosis; infections disease; ds.

Chlamydia trachomatis; fusion

(first

27-JUN-2000

AAA08120;

Chlamydia trachomatis

C. trachomatis MOMP containing fusion protein nucleotide sequence #1

us-09-391-606-14.rng

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ï
 The present invention describes fusion proteins (I) comprising at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis, at least one hydrophilic polypeptide having no immunoreactivity to human serum and their connected part. AAA08120 to AAA08125 encode specifically claimed examples of the fusion proteins given in AAY82388 (Chlamydia trachomatis antibody using (I) as the antigen. (I) is used for the diagnosis of Chlamydia trachomatis infectious diseases. The method can diagnose Chlamydia trachomatis infectious diseases precifically in a
 1000
 1021
 1081
 1262 cagtaggaacaactattgtggatgcagacaaatacgcagttacagttgagactcgcttga 1321
 1142 acccaactattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagata 1201
 823
 901
 703
 accettetteactaggaaatgecacageattgtetactactga---ttegtteteagaet 940
 Gaps
 sful for diagnosis of Chlamydia infection, major outer membrane protein (MOMP) of
 acggagttgttgaactttacacagacacctctttctctttggagcgtaggcgctcgtggag
 cettatgggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaac
 1202 ccatgcaaatcgttccttgcaattgaacaagatgaaatctagaaaatcttgcggtattg
 842 ctaaagtcgaagaattaaacgttctctgtaacgcagctgagtttactatcaataagccta
 agggetataaaaggegttgettteeecttgeeaacagaegetggegtageaacagetaetg
 gaacaaagtctgcgaccatcaattatcatgaatggcaagtaggagcctctctatcttaca
 824 ataacatccgcattgctcagccaaaactacctacagctgttttaaacttaactgcatgga
 tcatgcaaattgtttcctgtcagatcaacaagtttaaatctagaaagcttgtggagtta
 Length 1362;
 3;
 Indels
 Sequence 1362 BP; 383 A; 283 C; 324 G; 372 T; 0 other;
 21;
 1061 ttaacgagagactgctcacgtatctggtcagttcagattc 1101
 Score 287.4; DB 21;
Pred. No. 1.8e-77;
0; Mismatches 211;
 0; Mismatches
 Page 28; 37pp; Japanese.
 nseful
 26.1%;
66.6%;
 of
 fused protein used least part of trachomatis -
 Conservative
 Query Match
Best Local Similarity
Matches 427; Conserv
 sensitivity
 A soluble f
comprises
Chlamydia t
 Claim 16;
 high
 524
 584
 902
 962
 884
 782
 464
 644
 1001
 704
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"Fusion protein containing at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis; no stop codon given"
 The present invention describes fusion proteins (I) comprising at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis, at least one hydrophilic polypeptide having no immunoreactivity to human serum and their connected part. AAA08125 on AAA08125 encode specifically claimed examples of the fusion proteins given in AAY82388 (Chlamydia trachomatis antibody using (I) as the antigen. (I) is used for the diagnosis of Chlamydia trachomatis infectious diseases. The method can diagnose Chlamydia trachomatis infectious diseases specifically in a
 583
 970
 643
 910
 703
 Gaps
 A soluble fused protein useful for diagnosis of Chlamydia infection, comprises at least part of major outer membrane protein (MOMP) of Chlamydia trachomatis -
 ccitatgggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaac
 aaggatatgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacag
 464 acggagttgttgaactttacacagacactctttctctttggagcgtaggcgctcgtggag
 ctaaagtcgaagaattaaacgttctctgtaacgcagctgagtttactatcaataagccta
 agggctataaaggcgttgctttccccttgccaacagacgctggcgtagcaacagctactg
 DB 21; Length 1371;
 3;
 Indels
 Sequence 1371 BP; 390 A; 276 C; 324 G; 381 T; 0 other;
 0; Mismatches 211;
 26.1%; Score 287.4; DB 2:
llarity 66.6%; Pred. No. 1.8e-77;
Conservative 0; Mismatches 211
 Claim 12; Page 26-27; 37pp; Japanese.
 Location/Qualifiers
 (ELED) DENKI KAGAKU KOGYO KK.
 98JP-0213212.
 98JP-0213212
 /*tag=
 2000-295780/26
 Query Match
Best Local Similarity
Matches 427; Conserv
 P-PSDB; AAY82388.
 JP2000041678-A.
 38-JUL-1998;
 28-JUL-1998;
 Synthetic
 524
 791
 851
 644
 911
 Key
g
 ογ
Op
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 ..δ
 q
 Qγ
 g
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1;

AAA08120 standard; DNA; 1371 BP

RESULT 1 AAA08120 ID AAA0

807

924

Fri Feb

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/*tag= a
/note= "Fusion protein containing at least part of a
major outer membrane protein (MOMP) of Chlamydia
trachomatis; no stop codon given"
 ettactgcagaagetcgtttaattaacgagagagetgctcacgtatctggtcagttcaga 1098
 979 totagaaaagcttgtggagttactgtaggagctactttagttgatgctgataaatggtca 1038
 544 tetagaaaagettgtggtgtagetgttggtgcaaegttaategaegetgaeaaatggtea 603
 gcaacttttgatgetgataacateegeattgeteageeaaaetaeetaeegetgtttta 867
 C. trachomatis MOMP containing fusion protein nucleotide sequence #3.
 Chlamydia trachomatis; fusion protein; major outer membrane protein; MOMP; hydrophilic polypeptide; antibody; detection; diagnosis; infection; infectious disease; ds.
 184 cacaaaccaagaggctataaaggagctagctcgaattttcctttacctataacggctgga
 304 ctcgccctgtcttacagattgaatatgcttgttccatatattggcgtaaactggtcaaga
 geetetetatettacagaetaaaetetttagtgeeataeattggagtaeaatggtetega
 aacttaactgcatggaacccttctttactaggaaatgccacagcattgtctactact---
 Location/Qualifiers
1..1362
634 aacaaacccaagggctataaaggcgtt---
 BP.
 AAA08122 standard; DNA; 1362
 (first entry)
 Chlamydia trachomatis. Synthetic.
 JP2000041678-A.
 ttc 1101
 28-JUL-1998;
 27-JUN-2000
 15-FEB-2000
 AAA08122;
 14
 898
 424
 808
 Key
 AAA08122
 QQ
 Qγ
 q
 δλ
 g
 Qγ
 a
 qq
 QΥ
 QQ
 ^{\circ}
 QΥ
 5
 This DNA sequence codes for a major outer membrane protein (MOMP)

cockatiel isolate (the MOMP gene sequence of this isolate is

cockatiel isolate (the MOMP gene sequence of this isolate is

identical to that of C. psittaci Avian Type C). The MOMP

colypeptide comprises regions VD3 and VD4 of native MOMP. See

also AAW98187), i.e. it lacks regions VD1 and VD2 of MOMP. DNA

encoding the MOMP polypeptide was obtained by PCR amplification

(see also AAX25049 and AAX25051) of C. psittaci LSUWTCK DNA. A

claimed vaccine composition includes this MOMP polypeptide,

coptionally fused to a maltose binding protein. Also claimed

an isolated nucleic acid encoding the polypeptide, a vector,

and a method of preventing C. psittaci infection by administering

the vaccine containing the MOMP polypeptide. Vectors ancoding MOMP

polypeptides lacking regions VD1 and VD2 are useful for genetic

(naked nucleic acid) vaccination. The vaccines are used to prevent

C. psittaci infection, especially in birds.
 tetttaagtaaeggagttgttgaaetttaeaaeagaeaectetttetettggagegtagge 513
 DB 20; Length 726;
 Major outer membrane protein; MOMP; psittacosis; infection; vaccine; genetic immunisation; ss.
 Chlamydia psittaci MOMP (minus VD1 and VD2 region) DNA
 Sequence 726 BP; 221 A; 153 C; 144 G; 208 T; 0 other;
 Chouljenko VN, Kousoulas KG, Tully TN;
 0; Mismatches 182;
 29.2%; Score 321.8; DB 2 70.3%; Pred. No. 4.2e-88;
 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE.
 Example 2; Page 43-45; 72pp; English
 Location/Qualifiers
1..669
/*tag= a
 BP.
 AAX25044 standard; DNA; 726
 98WO-US17943
 97US-0057147
 (first entry)
 Conservative
 WPI; 1999-254214/21.
 Best Local Similarity
 Chlamydia psittaci
 P-PSDB; AAW98183
 WO9910005-A1
 28-AUG-1997;
 28-AUG-1998;
 05-JUL-1999
 Matches 466;
 Baghian A,
 Query Match
 AAX25044;
 454
 4
 514
 AAX25044
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(ELED ) DENKI KAGAKU KOGYO KK

WPI; 2000-295780/26. P-PSDB; AAY82390.

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98JP-0213212.

28-JUL-1998;

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tittctatgggagccaagccta....ctggatccgctgctacaaactatactactgcc 234
 göaggetteattgeettaaaeatttgggategetttgatgtttetgtaetttaggaget 354
 aaaggtactactgtaaatgcaaatgaactaccaaacgtttctttaagtaacggagttgtt 474
 aatg-----agaaccatgctacagtttcagatagtaagcttgtacca 462
 gaactttacacagacacctctttctcttggagcgtaggcgctcgtggagccttatgggaa 534
 gggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacaggaactaaggat 657
 atigotoagcoaaaactacctacagctgttttaaacttaactgcatggaacccttcttta 894
 getggagetggegatgtgaaagetagegeagagggteageteggagataeeatgeaaate 897
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 ctaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgcaaatt 951
 tctaatggttacattagaggaaactctacagcgttcaatccgttggtttattcggagtt
 ggcgttgctttccccttgccaacagacgctggcgtagcaacagctactggaacaagtct
 ttagtgccatacattggagtacaatggtctcgagcaacttttgatgctgataacatccgc
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 gegaceateaattateatgaatggeaagtaggageetetetatettacagaetaaaetet
 gctggattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaaaca
 gctgctcacgtatctggtcagttcagattc 1101
 aatatgagcttagatcaatct-----
 235
 535
 484
 658
 718
 178
 1012
 1072
 301
 355
 361
 415
 475
 463
 595
 598
 835
 895
 838
 868
 928
 1018
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 181
 181
 295
 421
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 5;
 The present invention describes fusion proteins (I) comprising at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis, at least one hydrophilite polypeptide having no immunoreactivity to human serum and their connected part. AAAA08120 to AAA08125 encode specifically claimed examples of the fusion proteins given in AAY82388 to AAA8333. Also described is a method (A) for the detection of Chlamydia trachomatis antibody using (I) as the antigen. (I) is used for the diagnosis of Chlamydia trachomatis infectious diseases. The method can diagnose Chlamydia trachomatis infectious diseases specifically in a
 /note- "Fusion protein containing at least part of a major outer membrane protein (MOMP) of Chlamydia 'trachomatis; no stop codon given"
 675
 ggtgctgcaggagatccttgcgatccttgcgctacttggtgcgacgctattagcttacgt 120
 Gaps
 1 atgttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaa 60
 1 atgotgoctgtggggtaaccctgctgaaccaagccttatgatcgacgggatcctatgggaa 60
 A soluble fused protein useful for diagnosis of Chlamydia infection, comprises at least part of major outer membrane protein (MOMP) of Chlamydia trachomatis -
616 tggtcaatcactggtgaagcacgcttaatcaatgaaagagccgctcacatgaatgctcaa
 protein nucleotide sequence
 Score 328.8; DB 21; Length 1047;
Pred. No. 3.7e-90;
0; Mismatches 367; Indels 72;
 Chlamydia trachomatis; fusion protein; major outer membrane pr
MOMP; hydrophilic polypeptide; antibody; detection; diagnosis;
infection; infectious disease; ds.
 Sequence 1047 BP; 315 A; 209 C; 233 G; 290 T; 0 other;
 C. trachomatis MOMP containing fusion
 Claim 20; Page 29-30; 37pp; Japanese.
 Location/Qualifiers
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 BP
 (ELED) DENKI KAGAKU KOGYO KK
 DNA; 1047
 Query Match 29.9%;
Best Local Similarity 60.5%;
Matches 671; Conservative
 98JP-0213212.
 98JP-0213212
 (first entry)
 Chlamydia trachomatis. Synthetic.
 WPI; 2000-295780/26.
P-PSDB; AAY82392.
 1093 ttcagattc 1101
 AAA08124 standard;
 684
 high sensitivity
 676 ttcagattc
 JP2000041678-A.
 28-JUL-1998;
 28-JUL-1998;
 27-JUN-2000
 15-FEB-2000
 AAA08124;
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714

774

834

13

RESULT

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594 539 654 597

414

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Db 734327 gaacaactattgtggatgcagacaaatacgcagttacagttgagactcgcttgatcgatg 734386
 733847 gggaatatggatgcgcgactttaggcgcntctttccaatacgctcaatccaagcctaaag 733906
 tegaagaattaaaegttetetgtaaegeagetgagtttaetateaataageetaaaggat 733966
 733967 atgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacaggaacta 734026
 734266
 ttgttgagttgtatacagatactacttttgcttggagtgctggagctcgtgcagctttgt 733846
 ataaaggcgttgctttccccttgccaacagacgctggcgtagcaacagctactggaacaa 709
 tocgcattgctcagccaaaactacctacagctgttttaaacttaactgcatggaaccctt
 734207 ctattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagataccatgc
 Db 734267 aaatcgtttccttgcaattgaacaagatgaaatctagaaaatcttgcggtattgcagtag
 agtetgegaceateaattateatgaatggeaagtaggageetetetatettaeagaetaa
 actetttagtgecatacattggagtacaatggtetegageaacttttgatgetgataaea
 ctttactaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgc
 aaattgtttcctgtcagatcaacaagtttaaatctagaaaagcttgtggagttactgtag
 gggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaag
 psittacosis; infection;
 Chlamydia psittaci MOMP (minus VD1 and VD2 region) DNA
 LOUISIANA & AGRIC & MECH COLLEGE
 1067 agagagctgctcacgtatctggtcagttcagattc 1101
 ter membrane protein; MOMP; genetic immunisation; ss.
 Location/Qualifiers
 BP
 98WO-US17943
 97US-0057147
 DNA; 744
 (first entry)
 Chlamydia psittaci.
 AAX25045 standard;
 (LOUU) UNIV
 WO9910005-A1
 28-AUG-1997;
 05-JUL-1999
 outer
 04-MAR-1999
 AAX25045;
 vaccine;
 Major
 11
 530
 290
 650
 710
 734027
 770
 734087
 830
 890
 733907
 Db 733787
 AAX25045
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 Dp
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This DNA sequence codes for a major outer membrane protein (MOMP) polypeptide (see AAW98183) of Chlamydia psittaci strain B577. The MOMP polypeptide comprises regions VD3 and VD4 of native MOMP (see also AAW98188), i.e. it lacks regions VD1 and VD2 of MOMP. DNA encoding the MOMP polypeptide was obtained by PCR amplification (see also AAX25049 and AAX25052) of C. psittaci B577 DNA. A claimed vaccine composition includes this MOMP polypeptide, optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides are useful for genetic (naked nucleic acid) vaccination. The vaccines are used to prevent C. psittaci infection, especially in birds.
 tetttetettggagegtaggegetegtggageettatgggaatgeggttgtgeaaetttg 552
 ggagcagagttccaatacgctcagtctaatcctaaaattgaaatgttgaatgtagtctcc 195
 672
 732
 cetetaacagetigitactgateaggeaactgacactaagteggetacaattaaataceae 315
 792
 gaatggcaagttggtttagcgctctttatcgattgaacatgcttgttccttacattagc 375
 852
 435
 912
 ttgtctactactgattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaag 972
 433 gcaaatgaactaccaaacgtttctttaagtaacggagttgttgaactttacacagacac 492
 Gaps
 ccaacagacgctggcgtagcaacagctactggaacaaagtctgcgaccatcaattatcat
 cetacagetgttttaaacttaactgcatggaaceettetttactaggaaatgecacagea
 16 gctgatcagcttcccaatgtaggcatcactcaaggaatcgttgaattttatacagataca
 aacgtatcgcaattctctgtaaacaaacccaagggctataaaggcgttgctttccccttg
 gaatggcaagtaggagcctctctatcttacagactaaactctttagtgccatacattgga
 gtacaatggtctcgagcaacttttgatgctgataacatccgcattgctcagccaaaacta
 ó
 Length 744;
 Indels
 Sequence 744 BP; 213 A; 164 C; 157 G; 210 T; 0 other;
ŢN;
 Score 352.2; DB 20;
Pred. No. 2.3e-97;
0; Mismatches 198;
Tully
 psittaci infections
Kousoulas KG,
 Example 2; Page 47-48; 72pp; English
 .32.0%;
Local Similarity 70.4%;
Les 471; Conservative (
 A new vaccine for Chlamydia
Chouljenko VN,
 WPI; 1999-254214/21
 P-PSDB; AAW98184
 Baghian A,
 Query Match
 913
 Best Loc
Matches
 196
 376
 136
 613
 673
 256
 733
 316
 793
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tggtcacttactgcagaagctcgtttaattaacgagagagctgctcacgtatctggtcag 1092

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WO9928475-A2

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Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 1006
 1066
 2014
 2374
 2434
 1834
 2074
 2134
 2194
 469
 649
 709
 769
 889
 829
 946
 1715 giggatatettaaaggaaatteageatettteaaettagtiggettatteggagataatg
 2015 atgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacaggaacta
 710 agtotgogaccatoaattatoatgaatggoaagtaggagootototatottacagactaa
 2135 atatyttcactccctacattygayttaaatyytctcyaycaaytttyatycagacacya
 ttcgtattgctcagccgaagtcagctacaactgtctttgatgttaccactctgaacccaa
 2375 gaacaactattgtggatgcagacaaatacgcagttacagttgagactcgcttgatcgatg
 atggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagtta---
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 gggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaag
 650 atamaggegttgettteeeettgeeaacagaegetggegtageaacagetaetggaacaa
 actetttagtgecatacattggagtacaatggtetegageaacttttgatgetgataaca
 890 ctttactaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgc
 2255 ctattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagataccatgc
 aaattgtttcctgtcagatcaacaagtttaaatctagaaaagcttgtggagttactgtag
 Complete genome seguence of Chlamydia trachomatis
 2435 agagagctgctcacgtaaatgcacaattccgcttc 2469
 agagagctgctcacgtatctggtcagttcagattc 1101
 BP.
 DNA; 1038602
 (first entry)
 Chlamydia trachomatis
 standard;
 07-0CT-1999
 AAZ01425
 AAZ01425;
 1775
 1955
 RESULT 10
 416
 470
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The present sequence represents the complete genome of Chlamydia trachomatis. Open reading frames (ORFS) of the genome encode polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonecoccal uretritis, pentralis, cervicitis, salpingitis, penthapatitis, bartholinitis; peneumopathy in breast feeding infants; and veneral lymphographlomatosis. The polypeptides of the invention may be of use in
 733307 tgcctgtggggaatcctgctgaaccaagccttatgatcgacggaattctatgggaaggtt 733366
 733426
 733666
 Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432 other;
 184
 Gaps
 64
 Length 1038602;
 733667 giggatatottaaaggaaattoagoatotttoaaottagtigggttattoggagataatg
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 Score 397.2; DB 20;
Pred. No. 1.4e-109;
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 Genome sequence of Chlamydia trachomatis
 Claim 1; Page 373-656; 1755pp; English.
 98US-0107077.
97FR-0015041.
97FR-0016034.
 36.1%;
66.4%;
 98WO-IB01939
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 treating these diseases
 WPI; 1999-371125/31
 Queřy Match
Best Local Similarity
Matčhes 740; Conserv
 (GEST) GENSET
 04-NOV-11998;
|28-NOV-11997;
|17-DEC-1997;
 27 - NOV - 1998;
 10-JUN-1999
 Griffais R;
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 185
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 359
Db
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1066
 1715 gtggatatcttaaaggaaattcagcatctttcaacttagttggcttattcggagataatg 1774
 946
 actetttagtgecatacattggagtacaatggtetegageaaettttgatgetgataaea
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 6
 2195
 890
 830
 1007
 416
 1775
 470
 530
 590
 650
 RESULT
AAN60007
ID AAN6
XX
AC AAN6
XX
DT 30-J
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ctgcaggagatccttgcgatccttgcgctacttggtgcgacgctattagcttacgtgctg 124
 358
 DNA obtd. from C.trachomatis serovar L2 was partially digested with DNAse I and inserted into vector lambda gtll. Clone lambda gt/l1/L2/ 333 (AAN60006) reacted with the pool and was subsequently shown to produce a polypeptide that displays species-, subspecies- and typerspecific epitopes of the chlamydial MOMP. L2 B9-F DNA (AAN60007) is comprised of lambda 1059 recombinants shown to be homologous with lambda gtll/L2/33.
 toggoggacatocttgogatocttgoaccacttggtggtgacgctatoagcatgcgtatgg
 tgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggtg
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 , DNA constructs and polypeptide(s) - displaying antigenicity major outer membrane protein of Chlamydia trachomatis \,
 Length 3133;
 Sequence 3133 BP; 911 A; 673 C; 606 G; 943 T; 0 other;
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Pred. No. 2e-134;
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 GT;
 cervicitis;
 Mullenbach
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 a major outer
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 85US-0692001
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Best Local Similarity 66.2
Matches 738; Conservative
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 Chlamydia trachomatis
 Agabian N, Stephens
 WPI; 1986-226702/35.
P-PSDB; AAP60004.
 CORP.
e encoding of DNA.
 misc_difference
 (CHIR-) CHIRON
 14-JAN-1985;
 10-JAN-1986;
 mat_peptide
 27-AUG-1986
 Sequence
L2 B9-F D
 Vaccine;
 New DNA
 1415
 1475
 185
 Key
 Dp.
 δy
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 δ
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3,

BP

3133

AAN60007 standard;

(first entry)

30-JUL-1991

AAN60007;

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10192388
 LOCUS
 ORGANISM
 ACCESSION
VERSION
KEYWORDS
SOURCE
 844
 1084
 TITLE
JOURNAL
 MEDLINE
PUBMED
 gene
 904
 1286
 REFERÊNCE
 AUTHORS
 REFERENCE
 AUTHORS
 RESULT
AE001652
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 TITLE
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KGTTYNANELPNVSLSNGVVELYTDTSFSWSVGARGALWECGCATLGAEFQYAQSKPK
VELNVILVNVSOFSVWRFWSTFDADAFPTDTDAGATATGTFSATINYERWQVGASLSY
RLNSLVPYIGVQWSATFDADAIRTAQPKLFTDATAGATATGTTTDSFS
DFWQIVSCQINKFKSRKACGVTVGATLVDADKWSLFARANYSGQFRF"
 ö
 565
 243
 625
 363
 745
 423
 805
 483
 865
 543
 925
 603
 783
 843
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 Length 1830;
 Indels
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 575
 Б
 386. .1483
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1502. .1528
a 383 c 355 g
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 517
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 BASE COUNT
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 1046
 724
 1106
 446
 999
 304
 986
 64
 124
 184
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 424
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AGDPCDATWCDAISLRAGFYGDYVFDRIIKVDARFTFSWGAKPTGSAAANTTAVD
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VEELNVICNVSOFSVNKPKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSY
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Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA Location/Qualifiers

1. 20057
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Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis 9206606
1166 TACATTGGAGTACAATGGTCTCGAGCAACTTTTGATGCTGATAACATCCGCATTGCTCAG 1225
 963
 01-DEC-2000
 of 103 of the complete genome
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Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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 major outer membrane protein.
Chlamydia pneumoniae DNA.
Chlamydia pneumoniae
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
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Sequence analysis of the major outer membrane protein
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DEFINITION
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TITLE
 JOURNAL
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 610
 0.29
 724
 190
 784
 844
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 544
 604
 RBS
 CHTMOMPP
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VPY ICVOWSRATFDADINIR TAGYELPTAVINILTANNPSLLGNATALSTTDSFSDFWQIY
SCQINKFKSRKACGVTVGATLYDADKWSLTAEARLINERAAHVSGOFRF"
 genome
 ;
0
 Ξ
 Takeuchi A., Nishida J., Shibata K., Fujinaga R., Yoneda H., Matsushima
Tanaka C., Furukawa S., Miura K., Nakazawa A., Ishii K., Shiba T.,
Hattori M., Kuhara S.;
 483
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 123
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 Gaps
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Matches 1098; Conserv
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Shirai
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729 723 789 783 849 843

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Submitted (25-ocr-1999) to the EMBL/GenBank/DDBJ databases.
Hideki Hirakawa, Kyushu University, Graduate School of Genetic Resources
Technology: 6-10-1 Hakozaki, Higashi-ku, Fukuoka, Fukuoka 812-8881, Japan
(E-mall:hirakawa@grt.kyushu-u.cip, URL:http://www.grt.kyushu-u.ac.jp,
Tel:81-92-642-3043, Fax:81-92-642-3043)
 849
 606
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Chlamydiales; Chlamydiaceae; Chlamydophila
 Chlamydophila pneumoniae ompA gene for major outer
 Last updated, Version 1)
 BP.
 DNA; PRO; 1170
 Created)
 major outer membrane protein.
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 Hirakawa H., Shirai M.;
 61,
61,
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Bacteria; Chla
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 AB033787.1
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VEELNVICNVSQFSVNKPKGYKGYKGVAFPLPTDAGVATATGTKSATINYHEWQVGASLSY
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Submitted (26-FEB-1999) Pathology, Vanderbilt University, C-3321
Medical Center North, Nashville, TN 37232, USA
Location/Qualifiers
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 Gaps
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Matches 1098; Conservative
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 BASE COUNT
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 424
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(without alignments)
1485.051 Million cell updates/sec
 US-09-391-606-14
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 2944280
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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 Database :
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| - 14 . | Result                                                  | Scor           | a)                              | Query<br>Match                                  | Length                                                                     | DB                     | ID                               | Description                               |
|--------|---------------------------------------------------------|----------------|---------------------------------|-------------------------------------------------|----------------------------------------------------------------------------|------------------------|----------------------------------|-------------------------------------------|
|        | -                                                       | 109            | 1 86                            | 7.66                                            |                                                                            |                        | AF131889                         | 31889 C                                   |
|        | 5                                                       | 109            | 86                              | 99.7                                            | 1170                                                                       |                        |                                  | Ab033787 Chlamydop                        |
|        | m <b>-</b>                                              | 0              | 00 0                            | 99.7                                            | 18                                                                         |                        | CHTMOMPP<br>AFOO1652             | M69230 Chlamydia p<br>AE001652 Chlamydia  |
|        | 4 r.                                                    | $\sim$ $\circ$ | ρœ                              | 7.00                                            | 2 5                                                                        |                        | AE001632<br>AE002167             | AE002167 Chlamydop                        |
|        |                                                         | $\circ$        | 0 00                            | 99.7                                            | lιΩ                                                                        |                        | AP002547                         | AP002547 Chlamydop                        |
| •      | 7                                                       | 9              | 4                               | 966                                             | Π.                                                                         |                        | CHTMOMPB                         | M64064 Chlamydia p                        |
| •      | <b>∞</b> α                                              | 10             | 9 0                             | 96.8                                            | . 19                                                                       |                        | CPMOMPX                          | X/ZUZ3 Chlamydophi<br>I.04982 Chlamydia p |
|        | 10                                                      | 96             | 7.5                             |                                                 | 15                                                                         |                        | CHIOMPAI                         | M73038 Chlamydophi                        |
|        | 11                                                      | 89             | 4                               |                                                 | Ψ,                                                                         |                        | AF131230                         | AF131230 Chlamydop                        |
|        | 12                                                      | 65             | ر<br>در د                       |                                                 | 9 7                                                                        |                        | AF131229<br>AF269259             | AF131229 CHIAMIYUOP<br>AF269259 Chlamydop |
|        | 14                                                      | 600            | . ~                             | 54.5                                            | 11                                                                         |                        | AF272945                         | AF272945 Chlamydop                        |
|        | 15                                                      | 00             | 7.0                             |                                                 | 17                                                                         |                        | CHTOMPAAD                        | M73036 Chlamydophi<br>x51859 Chlamydophi  |
|        | 17                                                      | 009            | 70                              |                                                 | <b>∓</b> ∺                                                                 |                        | CFUMP<br>CHTOMPAAA               | L39020 Chlamydophi                        |
|        | 18                                                      | 009            | . 7                             |                                                 | 14                                                                         |                        | AF269256                         | AF269256 Chlamydop                        |
|        | 19                                                      | 595            | ص <u>ب</u>                      |                                                 | 17                                                                         |                        | AF269267<br>aF269266             | AF26926/ Chlamydop<br>AF269266 Chlamydop  |
|        | 2 12                                                    | 590            |                                 | 53.6                                            | i ;                                                                        |                        | AF269279                         | AF269279 Chlamydop                        |
|        | 22                                                      | 585            | 8                               |                                                 | Ξ,                                                                         |                        | CHIMOMPXA                        | L25436 Chlamydia p                        |
|        | 23                                                      | 585            | ထ္ဝ                             |                                                 | 77.                                                                        |                        | AF26926U<br>AF269261             | AF269260 CHIAMAGE<br>AF269261 Chlamydop   |
|        | 25                                                      | 581            | . ~                             |                                                 | 17                                                                         |                        | AF269282                         | AF269282 Chlamydop                        |
|        | 26                                                      | 573            | 4.                              |                                                 | H :                                                                        |                        | AF269257                         | AF269257 Chlamydop                        |
|        | 27                                                      | 573            | 4. 4                            |                                                 |                                                                            |                        | AFZ69Z58<br>CHTOMPAAH            | AF209250 CHIEMYGOP<br>M73037 Chlamydophi  |
|        | 50                                                      | , io           | 73                              |                                                 | 12                                                                         |                        | AF269280                         | AF269280 Chlamydop                        |
|        | 30                                                      | 571            | œ. ر                            |                                                 | 6                                                                          |                        | CPFPNMOMP                        | X61096 Chlamydophi                        |
|        | 32<br>32                                                | 552            | ٥,٢                             |                                                 | 7.7                                                                        |                        | AF 203203<br>CPDNAX              | Z18756 Chlamydophi                        |
|        | 33                                                      | ľ.             | 43                              |                                                 | 3                                                                          |                        | CHTOMPAAK                        | M73040 Chlamydophi                        |
|        | 34                                                      | 534            | 36                              |                                                 | <b>~</b> 10                                                                |                        | CPAJ561/<br>CPAJ5613             | AJ005613 Chlamydop                        |
|        | 36                                                      | 534            |                                 |                                                 | . i                                                                        |                        | CPAJ5614                         | AJ005614 Chlamydop                        |
|        | 37                                                      | 532            |                                 |                                                 | 4 4                                                                        |                        | CPAJ5615<br>CPAJ5618             | AJUUSEIS CRIAMYGOP<br>AJUUSEIB Chlamydop  |
|        | 36                                                      | 532            |                                 |                                                 | i —                                                                        |                        | CPJ004875                        | AJ004875 Chlamydop                        |
|        | 40                                                      | 529            |                                 |                                                 |                                                                            |                        | AFZ69Z65<br>CHTMOMPXX            | Arzeszes chiamydop<br>L04980 Chlamydia p  |
|        | 42                                                      |                |                                 |                                                 | 0                                                                          |                        | CPJ004874                        | AJ004874 Chlamydop                        |
|        | 44                                                      |                | 8<br>7<br>8                     | 4 4<br>8 8                                      | 0 139<br>0 143                                                             | 5 C                    | AF269264<br>AF269264             | AF269264 Chlamydop                        |
|        | 45                                                      | Ŋ              |                                 |                                                 | 143                                                                        |                        | AF269263                         | AF269263 Chlamydop                        |
|        |                                                         |                |                                 |                                                 |                                                                            |                        |                                  |                                           |
|        |                                                         |                |                                 |                                                 |                                                                            |                        | ALIGNMENTS                       |                                           |
|        | ,                                                       |                |                                 |                                                 |                                                                            |                        |                                  |                                           |
|        | AF131889<br>LOCUS<br>DEFINITION<br>ACCESSION<br>VERSION | 1 CON          | AF1<br>Chl<br>Com<br>Com<br>AF1 | AF131889<br>Chlamydia<br>complete c<br>AF131889 | 1170<br>a pneumoni<br>cds.                                                 | 70 by<br>oniae<br>4545 | NA BC<br>c outer membrane        | T. 31-MAR-1999<br>protein (MOMP) gene,    |
|        | KEYWORDS                                                |                | . [                             | ماسي                                            | nh:12                                                                      | Ē                      | 4                                |                                           |
|        | SOURCE                                                  | ISM            | Ch1                             | amydd<br>amydo<br>teria                         | phila p<br>phila p<br>Chlam                                                | neum<br>neum<br>vdia   | hlamydiaceae;                    | Chlamydophila.                            |
|        | REFERENCE<br>AUTHORS<br>TITLE                           | ыS             | Sri<br>Mul                      | (base<br>ram, S<br>tiple                        | 1 (bases 1 to 1170)<br>Sriram,S., Mitchell,W.M. Multiple sclerosis associa | 1170<br>hell<br>sis    | and Stratton,C<br>ated with Chla | a pneumoniae infection                    |
|        | JOURNAL                                                 |                | Neu                             | rolog                                           | NS<br>IY 50 (2                                                             | , 5                    | 71-572 (1998)                    |                                           |
|        | MEDLINE<br>REFERENCE<br>AUTHORS                         |                | 981<br>2<br>Mit                 | 98145402<br>2 (bases<br>Mitchell,W              | 12<br>es 1 to<br>1, W.M.,                                                  | 1170)<br>Tharp,        | )<br>p,A.C., Stratton,C.W. and   | d Sriram,S.                               |
|        | TITLE                                                   |                | Dir                             | ect 5                                           | 뒽                                                                          | on                     |                                  |                                           |

Fri Feb

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us-09-391 4606-9.rpr

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Copyright (c) 1993 - 2000 Compugen Ltd.
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February 7, 2002, 21:38:07 ; Search time 96.2 Seconds
(without alignments)
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Minimum DB seq length: 0 ... Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| ٠         | Description   | hypothetical 76K p | Ω      | CHLPN 76 kDa homol | hypothetical prote | probable membrane |        | extracellular matr | EF protein - Strep | Htr7 transducer (i | halobacterial tran | Htr14 transducer [ | R27-2 protein - Tr | hypothetical prote | transducer protein | probable secreted | transducer protein | Htrl transducer (i | halobacterial tran | Htr5 transducer [i | lmp1 protein - Myc | methyl-accepting c | nucleolar phosphop | related to transcr | Htr2 transducer [i | transducer protein | hypothetical prote | tail fiber protein | phage lambda-relat | surface antigen sp |
|-----------|---------------|--------------------|--------|--------------------|--------------------|-------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ΙĐ            | 140729             | D72042 | E86581             | G71490             | C85693            | G64887 | T31110             | S33441             | E84327             | T46811             | F84194             | T30296             | T34434             | T44938             | T34852            | A47190             | E84318             | T46810             | F84327             | T30822             | C82206             | 151618             | T50985             | A84328             | T44946             | T22523             | T14650             | T14968             | 806839             |
|           | 80            | 7                  | ~      | 7                  | 7                  | ~                 | 7      | 7                  | 7                  | ~                  | 7                  | N                  | 7                  | 7                  | ~                  | 7                 | П                  | ~                  | 7                  | 7                  | 7                  | ~                  | ~                  | ~                  | ~                  | Н                  | 7                  | ~                  | 7                  | 7                  |
|           | Length        | 715                | 651    | 651                | 647                | 973               | 1122   | 2055               | 1822               | 545                | 545                | 627                | 1128               | 2232               | 544                | 1156              | 536                | 536                | 810                | 810                | 1365               | 641                | 990                | 892                | 764                | 765                | 1262               | 860                | 978                | 1561               |
| æ         | Query         | 97.9               | 96.8   | 96.8               | 20.0               | •                 |        | 8.1                | •                  |                    |                    |                    |                    | 7.4                | •                  | 7.0               | 7.0                | 7.0                | 7.0                | 7.0                | 7.0                | 6.9                | 6.9                | 6.9                | 9.9                | 6.9                | 6.8                | 6.7                | 6.7                | 6.7                |
|           | Score         | 2214               | 2188   | 2188               | 451.5              | 201               | 188    | 182.5              | 177.5              | 174.5              | 174.5              | 171                | 166.5              | 166.5              | 160.5              | 158.5             | 158                | 158                | 158                | 158                | 158                | 156.5              | 156                | 155                | 154.5              | 154.5              | 154.5              | 152.5              | 152.5              | 152                |
|           | Result<br>No. | 1                  | 7      | Э                  | 4                  | 5                 | 9      | 7                  | 80                 | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 26                 |                    | 28                 | 29                 |

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421 ALEAALGKAGQQQGILNALGQIASAAVVSAGVLPLQQVL 459

| intermediate filam | probable exonuclea | surface antigen A | transducer protein | hypothetical prote | probable membrane | saliva-interacting | hypothetical prote | surface-located me | transducer protein | microtubule-associ | hypothetical prote | hypothetical prote | Htr8 transducer [1 | multifunctional am | Htrl6 transducer [ |
|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S24545             | T03465             | A60338            | T44253             | E70803             | S56032            | A60988             | T35781             | JC6009             | T48897             | T13564             | н83098             | D86164             | H84305             | \$18644            | F84219             |
| 7                  | ~                  | 7                 | Н                  | 7                  | ~                 | 7                  | 7                  | -                  | 7                  | 7                  | 7                  | N                  | 7                  | -                  | 7                  |
| 582                | 1238               | 1528              | 642                | 729                | 881               | 1556               | 1147               | 1302               | 778                | 5327               | 446                | 571                | 643                | 1714               | 628                |
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| 151.5              | 151.5              | 150.5             | 1.49               | 1.48               | 1.48              | 1.48               | 147.5              | 147.5              | 1.47               | 147                | 146.5              | 146.5              | 146.5              | 146                | 145.5              |
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|                    | ٠                  |                   |                    |                    |                   | •-                 |                    | •                  | 3.                 |                    |                    |                    |                    |                    |                    |

## ALIGNMENTS

|              | _                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|--------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| PECIIL       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 140729       | 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| hypc         | hypothetical 76k protein - Chlamydophila pneumoniae (strain AR39)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| C; SF        | G:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| C; Ac        | C. Accession: I40729                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| R; Pe        | R; Perez-Melgosa, M.; Kuo, C.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| A; Ti        | Interc. Immun. 02, 800 900, 1394<br>Affile: Isolation and characterization of a gene encoding a Chlamydia pneumoniae 76                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| A; Re        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| A; Ac        | A; Accession: I40729                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| A; St        | A;Status: translated from GB/EMBL/DDBJ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| A; MC        | A) MOLECULE (1Per JDA)<br>A Readdings 1-715 (APES)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| A; CI        | A)Crosis-references: GBLL23921; NID:9435961; PIDN:AAA23117.1; PID:9435962                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| A; E         | 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <u>.</u>     | omment. This is the hypothetical transfacton of a sequence that was reported as t                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| nō<br>,.     | . 97.98;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|              | Best Local Similarity 98.9%; Pred. No. 1.4e-110;<br>Matches 454; Conservative 2; Mismatches 3; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| - ô          | 1 MVNPIGPGPIDETERTPPADLSAOGLEASAANKSAEAORIAGAEAKPKESKTDSVERWSI 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| , <u>, ,</u> |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 2            | 23/ LVIRTIGEGETIUDIERIKFADLDANGELEASAANNSAEAUKIAGAEANFKESKIUSVEKWSI 510                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Óy           | 61 LRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT 120                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| qá           | 317 .LRSAVNALMSLADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTFDDYKTQAQTAYDT 376                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|              | 131 TOWCHELANTOARIVETORANMIERAMAMERDOMATAARINDMAKARATUSOAATMETANU 100                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Ž            | TETSTSTANDING SEQUENTIAND SET STANDARD SET S |
| q            | 377 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAVKVGAQITELAKY 436                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| ζ            | 181 ASDNOAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAOSLVD 240                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| _ q.         | 437 ASDNQAILDSLGKLTSFDLLQAALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD 496                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| Qy           | 241 QTDATATQIEKDGNAIGDAYFAGONASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQ 300                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| qa           | 497 OTDATATQIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQ 556                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| Qy           | 301 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL 360                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| Q .          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |

J138)

Chlamydophila pneumoniae (strain

Ouchi, K.; Shiba,

CHIPN 76 kDa homolog\_1 (CT622) [imported] - Chlamydophila pneumoniae (strail C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (strail C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 02-Mar-2001 C:Accession: E86581 # Kimpto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000 A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A; Reference number: A86491; MUID:20330349 A; Accession: E86581 A; Status: preliminary

A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-651 <STO> A; Cross-references: GB:BA000008; NID:g8979100; PIDN:BAA98935.1; GSFDB:GN00142 A; Experimental source: strain J138 C; Genetics: A; Genetics

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Conserved hypothetical protein CP0018 [imported] - Chlamydophila pneumoniae (strains CWI N.Alternate names: chlpn 76 kda homolog_1 (ct622); hypothetical protein CP00728

N.Alternate names: chlpn 76 kda homolog_1 (ct622); hypothetical protein CP00728

C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C.Species: Chlamydophila pneumoniae, Chlamydia II-May-2000

C.Species: Chlamydophila pneumoniae, C.; Fan, J.; Olinger, L.; Grimwod, J.;

Nature Genet. 21, 385-389, 1999

A.Title: Comparative genomes of clamydia pneumoniae and C. trachomatis.

A.Reference number: A72000; MUID:99206606

A.Reference number: A72000; MUID:99206606

A.Residues: 1.651 ARN>

A.Residues: 1.651 ARN>

A.Residues: 1.651 ARN>

A.Residues: 1.651 ARN>

A.Reference number: A81500; MUID:201555

A.Reference number: A81500; MUID:2015055

A.Reference number: A81500; MUID:2016055

A.Reference number: A81500; MUID:201605

A.Reference number: A81500; MUID:201605

A.Reference number: A81500; MUID:201606

A.Reference number: A81500; MUID:20160
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 300
 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL 360
 DDAENETASILMSGFROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK 420
 LRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT 120
 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKY 180
 Gaps
 1 MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI 60
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 ;
0
 651;
 Indels
 Length
 96.8%; Score 2188; DB 2;
98.9%; Pred. No. 3e-109;
iive 1; Mismatches 4;
ALEAALGKAGQQQGILNALGQIASAAVVSAGVLPLQQVL 715
 ALEAALGKAGQQQGILNALGQIASAAVVSAGVLP 454
 Conservative
 Query Match
Best Local Similarity
Matches 449; Conserv
 C;Genetics:
A;Gene: CPn0728; CP0018
 PIR: H71490).
 61
 61
 121
 181
 181
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 361
 421
 121
 677
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hypothetical protein CT622 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
N.Alternate names: chlpn 76kda homolog CT622
C.Species: Chlamydia trachomatis
C.Species: Chlamydia trachomatis
C.Species: Chlamydia trachomatis
C.Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C.Accession: G71490
R.Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitc Science 282, 754-759, 1998
C.Accession: G71490
A.Reference number: A71570; MUID:99000809
A.Reference number: A71570; MUID:99000809
A.Residues: 1-647 ARN>
A.Molecule type: DNA
A.Residues: 1-647 ARN>
A.Residues: 1-647 ARN>
A.Residues: 1-647 ARN>
A.Cross-references: GB:AE001333; GB:AE001273; NID:g3329068; PIDN:AAC68226.1; PID:g3
 ö
 360
 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL 360
 DDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK 420
 240
 300
 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKY 180
 180
 LRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT 120
 Gaps
 9
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 181 ASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD
 QTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQ
 1 MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI
 ..
O
 Length 651;
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3e-109;
 ALEAALGKAGQQQGILNALGQIASAAVVSAGVLP 454
 Pred. No. 3e-1
1; Mismatches
 96.8%; Score 2188; 98.9%; Pred. No. 3e
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PIDN: AAC74454.1; PID: 917876
 A;Cross-references: GB:AE000234; GB:U00096; NID:91787633; PIDN:AAC74454.1; PID:917876
 Isono, K.; Itoh, T.; Kasai,
Nishio, Y.; Oshima, T.; Sal
 N.T.; Burland, V.; Riley, M.;
 A; Molecule type: DNA
A; Residues: 1-1122 <BLAT>
A; Coss. references: GB: AE000234; GB: U00096; NID: 91787633; PIDN: AAC74454.1; PID: 91
A; Experimental source: strain K-12, substrain MG1655
A; Experimental source: strain K-12, substrain MG1655
A; Riaba, H.; Baba, T.; Fujita, K.; Hayashi, K.; Inada, T.; Isono, K.; Itoh, T.; Ka: MA McManura, K.; Motomura, K.; Nakade, S.; Nakamura, Y.; Nashimoto, H.; Nishio, Y.; Oshima, T.; DNA Res. 3, 563-377, 1996
A; Tille: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding A; Reference number: 216603; MUID: 97251357
A; Accession: T09189
 probable tail fiber protein GP37 - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jul-2000
C;Accession: G64887; T09189
R;Blattner, F:R.: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; R.A.: Dose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
 511 QKGTVQLSNATNSTSEM----LAATPKSVKAAYDLANGKYTAQDATTAQKGIVQLSSATN 566
 AVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTFT 123
 86 TSRSADVDSTTATAPTPPPFTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIK
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 457 AVALEDAS-----TTKKGIVQLSSATNSTSESLAATPKAVKAAYELANGKYTAQDATTA
 171 ASSSAGTASTKATEASKSAAAESSKSAAATSAGAAKTSET----NAAVSQQSAATSAS
 146 DTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALL
 -----NIDSAKAAIATAKTQIAE-----AQKKFPDSPILQEAEQMVIQAEKDLK
 397 ASKDEATROASAAKSSATTASTKATEAAGSATAAAQSKSTAESAATRAETAAKRAEDIAS
 8 GPIDETERTPPA----DLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRS
 OSVANNNKAAELLKEMODNPVVPGKTPA----IAQSLVDQTDATATQIEKD----
 -----GNAIGDAYFAGQNASGA---VENAKSNNSIS------
 A;Status: nucleic acid sequence not shown; translation not shown
 Length 1122
 A; Reference number: A64720; MUID: 97426617
 NIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSG--
 ||: || ||::|| SASETLAATPKAVKAAND------NANGRVPSARKVNGKAL
 SAAÄALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAGVL
 203;
 8.3%; Score 188; DB 2;
23.0%; Pred. No. 0.014;
iive 68; Mismatches 203;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 FRQMIHMFNTENPDSQAAQQELAAQARAAKAAGD-
 Conservative
 <AIB>
 Similarity
 A; Molecule type:
A; Residues: 3-112
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 probable membrane protein of prophage CP-933X Z1918 [imported] - Escherichia coli (strai C; Species: Escherichia coli (Species: Escherichia coli (C; Species: Escherichia coli (C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 (C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 (F; Date: 16-Feb-2001 (F; Date: 17: Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 (F; Appodaca, A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A; Reference number: A68480; MUID:21074935; PMID:11206551
 GSPDB:GN00145; UWGP:Z1
 part of a sequence
 14;
 14;
 RSAVNALMSLADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTSDDY----KTQAQTAY 118
 119 DTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELA 178
 238
 109 SGLENATILAEYETKMADLMAALQDMERLAKQKAEVTRIKEALQEKQEVID---KLNQLV 165
 355 -----RVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAK---A 405
 Gaps
 52
 2 VNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSIL 61
 26 LEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSS 85
 KYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSL
 239 VDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAALATAKTQIAE
 AQKK ---FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSI-
 t
t
 Indels 130;
 Length 647;
 A Status: preliminary
A Molecule type: DNA
A Molecule type: DNA
A Residues: 1-973 <ST0>
A Cross-references: GB.AE005174; NID:g12514847; PIDN:AAG56007.1;
A Experimental source: strain 0157:H7, substrain EDL933
A Genetics:
A Genetics:
 homologous
 Length 973;
 Indels
 AGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAG 451
 Ital source: serotype D, strain UW-3/Cx This sequence was originally identified as
 Query Match 8.9%; Score 201; DB 2; L. Best Local Similarity 22.9%; Pred. No. 0.0024; Matches 120; Conservative 64; Mismatches 210;
 DB 2;
 Query Match
Best Local Similarity
Matches 138; Conserv
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PIR:E72042).
 C;Genetics:
A;Gene: CT622
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| Db 150 AADSARAASTSAGQAAS-SAQSASSAGTASTKATEASKSAAAAESSKSAAATSAGAAKT 208  Qy 124 STSLADIOAALVSLQDAVTNIKDTAATDEETARAEWETKNADAIKVGAQITELAKYASD 183                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Oy 342 GGSKQOGS-SIGSI-RVSMLLDDAENETASILMSGFROMIHMFNTENPDSQ 390  1696 TAKQNEGTKAINDVPQTPTAKTDAKNAVDQAATDKKSAIENDPALTREEKD 1746  OY 391 AAQQELAAQARAKAAGDDSAAAALADAQKALEAALGKAGQOGGILNALGQIASA 445                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| SULT 7 Litacellu Litacellu Species: 30 Actes: 00 Actes: | Ouery Match Best Local Similarity 23.6%; Score 1775; DB 2; Length 1822; Best Local Similarity 23.6%; Pred, No. 0.095; Indels 103; Gaps 21; Best Local Similarity 23.6%; Pred, No. 0.095; Indels 103; Gaps 21; Oy 13 TEKTEPADLSAGGLEASANKSAEORIAGAEAKRAKENEEEBATKVEKLAEDTEKA 1260  Oy 11 LENAKAAELAGEKSESTERSAD-VUSTTATAFTPEPEPERSONYRITOAGATATETETSLAD 129  ON 71 LADKLGASSNSSSTRSAD-VUSTTATAFTPEPEPEDYKTOAGATATETETSLAD 129  ON 71 LADKLGASSNSSSTRSAD-VUSTTATAFTPEPEPEPEDYKTOAGATATETETSLAD 129  ON 71 LADKLGASSNSSSTRSAD-VUSTTATAFTPEPEPEPEDYKTOAGATATETAKASAD 1309  ON 130 IQAALVSLQDAVTHKATAATDETALA-TENETKANDIKTGAAGATTATAKASADAN 1364  ON 130 IQAALVSLQDAVTHKATAATDETALA-TENETKANDIKTGAAGATTAAKASADAN 1364  ON 130 IQAALVSLQDAVTHKATAATDETALA-TENETKANDIKTGAAGATTAAKASADAN 1364  ON 241 OTDATA-TOIEKDGNAIGDAYAGACAAELKEMONPWVEKTPATAAGSLVD 240  DD 1310 LEKAAVDARAANADAAKAADANSAAAAAAAAAAAAAAAAAAAAAAAAAA |
| OY 283 DEAKAIATRIQIARAO(K-KEPDSPILOEAROMYIQAEKDIKNIKRADGSDVPNPGTTV 341  1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | HIT/ transducer limported; - Halobacterium Sp. NRC-1<br>C:Species: Halobacterium sp. NRC-1<br>C:Spate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

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TPAIAQSLVDQTDAT --
 Query Match
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Matches 120; Conserv
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Les 100; Conserv
 <ST0>
 A; Accession: F84194
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-627 <STC
 Query Match
Best Local Si
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 Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, Y. 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483
A; Accession: E84327
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-545 <STO>
 C; Accession: T46811
R; Rudolph, J; Nordmann, B.; Storch, K.F.; Gruenberg, H.; Rodewald, K.; Oesterhelt, D. FEMS Microbiol. Lett. 139, 161-168, 1996
A; Title: A family of halobacterial transducer proteins.
A; Reference number: Z24094; MUID:96275896
 17;
 A; Gross-references: GB: AE004437; NID: 910581214; PIDN: AAG19985.1; GSPDB: GN00138 C; Genetics:
 PID:91435132
 RESULT 10
746811
halobacterial transducer protein V [imported] - Halobacterium salinarum
C; Species: Halobacterium salinarum
C; Species: Halobacterium salinarum
C; Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 15-Sep-2000
 LAKYASDNQAILDSLGKLT----SFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGK 230
 TPAIAQSLVDQTDAT-----ATQIEKDGNAIGD--AYFAGQNASGAVENAKSNNS 278
 |: |: |: | |: |
398 IAELIEEVQSQTATTVEEI--------RVAEQRVNDGAAAVEETVDAFGAVTENI 444
 118 EEERA-----EAERAREKAEQKQAEAER----QTAEAESAKQDARERSAEIEQLAADLESQ 169
 SLADIQAALVSLQDAVTNIKDT-----AATDEE----TAIAAEWETKNADAIKVGAQITE 176
 -VDDIATISQATA 483
 Gaps
 ETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSL 71
 ADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPT-SDDYKTQAQTAYDTI-----FTST
 ISN-IDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNP
 GTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELA
 89;
 Length 545;
 A;Residues: 1-545 <RUD>
A;Cross-references: EMBL:X95589; NID:91435130; PIDN:CAA64842.1;
 A;Gene: htpV
C;Superfamily: Halobacterium salinarum transducer protein htrI
 Superfamily: Halobacterium salinarum transducer protein htrI
 Indels
 484 DRAENVSAASEEQ-TASITEVISSLQSLAAQADTLEDRLN 522
 Ouery Match 7.7%; Score 174.5; DB 2; Best Local Similarity 21.7%; Pred. No. 0.029; Matches 100; Conservative 79; Mismatches 192;
 398 AQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGILN 437
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 445 QETTDGVQE-----ISQAMDEQAQRSERVVSS---
 A; Molecule type: DNA
E84327
 A; Accession: T46811
 C; Genetics
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Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lask f. Leithauser, B.; Kellar, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; J. Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hcu, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M. A;Tille: Genome sequence of Halobacterium species NRC-1. 17; 27; A;Cross-references: GB:AE004437; NID:910579976; PIDN:AAG18922.1; GSPDB:GN00138 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001 C;Accession: F84194 ADKLGIASSNSSSTSRSADVDSTTATAPTPPPPT-SDDYKTQAQTAYDTI-----FTST 125 SLADIQAALVSLQDAVTNIKDT----AATDEE----TAIAAEWETKNADAIKVGAQITE 176 ---ATQIEKDGNAIGD--AYFAGQNASGAVENAKSNNS 278 ISN-IDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNP 337 IAELIEEVQSQTATTVEEI------RVAEQRVNDGAAAVEETVDAFGAVTENI 444 GTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELA 397 -- VDDIATISQATA 483 PALDESVPGAFGESITEMADSLEAYTAELEDKTAELEHQQAELERQSEQLRALVDALSEA 204 ADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTSDDYKTQA-----QTAYDTIFTS 124 Gaps ETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSL 71 PPADLSAQGLEASAANKSAEAQRIAGAEAKPK----ESKTDSVERWS-ILRSAVNALMSL 71 LAKYASDNQAILDSLGKLT----SFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGK Indels 122; Length 545; Length 627; Superfamily: Halobacterium salinarum transducer protein htrI :| :| :| :| || 484 DRAENVSAASEEQ-TASITEVTSSLQSLAAQADTLEDRLN 522 7.6%; Score 171; DB 2; L. Lalarity 23.4%; Pred. No. 0.053; Conservative 87; Mismatches 184; AQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGILN 437 7.7%; Score 174.5; DB 2; .larity 21.7%; Pred. No. 0.029; Conservative 79; Mismatches 192; Htrl4 transducer [imported] - Halobacterium sp. NRC-1 445 QETTDGVQE-----ISQAMDEQAQRSERVVSS---q

| QY 125 TSLADIQAALVSLQDAVTNIKDIAATDETAIAAEWETKNADA 167                                                                                                                                                                           |                                                                                                                                                                                                                                              |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 276 NNSISNIDSAKAAIATAKTQIAEAQKKFPDSP-ILQEAEQMYIQAEKDLAEETREQ 420 276 NNSISNIDSAKAAIATAKTQIAEAQKKFPDSP-ILQEAEQMYIQAEKDLKNIKP 328 1                                                                                               | RESULT 13 T34434  hypothetical protein K06A9.la - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 18-Feb-2000 C;Accession: T34434 |
| :     :                                                                                                                                                                                                                         | RyGeisel, C.; Gattung, S. submitted to the EMBL Data Library, December 1996 AyDescription: The sequence of C. elegans cosmid K06A9. AyReference number: Z21525 AyAccession: T34434 AyStatus: preliminary, translated from GB/EMBL/DDBJ       |
| OY 419 OKALEAALGKAGOQOGILNALGQIASAAVVSAG 451      :                                                                                                                                                                             | A; Molecule type: DNA<br>A; Residues: 1-2232 <gel><br/>A; Cross-references: EMEL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a<br/>A; Experimental source: strain Bristol N2; clone K06A9</gel>                                      |
|                                                                                                                                                                                                                                 | A;Gener.CESP:K06A9.la<br>A;Map position: X<br>A;Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 20                                                                                                          |
| C:Species: Trypanosoma cruzi<br>C:Date: 22-0ct-1999 #sequence_revision 22-0ct-1999 #text_change 17-Mar-2000<br>C:Accession: T30296<br>R:Otsu, K.: Donelson, U.E.; Kirchhoff, L.V.<br>Mol. Biochem. Parasitol, 57, 317-330, 1993 | Query Match 7.4%; Score 166.5; DB 2; Length 2232; Best Local Similarity 19.7%; Pred. No. 0.47; Matches 79; Conservative 70; Mismatches 174; Indels 79; Gaps 11;                                                                              |
| Aritle: Interruption of a Trypanosoma cruzi gene encoding a protein containing 14-amind A.Reference number: 220813; MUID:93165082 A.Accession: T30296 A.Stetus: preliminary: translated from GB/EMBL/DDBJ                       | QY 4 PIGPGPIDETERTPPADLSAQGLEASAANKSAEAGRIAGAEAKPKESKTDSVERWS 59                                                                                                                                                                             |
| A;Molecule type: DNA<br>A;Residues: 1-1128 <ots><br/>A;Cross-references: EMBL:L04603; NID:g385171; PID:g1256742; PIDN:AAA96494.1<br/>C;Superfamily: neurofilament triplet H protein</ots>                                       |                                                                                                                                                                                                                                              |
| Query Match Best Local Similarity 23.9%; Pred No. 0.2; Length 1128; Matches 110; Conservative 7.1: Mismatches 202: Indels 77: Gaps 19:                                                                                          | OY 118 YDTIET-STSLADIQAALVSLQDAVTNIKDTAATDEETALAAEWETKNADAIKVGACITE 176  1                                                                                                                                                                   |
| IDETERTPADISAQGLEASAANKSAEAQRIAGABA-KYRESKTDSVERWSILKSA 64                                                                                                                                                                      | 237 SLVDOTDATATOIEKDGNAIGDAYFAGONASGAVENAKSNNSISNIDSAKAAIATAK                                                                                                                                                                                |
| OY 65 VNALMSLADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTSDDXKTQAQTAYDTIFTS 124  DD 702 EKQKAABATKVABAEKQKAAEATKVABAEKQKAAEATTK 753                                                                                                       | Db 794 ALLTSTQQSVSTNSPGSTVTRPSTVSGSTSGSSTVTVGSTEASTSGSSVASSSPAPSTSQ 853 OY 294 TQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTVGGSKQQ 347                                                                                                     |
| 125 ISLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITEL                                                                                                                                                                       |                                                                                                                                                                                                                                              |
| QY 178 AKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPEKT 231                                                                                                                                                               | bb 904 STTIGSTQGSTSPGISTTSEEMTSQGSTQTPGS 936                                                                                                                                                                                                 |
| OY 232 PAIAQSLVDQTDATATQ1EKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDS 284                                                                                                                                                                | ă Li di                                                                                                                                                                                                                                      |

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Length 1156; Indels

DB 2;

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-- LADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLA 128
 DIQAA-LVSLQDAVTNIKDTAATDEETAIAAE-WETKNADAIKVGAQITELAKYASDNQA 186
 DSAAAHAEKAADAADAAADAAGEADDYANKAKAWA---ADSVAA---AELAAKAVDDAR 535
 AVEAAAREAEAEKLAHDTEOSLAEAREMA--AAEAEDREAARN----AATEADRLDAQT 588
 TQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDS 306
 PILOEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENE 366
 - IHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAALADA 418
 689 VRNFLTTGIHEAAALDRRVDILRILGDNPGK-----AVKDAAQAALDDGSPSALHAF 740
 : : | | | : | : | | : | DASKTKAAREJAAAGALAAAQTATQAAAAAGISAAATARDSAAAAQQA
 ILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATA
 ----KDFISRAEAAYASGDTASALANGR------KAAVNLISTTIGTWSRAAAEY
 427 AVÄAQASGAAQSEAAVARAAAEADAQAARA----TKAANRAQSLANTAASAAAARKAA
 12 ETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMS-
 FRALPDKAALDDRATILTILNTAGPYTAAAAQVA----LEGTSWMR
 QKAL - - BAALGKAGQQQGILNALGQIASAAVVSAGVLPLQQVLWIR
 75; Mismatches 227;
 Score 158.5; DF pred No. 0.54;
 21:38:09
 7, 2002,
 21.2%;
 Conservative
 completed: February.
He: 7098 sec
 367 TASILMSGFROM----
 Best Local Similarity
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 Richard, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.

Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4654, 1996

Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4654, 1996

A.Title: Signal transduction in the archaeon Halobacterium salinarium is processed throu A.Reference number: 222804; MUID:96209786

A.Accession: T44938

A.Accession: T44938

A.Accession: T44938

A.Accession: T44038

A.Accession: T44038

A.Residues: 1-544 <2HA>
A.Residues: 1-544 <2HA>
A.Residues: 1-544 <2HA>
A.Residues: 1-545 <2HA>
A.Accession: T44038

A.Accession: Alaboracterium salinarum transducer protein htrI
C.Superfamily: Halobacterium salinarum transduction; transmembrane protein
F; 246-502/Region: MCP signalling domain similarity
 probable secreted protein - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: OS-Nov-1999 *sequence_revision OS-Nov-1999 #text_change OS-Nov-1999 C; Accession: T34852 R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1999 A; Reference number: 221559 A; Reference number: 221559 A; Accession: T34852 A; A; A; Detailminary; translated from GB/EMBL/DDBJ
 A;Cross-references: EMBL:AL035478; PIDN:CAB36606.1; GSPDB:GN00070; SCOEDB:SC2G5.19 A;Experimental source: strain A3(2) C;Genetics: A;Gene: SCOEDB:SC2G5.19
 19;
 175 TELAKYASDNQAILDSLGKLT----SFDLLQTALLQSVANNNKAAELLKEMQDNPVVP 228
 GKTPAIAQSLVDQTDAT-----ATQIEKDGNAIGD--AYFAGQNASGAVENAKSN 276
 --- LQEAE 313
 395 KDIAELIEEVQSQTATTVEEIRVAEQRVNDGAAAVEETVDAFGAVTENIQETTDGVQEIS 454
 Gaps
 118 EEERA----EAERAREKAEQKQAEAER-QTAEAQSQTGRTGTQRE---IEQLAADLESQ 168
 125 TS-----LADIQAALVSLQDAVTNIKDTAATDEE----TAIAAEWETKNADAIKVGAQI 174
 340 -----IAELISDIAEQTNMLALNANIEAARAGSGGGTNGDGFAVVADEVKELATESQRSA 394
 ETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSL 71
 ADKLGIASSNSSSTSRSADVDSTTATAPTPPPPT--SDDYKTQAQT-----AYDTIFTS
 228 ASREATGGAKEIQVASQTVSESVQEI--AAGTDDQREQLESVAEEMDSYSATVEEVAATA
 Q------MVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDA
 95;
 Length 544;
 Indels
 183;
 DB 2;
 0.16;
 22.3%; Pred. No. 0.16, ive 74; Mismatches
 277 NSISN-IDSAKAAIATAKTQIAEAQKKFPDSPI----
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QADTLEDRINEFRTEATGTAHGERTDAPAGOSD 544
 Score 160.5;
 364 ENETASILMSGFR-QMIHMFNTENPDSQAAQQE
 Query Match
Best Local Similarity 22.3%
Matches 101; Conservative
 A; Molecule type: DNA
A; Residues: 1-1156 <OLI>
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C;Accession: T
R;Zhang, W.; E
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## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 7, 2002, 21:42:42 ; Search time 76.51 Seconds
(without alignments)
221.877 Million cell updates/sec Run on:

US-09-391-606-9
2261
1 MVNPIGPGPIDETERTPPAD.....SAAVVSAGVLPLQQVLWIRA 463 Title: Perfect score: Sequence:

BLOSUM62 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | P76072     | Q48318 halobacteri |            |            |            | Q9hp81 halobacteri |            |            |            |            |            |            |            | P03764 bacteriopha |            | Q02113 bacillus su | P11657 streptococc | P80544 staphylococ |            |            | P28968 equine herp |            | P25054 homo sapien | mus m      | _          |            | P33955 halobacteri | P02468 mus musculu | P26039 mus musculu | Q61315 mus musculu | _          | 2844 | O14066 schizosacch |
|-----------|---------------|------------|--------------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|--------------------|------------|--------------------|--------------------|--------------------|------------|------------|--------------------|------------|--------------------|------------|------------|------------|--------------------|--------------------|--------------------|--------------------|------------|------|--------------------|
| SUMMARIES | ID            | STFR_ECOLI | HTR5_HALN1         | HTR1_HALN1 | HTR4_HALN1 | HTR4_HALSA | HTR2_HALN1         | HTR2_HALSA | SPAP_STRMU | HRPK_PSESY | SPAA_STRDO | FLJB_SALTY | YJH8_YEAST | HTR6_HALSA | STF_LAMBD          | SYEP_DROME | CWBA_BACSU         | PAC_STRMU          | MRSP_STAAU         | MSB2_YEAST | HTR6_HALN1 | VGLX_HSVEB         | LMG1_HUMAN | APC_HUMAN          | NCR1_MOUSE | TALA_DICDI | FLJB_SALAE | HTR1_HALSA         | LMG1_MOUSE         | TALI_MOUSE         | Σ                  | TRC4_ECOLI | - 1  | YFF9_SCHPO         |
|           | 80            |            | Н                  | ~          | 7          | 1          | П                  | -          | -          | Н          | 7          | ٦          | ~1         | ٦          | Н                  |            |                    | <del>, - 1</del>   |                    | -          | Н          |                    | -          | -                  | -          | Н          | П          | -                  | П                  | <b>~</b>           | Н                  | Н          |      |                    |
|           | Length        | 11         | 545                | 535        | 810        | 810        | 763                | 7          | 1561       | 641        | 1528       | 505        | 881        | 778        | 774                | 1714       | 705                | 1565               | 1637               | 1306       | 778        | 797                | 1609       | 2843               | 2453       | 2492       | 200        | 535                | 1607               | 2541               | 2845               | 1061       | 1969 | 1379               |
| æ         | Query         |            | 7.7                | 7.0        | 7.0        | 7.0        | 9.8                | e.9        | 6.7        | 6.7        | 6.7        | 6.5        | 6.5        | 6.5        | 6.5                | 6.5        | 6.4                |                    | 6.4                | 6.3        | 6.3        | 6.1                | 6.1        | 6.1                | 6.1        | 6.1        | 6.1        | 6.1                | 6.1                |                    |                    | 0.9        |      | 9.0                |
|           | Score         | 188        | 174.5              | 158        | 158        | 158        | 154.5              | 154.5      | 152        | 151.5      | 150.5      | 148        | 148        | 147        | 146.5              | 146        | 145                | 145                | 144                | 143.5      | 142.5      | 139                | 138        | 138                | 137.5      | 137.5      | 137        | 137                | 137                | 136                | 136                | 135.5      | 35   | 135                |
|           | Result<br>No. | 1          | 7                  | m          | 4          | 'n         | 9                  | 7          | œ ·        | on i       | 10         | 11         | 12         | 13         | 14                 | 15         | 16                 | 17                 | 18                 | 19         | 20         | 21                 | 22         | 23                 | 24         | 25         | 26         | 27                 | 28                 | 29                 | 30                 | 31         | 32   | 33                 |

| 401 streptococc | 212 neurospora |         |            |            |            |           |            | 247500 escherichia |            |            | _          |
|-----------------|----------------|---------|------------|------------|------------|-----------|------------|--------------------|------------|------------|------------|
| P19             | P19            | P70     | P40        | P25        | 013        | P20       | 052        | 047                |            | P16        | . P42      |
| M12_STRPY       | NIT2_NEUCR     | APC_RAT | YEY8_YEAST | SED4_YEAST | TCOF_HUMAN | TRX_DROME | MOTD_RHIME | CE05_ECOLI         | ST20_CANAL | SSP5_STRGN | HTR2_NATPH |
| г               | -              | П       | П          | Н          | Н          | -         | Н          | Н                  | Н          | Н          | -          |
| 564             | 1036           | 2842    | 573        | 1065       | 1411       | 3726      | 475        | 490                | 1230       | 1500       | 534        |
| 5.9             | 5.9            | 5.9     | 5.9        | 5.8        | 5.8        | 5.8       | 5.7        | 5.7                | 5.7        | 5.7        | 5.7        |
| 134             | 134            | 134     | 132.5      | 131.5      | 131.5      | 130.5     | 130        | 130                | 130        | 129        | 128.5      |
| 34              | 32             | 36      | 37         | 38         | 39         | 40        | 4          | 42                 | 43         | 44         | 45         |

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 :|| :: :|| :: ---ESAASSASTATTKAGEATEQ- 347
 304 PDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDA 363
 ----ASAAARSASAAKTSETNAKASETSAESSKTAAASSASSAASSASASK--DEA 400
 401 TRQASAAKSSATTASTKATEAAGSATAAAQSKSTAESAATRAETAAKRAEDIASAVALED 460
 STSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASD 183
 NQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTD 243
 258 SSAASSATAAGNSAKAAKTS----ETNARSSETAAGQSASAAAGSKTAAASSASAASTS 312
 ATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKF 303
 364 ENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQA-----RAAKAAGDDSAAAALAD 417
 AVNALMSLADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFT 123
 207 SETNAS-----ASLQSAATSASTATTKASEAATSA----RDAAASKEAAKSSETNASSSA 257
 Gaps
 8 GPIDETERTPPA----DLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRS 63
 MEDLINE-20504483; PubMed-11016950;
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 Pred. No. 0.012;
68; Mismatches 2
 Score 188;
 313 A-----GQASASATAAGKSA------
 Halobacterium sp. (strain NRC-1), and Halobacterium salinarium.
 418 AQKALEAALGKAGQQQGILNALGQIASA 445
 461 ASTT-----KKGIV----QLSSA 474
 SPECIES=H.salinarium; STRAIN=S9;
8.3%;
 Conservative
 NCBI_TaxID=64091, 2242;
 SEQUENCE FROM N.A.
 Similarity
 [2]
SEQUENCE FROM N.A.
 Halobacterium
 STRAIN=NRC-1
 Matches 103;
 Query Match
 Best Local
 348
 184
 64
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 17;
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 SERATAGAKEIQDASQTVSESVQEIAAGTDDQREQLESVAEEMDSYSATVEEVAATAQS 288
 278
 337
 397
 --VDDIATISQATA 483
 72 ADKLGIĄSSNSSSTSRSADVDSTTATAPIPPPPT-SDDYKTQAQTAYDTI-----FTST 125
 126 SLADIQAALVSLQDAVTNIKDT-----AATDEE----TAIAAEWETKNADAIKVGAQITE 176
 LAKYASDNQAILDSLGKLT-----SFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGK 230
 118 EEERA----EAERAREKAEQKQAEAER---QTAEAESAKQDARERSAEIEQLAADLESQ 169
 SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
 Gaps
 HTRI_HALNI STANDARD; PRT; 535 AA.
P3741; OHPPF6;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SENSORY RHODOPSIN I TRANSDUCER (HTR-I) (METHYL-ACCEPTING PHOTOTAXIS PROTEIN I) (MPP-I).
HTRI OR HTRI OR VNG1659G.
FUNCTION: POTENTIALLY INVOLVED IN CHEMO- OR PHOTOTACTIC SIGNAL
 398 IAELIEEVQSQTATTVEEI-------RVAEQRVNDGAAAVEETVDAFGAVTENI
 ETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSL
 170 ATEVG-ATLEAASDGDLTARVDATTDNAEIAEVATVVNDMLTTMERTIDEIQGFSTNVTT
 231 TPAIAQSLVDQTDAT-----ATQIEKDGNAIGD--AYFAGQNASGAVENAKSNNS
 279 ISN-IDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNP
 338 GTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELA
 Length 545;
 Indels
 FDD870389C2F428B CRC64;
 445 QETTDGVQE-----ISQAMDEQAQRSERVVSS-----
 7.7%; Score 174.5; DB 1;
21.7%; Pred. No. 0.024;
ive 79; Mismatches 192;
 :| :| :: :|: :|: || DRAENVSAASEEQ-TASITEVTSSLQSLAAQADTLEDRLN
 398 AQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGILN
 EMBL; AE005080; AAG19985.1; -.
EMBL; X95589; CAAG4842.1; -.
InterPro; IPR000122; Chemotaxis_transducer.
InterPro; IPR003660; HAMP.
 POTENTIAL.
 POTENTIAL
 POTENTIAL
 Iransducer; Transmembrane; Complete
IRANSMEM 10 30 POTENTI
 MM;
 Pfam; PF00015; MCPSignal; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
 64
100
57070 M
 Local Similarity 21.7
 545 AA;
 TRANSMEM
 TRANSMEM
 SEQUENCE
 Query Match
 RESULT 3
HTR1_HALN1
 Matches
 12
 229
 177
 341
 484
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98

SILRSAVNALMSLADKLGIASSNSSSST

59

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 MEDLINE=20504483; PubMed=11016950;
NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Well D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isebbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
"Genome sequence of Halobacterium species NRC-1.";
"Genome sequence of Halobacterium species NRC-1.";
 SPECIES-H.halobium; STRAIN-FLXSR;
MEDLINE-9101637; PubMed-1465418;
Yao V.J., Spudich J.L.;
Yao yuloo J.L.;
Primary structure of an archaebacterial transducer, a methyl-accepting procein associated with sensory rhodopsin I.";
Proc. Natl. Acad. Sci. U.S.A. 89:11915-11919(1992).
-!- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSORY RHODOPSIN I (SR-I) TO THE FLAGELLAR MOTOR. RESPONDS TO LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
-!- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
 SEQUENCE FROM N.A., AND SEQUENCE OF 1-10; 350-377 AND 457-476.
 Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 B9945E4F66A9D091 CRC64;
 Transmembrane; Methylation
 CYTOPLASMIC (POTENTIAL).
 EMBL, L05603; AAA72315.1; -.
PIR, A47190, A47190.
InterPro; IPR000122; Chemotaxis_transducer.
InterPro; IPR000658; DUF5.
InterPro; IPR003660; HAMP.
Pfam; PF00672; DUF5; 1.
Pfam; PF00015; MCPSignal; 1.
 METHYLATION
 METHYLATION
METHYLATION
 METHYLATION
 METHYLATION
 (strain NRC-1), and
 EMBL; AE005075; AAG19913.1; -.
 56544 MW;
 Transducer; Photoreceptor;
 SM00304; HAMP; 2.
Halobacterium sp. (stra
Halobacterium halobium.
 NCBI_TaxID=64091, 2242;
 535 AA;
 SEQUENCE FROM N.A.
 Halobacterium.
 STRAIN-NRC-
 DOMAIN
TRANSMEM
DOMAIN
 DOMAIN
 MOD_RES
MOD_RES
SEQUENCE
 INIT_MET
 MOD_RES
 SMART;
 SMART;
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15; Gaps 8 GPIDETERTPPADLSAQGLEASAANKSAE--AQRIAGAEAKPKE---SKTDSVERW---- 58 7.0%; Score 158; DB 1; Length 535; 18.7%; Pred. No. 0.17; ive 83; Mismatches 189; Indels 110; ; DB 1; Length 535; 0.17; 88; Conservative Query Match Best Local Similarity

Best Loca

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 ----WETKNADAIKVGAQITELAKYASDNQAIL 188
 DSLGKLTSFDLLQTALLQSVANNN------KAAELLKEMQDNPVVPGKTPAIAQS 237
 : | : | : | : | : : | 330 TEIGEQTIMILALNASIEAARAGGNADGDGFSVVADEVKDLAEETQDR---ANEIAAVVEK 386
 LVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIA 297
 EIQRITSEQAETVQSTATSVERVAGLSDDTTALASDAE---SAVIGQRESAEEIAA---- 487
 TRANSDUCTION (BY SIMILARITY).
 387 VTAQTEDVTASIQQTRTRV-----ESGSETVE----STLRDIRTIADSIAEVSNSID 434
 EAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVS 357
 MEDLINE-20504483; Pubmed=11016950; MG W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shugha H.D., Lasky S.R., Baliga N.S., Thorson V., Sbrogna J., Shugha H.D., Lasky S.R., Baliga N.S., Thorson W. Sbrogna J., Leithauser B., Keller K., Cruz R., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-Lisenbardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S., Encome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 SRSADVDST - - - TATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTN
 --SADIEASAGDTVEAVSKIESQANDQRTELDSAAD-----DVQQVSASAEEIAAT
 EAAATGDLTQRVDVDTDHEAMETVGTAFNQMMDDLQATVRTVTTVADEIEAKTERMSET-
 488 -SLEQFQNTAVEQLQS----RVASFTVATEDSETAGGSVEQPVMRAGADG 532
 Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 MLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAG
 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HARS OR HTPIV OR VNG1760G.
 InterPro; IPR000122; Chemotaxis_transducer
 or send an email to license@isb-sib.ch).
 PRT;
 Halobacterium sp. (strain NRC-1).
 InterPro; IPR003660; HAMP.
Pfam; PF00672; DUF5; 1.
Pfam; PF00015; MCPsignal; 1.
 EMBL; AF005080; AAG19986.1;
 144 INDIAATDEETAIAAE-----
 InterPro; IPR000658; DUF5
 STANDARD;
 SEQUENCE FROM N.A.
 NCBI_TaxID=64091;
 Halobacterium
 RESULT
HTR4_HALN1
HTR4_HALN1
NPR4;
 435
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 189
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39
60
324
345
810 AA;
 AE----
 HTR2_HALN1
 DOMAIN
TRANSMEM
 DOMAIN
 TRANSMEM
 Query Match
 DOMAIN
 RESULT 6
HTR2_HALN1
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 319
 359
 398
 ID DT DT OS OS OS
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 22;
 261 FAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPD--SPILQEAEQMVIQ 318
 -----KDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSM 358
 693 ESMDAGIDAVEEVVDAFTAVSDHADETDTGVQEISDTTDDQAASTEEAVSMTEEVADLSD 752
 QTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAY 260
 -- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY
 TSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIK 145
 DTAATDEETAIAAEWETKNADAIKVGAQIT----ELAKYASDNQAILDSL-GKLTSFDLL 200
 EASAANKSA-EAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSS 85
 "A family of halobacterial transducer proteins.";
FEMS Microbiol. Lett. 139:161-168(1996).
-!- FUNCTION: POTENTIALLY INVOLVED IN CHEMO- OR PHOTOTACTIC SIGNAL
TRANSDUCTION.
 635 ANIEAARADKSGDGFAVVADEVKDLAEETQESAGDIERRITEV--QSQTTATVAEARAAE
 ×
 7.0%; Score 15%; DB 1; Length 810; 22.0%; Pred. No. 0.2%; and 74; Mismatches 169; Indels 118;
 Rodewald
 Archaea, Euryarchaeota, Halobacteriales, Halobacteriaceae,
Halobacterium.
 359 LLDDAENETASILMSGFRQMI-HMFNT-----ENPDSQAAQQE---
 POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
4BF36E4B7D22BD80 CRC64;
 CYTOPLASMIC (POTENTIAL).
 396 -LAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGILN 437
 | :|:: || :: || :: ||:: |:| |:| |: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
 STRAIN=S9;
MEDLINE-96275896; PubMed=8674984;
MEDLINE-96275896; PubMed=8674984;
Medolph J., Ovedmann B., Storch K.F., Gruenberg H.,
Oesterhelt D.;
"A family of halobacterial transducer proteins.";
 15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HALOBACTERIAL TRANSDUCER PROTEIN IV.
 Complete proteome
 810 AA
 (Rel. 37, Created)
(Rel. 37, Last seq
 MM;
 38
59
323
344
810
85219 M.
 SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
Transducer; Transmembrane;
 HTR5 OR HTPIV.
Halobacterium salinarium
 Conservative
 STANDARD;
 810 AA;
 Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=2242;
 AE----
 15-DEC-1998 (
15-DEC-1998 (
 HTR4_HALSA
Q48317;
 Best Local Sin
Matches 102;
 TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
SEQUENCE
 Query Match
 DOMAIN
 HTR4_HALSA
 319
 27
 398
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 146
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 22;
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 20-AUG-2001 (Rel. 40, Last sequence update)
SENSORY RHODOPSIN II TRANSDUCER (HTR-II) (METHYL-ACCEPTING PHOTOTAXIS PROTEIN II) (MPP-II).
HTR2 OR VNG1765G.
 ----- 395
 693 ESMDAGIDAVEEVVDAFTAVSDHADETDTGVQEISDTTDDQASSTEEAVSMTEEVADLSD 752
 DTAATDEETAIAAEWETKNADAIKVGAQIT----ELAKYASDNQAILDSL-GKLTSFDLL 200
 551
 201 QTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAY 260
 261 FAGGNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPD--SPILQEAEQMVIQ 318
 ----KDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSM 358
 TSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIK 145
 445 AERYSDVMAACADGDLTRRMPADDTDNEAMAAIAASF-NEMLAQWEHTIIDIQE----FA 499
 EASAANKSA-EAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSS
 7.0%; Score 158; DB 1; Length 810;
21.8%; Pred. No. 0.28;
ive 75; Mismatches 169; Indels 118;
 LLDDAENETASILMSGFRQMI-HMFNT-----ENPDSQAAQQE----
 EXTRACELLULAR (POTENTIAL)
 CYTOPLASMIC (POTENTIAL).
37B0F6046A39D9BA CRC64;
 -LAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGILN 437
 CYTOPLASMIC (POTENTIAL)
 AA.
 EMBL, X95589; CAA64841.1; -.
InterPro: IPR000122; Chemotaxis_transducer.
InterPro: IPR000658; DUF5.
InterPro: IPR03660; HAMP.
Pfam; PF00672; DUF5; 1.
Pfam; PF0015; MCPSignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
 . 763
 POTENTIAL.
 POTENTIAL
 Halobacterium sp. (strain NRC-1)
 85207 MW;
 Transducer; Transmembrane.
 Best Local Similarity 21.8 Matches 101; Conservative
 STANDARD;
 38
59
323
344
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 WEDLINE-20504483; Pubmed=11016950;
AM WUV, Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
ANDLINE-20504483; Pubmed=11016950;
AM Shukla H.D., Lasky S.F., Malia N.S., Thorsson V., Sbrogna J.,
Asartzell S., Weller K., Cruz R., Dahl T.A., Welti R., Goo Y.A.,
Alain B., Keller K., Cruz R., Dahl T.A., Mough D.W.,
Alam M., Freitas T., Houg P.E., Krebs M.P., Apudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
A. Genome sequence of Halobacterium species NRC-1.*
R. Changes Sci. U.S.A. 97:12176-12181(2000).
C. I- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSORY
C. RHODOPSIN II (SR-II) TO THE ELAGELLAR MOTOR. RESPONDS TO LIGHT
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 18;
 | || || || ::!| | ::! | |
396 RALESAAADYEEALTAVAD--GDLTRRVDASRDHDAMARIGHALNDMLDDIETSVAAATA 453
 SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
 ----DVDSTTATAPT 101
 Gaps
 8 GPIDETERTPPADLSAQGLEASAANKSAE-----AQRIAGAEAKPKE---SKIDSVERW 58
 102 PPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWE
 162 TKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEM
 454 FSDHVSDAAQRVEADAGDAIDAGT---DVSTAVDEISDGATE----QTDRLHEVAGEVD
 :| | : | | | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| | : :| DLSASAEEVAETVASLADTAGQAASAVDD-GRQATEDAVET--MDDVADDAEAAADAMDA
 93;
 QDNPVVP-GKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENA----
 DB 1; Length 763;
 Euryarchaeota; Halobacteriales; Halobacteriaceae;
 Indels
 EXTRACELLULAR (POTENTIAL)
 Transducer; Photoreceptor; Transmembrane; Methylation; Complete proteome.

INIT_MET 0 0 BY SIMILARITY.

ODMAIN 1 15 CYTOPLASMIC (POPENTIAL).
 CYTOPLASMIC (POTENTIAL).
CF7A8FF04DFF309A CRC64;
 CYTOPLASMIC (POTENTIAL).
 Score 154.5; DB 1;
Pred. No. 0.39;
1; Mismatches 196;
 59 SILRSAV----NALMSLADKLGIASSNSSSSTSRSA-----
 EMBL; AE005080; AAG19989.1; -.
InterPro: IPR000122: Chemotaxis_transducer.
InterPro: IPR000658; DUF5.
InterPro: IPR003660; HAMP.
Pfam; PF00672; DUF5; 1.
Pfam; PF0015; MCPSignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
 POTENTIAL.
 POTENTIAL.
 71;
 MW.
 6.8%;
 0
15
36
277
297
763
78911 N
 Conservative
 278
298
763 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 Halobacterium.
NCBI_TaxID=64091;
 SIMILARITY).
 105;
 FRANSMEM
 TRANSMEM
 SEQUENCE
 DOMAIN
 DOMAIN
 Matches
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 18;
 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
$ENSORY RHODOPSIN II TRANSDUCER (HTR-II) (METHYL-ACCEPTING PHOTOTAXIS
 Proc. Natl. Acad. Sci. U.S.A. 93:8230-8235(1996).
-i. FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSORY RHODOPSIN II (SR-II) TO THE FLAGELLAR MOTOR. RESPONDS TO LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
-i. SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
 Zhang W., Brooun A., Mueller M.M., Alam M.;
"The primary structures of the Archaeon Halobacterium salinarium blue
light receptor sensory rhodopsin II and its transducer, a methyl-
 DVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAA 392
 93; Gaps
 GPIDETERTPPADLSAQGLEASAANKSAE-----AQRIAGAEAKPKE---SKTDSVERW 58
274 -KSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGS
 :| :: :|:| |:
EESRDAAEDIESRLLALOGQVSDVADEMRATSDT--VSDGRATVGDAATALDDV-----
 DB 1; Length 764;
 Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
 Indels
 EXTRACELLULAR (POTENTIAL)
 393 QQELAAQARA-AKAAGD-----DSAAAALADAQKALEAALGK 428
 Transmembrane; Methylation.
 1E0D7B4E460FC588 CRC64;
 BY SIMILARITY.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
 CYTOPLASMIC (POTENTIAL)
 =
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::
 6.8%; Score 154.5; DB 1;
22.6%; Pred. No. 0.39;
iive 71; Mismatches 196;
 Ž
 InterPro; IPR000122; Chemotaxis_transducer.
InterPro; IPR000658; DUF5.
InterPro; IPR003660; HAMP.
 764
 POTENTIAL.
 MEDLINE=96323203; PubMed=8710852;
 MM.
 Pfam; PF00672; D0F5; 1.
Pfam; PF00015; MCPsignal; 1.
SWART; SM00304; HAMP; 2.
SWART; SM00283; MA; 1.
 EMBL; U62676; AAC44369.1; -
 Transducer; Photoreceptor;
INIT_MET 0 0
DOMAIN 1 15
 79187
 Query Match 6.81
Best Local Similarity 22.65
Matches 105; Conservative
 Halobacterium salinarium.
 STANDARD;
 277
298
764
 PROTEIN II) (MPP-II).
HTR2 OR HTRII.
 299
764 AA;
 accepting protein.
 SEQUENCE FROM N.A.
 NCBI_TaxID=2242;
 STRAIN-FLX15
 HTR2_HALSA
P71410;
 TRANSMEN
 TRANSMEM
 SEQUENCE
 DOMAIN
 333
 HTR2_HALSA
 699
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
 MEMBRANE ANCHOR.
CYTOPLASMIC (POTENTIAL).
HELICAL (POTENTIAL).
3 X TANDEM REPEATS, ALA-RICH.
3 X TANDEM REPEATS, PRO-RICH.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
 62 NLPEAQGSASKQAEQSQTKLERQMVHTIEVPKTDLDQAAKDAKSAGVNVVQDADVN-KGT 120
 Q---KKFPDSPILQEAE-QMVIQA-EKDLKNIKPAD------GSDVPNPGTTVG 342
 --KQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTE 385
 AATDEETAIAAEWE----TKNADAIK-----VGAQITELAKYASDNQAILDSLGK 193
 194 LTSFDLL-QTALLQSVANNNKAAEL----LKEMQDNPVVPGKTPAIAQSLVDQTDATAT 247
 OIE----KDGNAIGDAYFAGONASGAVENAKSNNSISNIDSAKAAIATAK----TOIAEA 299
 235 QAELKRVQEANAAAKAAY---DTAVAANNAKNTEIAAANEEIRKRNATAKAEYETKLAQY 291
 292 QAELKRVQEANAANEADYQAKLTAYQTELARVQRANADAKAAYEAAVAANNAKNAALTAE 351
 48 KESKTDSVERWSILRSAVNALMSLADKLGIASSN-SSSSTSRSADVDSTTATAPTPPPFT 106
 -----SDDYKTQAQTAYDTIFTST-----SLADIQAALVS-LQDAVTNIKDT 147
 2 KVKKTYGFRKSKISKTLCGAVLGTVAAVSVAGQKVFADETTTTSDVDTKVVGTQTGNPAT 61
 Interpro: IPR001899; Gram_pos_anchor.
Pfam; PF00746; Gram_pos_anchor; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Antigen; Signal; Transmembrane; Repeat; Cell wall; Dental caries.
 (PROBABLE)
 Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
 6.7%; Score 152; DB 1; Length 1561; 22.3%; Pred. No. 1.2;
 Mismatches 182; Indels
 540D92768FC8AB4B CRC64;
 386 NPDSQAAQQELAAQARAAKAA--GDDSAAAAL-ADAQKALEAALGK 428
 EXTRACELLULAR (POTENTIAL)
 CELL SURFACE ANTIGEN I.
 01-NoV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PATHOGENICITY LOCUS PROTEIN HRPK.
 641 AA
 PRT;
 82;
 EMBL; X17390; CAA35253.1; -.
 170060
 Conservative
 STANDARD;
 1536
1556
1561
 550
464
963
1533
 1561
 1561 AA;
 PIR; S06839; S06839
 Similarity
 39
997
39
1537
1557
 NCBI_TaxID=321;
 219
847
1528
 GS----
 HRPK_PSESY
P41501;
 104;
 Antigen; S
SIGNAL
CHAIN
 DOMAIN
TRANSMEM
DOMAIN
 SEQUENCE
 Query Match
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 HRPK_PSESY
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 $EQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-812 SERVITYPE C;
MEDLINE-91207143; PubMed-1982405;
Kelly C., Evans P., Ma J.K.C., Bergmeier L.A., Taylor W., Brady L.J.,
Lee S.F., Bleiweis A.S., Lehner T.;
"Sequencing and characterization of the 185 kDa cell surface antigen
of Streptococcus mutans.";
 455 FSDHVSDAAQRVEADAGDAIDAGT---DVSTAVDEISDGATE----QTDRLHEVAGEVD 506
 QDNPVVP-GKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENA----- 273
 564 IDSEMADIGEIVDVIADIADQTNMLAL-----NASIEAARTGADGDGFAVVADEVKTLA 617
 274 -KSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGS 332
 DVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAA 392
 337 GTLAESFRSMRDSLSESLTDAERAŤARAEDAREDAEQQRADAEAAREDAEAARKDAQETA 396
 -- DVDSTTATAPT 101
 397 RALESAAADYEEALTAVAD--GDLTRRVDASRDHDAMARIGHALNDMLDDIETSVAAATA 454
 102 PPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWE 161
 Kelly C., Evans P., Bergmeier L., Lee S.F., Progulske-Fox A., Harris A.C., Aitken A., Bleiweis A.S., Lehner T.; "Sequence analysis of the cloned streptococcal cell surface antigen
 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 of Streptococcus mutans.";
Arch. Oral Biol. 35:338-388(1990).
-!- FUNCTION: SUFFREE PROTEIN ANTICEN IMPLICATED IN DENTAL CARIES.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-!- SIMILARITY: TO OTHER STREFTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
 162 TKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEM
 :|:| :| | | : :|:
EESRDAAEDIESRLLALQGQVSDVADEMRATSDT--VSDGRATVGDAATALDDV-----
 -----VSFVADTDTAAGQIRAA---TDRQAHAASRVASAVDEV---
 393 QQELAAQARA-AKAAGD-----DSAAAALADAQKALEAALGK 428
 -!- SIMILARITY: BELONGS TO THE SPAP/SSP5/SPAA FAMILY.
 W-1991 (Rel. 20, Last sequence update)
2B-1996 (Rel. 33, Last annotation update)
SURFACE ANTIGEN I/II PRECURSOR.
 PRT; 1561 AA
 SILRSAV - - - - NALMSLADKLGIASSNSSSSTSRSA -
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN=NG5 SEROTYPE C;
 MEDLINE=90076473; PubMed=2687020;
 (Rel. 20, Created)
(Rel. 20, Last seq
 FEBS Lett. 258:127-132(1989).
 STANDARD;
 Streptococcus mutans.
 NCBI_TaxID=1309;
 Streptococcus
 01-NOV-1991
 01-NOV-1991
01-FEB-1996
 STRMU
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SPAP_STRMU
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 POTENTIAL.
CELL SURFACE ANTIGEN I.
CELL SURFACE ANTIGEN II.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE
 190 AQYE--QDLAANKAEVERSLMRMRKPRPIYEAK---LAQNQKDL--AAIQQANSDSQA-- 240
 TATÄAPTPPPPTSDDYKTQAQTAY-----DTIFTSTSLADIQAALVSLQDAVTNIKDTA 148
 TGNPATNLPDKQDNPSSQAETSQAQARQKTGAMSVDVSTSELDEAAKSPQEAGVTVSQDA 129
 ATDEETAIAAEWETKNADAIK--VGAQITELAKYASD-----NQAILDSLGKLTSFDL 199
 130 TVNKGTVEPSDEANOKEPEIKDDYSKQAADIQKATEDYKASVAANOAETDRINGEIAAKK 189
 LQTALLQSVANNNKAAE--LLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIG 257
 38 QRİAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSSTS--RSADVDST 95
 16 KRILGA-AKVKSGRTLS---GALLGTAI--LASGAGOKALAEETSTTSTSGGDTAVVGTE 69
 Streptococcus downei (Streptococcus sobrinus).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 MpDLINE-91310320; PubMed-1855987;
Hapolla R.J., Haron J.A., Kelly C.G., Taylor W.R., Bohart C.,
Hendricks M., Payati J., Graff R.T., Ma J.K.C., Lehner T.;
"Sequence and structural analysis of surface protein antigen I/II
(SpaA) of Streptococus sobrinus.";
 -> K (IN REF. 2).
-> K (IN REF. 2).
-> S (IN REF. 2).
-> S (IN REF. 2).
B235F9CCD92838E0 CRC64;
 InterPro: IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
Antigen; Signal; Transmembrane; Repeat; Cell wall.
 192;
 DB 1;
 A -> K (IN REF.
Q -> K (IN REF.
Q -> K (IN REF.
A -> S (IN REF.
A -> S (IN REF.
 Pred. No. 1.4;
68; Mismatches
 6.7%; Score 150.5;
 PROTEINS
 nfect. Immun. 59:2677-2685(1991)
 EMBL; X57841; CAA40973.1; -.
 165572
 23.5%;
 FROM N.A.
715 / SEROTYPE G;
 AAA26977.1;
 Best Local Similarity 23.5
Matches 110; Conservative
 427
431
434
531
600
 AA;
 Streptococcus.
NCBI_TaxID=1317;
 427
431
434
531
600
1528
 1503
 SEQUENCE FROM STRAIN=6715 /
 M38210;
 Antigen; SIGNAL
 CONFLICT
CONFLICT
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SEQUENCE
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 15;
 associated with
 DSVERWSILRSAVNALMSLADKLGIASSNSSSSTSRSADVDS----TTATAPTPPPPT 106
 53 DSPSSFSGTEQSGSSLAMSL----LTRSSSSESTS-SVDQDSDQVSPWTSVSSTASASPT 106
 SDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNI-----KDTAATDEETAIAAEWET 162
 163 KNADAIKVGAQITELAKYASDNQAILDSL-----GKLTSFDLLQTALLQSVANNN 212
 DGNV-----SAEGLKALIKSNPGLSG------TLKQSSNAWSQAGFLSQ 312
 AASNPANAPSATDAAFLDNSEYSSPEALKRWEPMVANLPPEEREQAAKELNRPIAAAWMA 166
 312 AEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAE-NETASI 370
 222 ADKDVAKYMEDNPGADPQSLEMVRSAAVMRANMPLATAADPHHAVGAADKTDV----- 274
 252 DGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQE 311
 313 VDEAGLIGRKKAAH-SPDQVFDASNMSEWI---RKSAPKNGGQFASMLSDAATLNSVAGI 368
 Gaps
 Xiao Y., Heu S., Yi J., Lu Y., Hutcheson S.W.;
"Identification of a putative alternate sigmma factor and
characterization of a multicomponent regulatory cascade controlling
the expression of Pseudomonas Syringae pv. syringae Pss61 hrp and
 371 LMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAALGK 428
 369 DISKLNAQVF----EKPKAYTGAQKAAVMIKLQQTQQSVIAGRDLRNTEKT-EAGLNE 421
 91;
 Length 641;
 "Nucleotide sequence and properties of the hrmA locus asso-
the Pseudomonas syringae pv. syringae 61 hrp gene cluster.
Mol. Plant Microbe Interact. 6:553-564(1993).
 Indels
 641 AA; 67678 MW; EC098941E5B46C8E CRC64;
 6.7%; Score 151.5; DB 1;
21.5%; Pred. No. 0.44;
Live 56; Mismatches 181;
 01-AUG-1991 (Rel. 19, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CELL SURFACE ANTIGEN I/II PRECURSOR.
SPAA.
 PRT; 1528 AA.
 Bacteriol. 176:1025-1036(1994)
 MEDLINE=94100578; PubMed=8274770;
 DIKAIN-F3301;
MEDLINE-94148760; PubMed-8106313;
 EMBL; U03855; AAA17653.1;
 Local Similarity 21.5
nes 90; Conservative
 STANDARD;
 SEQUENCE FROM N.A.
 FROM N.A.
 S., Hutcheson
 STRAIN-PSS61
 genes.
 SPAA_STRDO
P21979;
 SEQUENCE
 Query Match
 107
 23
 SPAA_STRDO
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Length 1528;

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 ----ASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKK 302
 303 FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDD 362
 363 AENETASIIMSGFRQMIHMFNTEN----PDSQAAQQELAAQARAAKAAGDDSAAAALADA 418
 241 -AYAAAKEAYDKEWARVQAANAAAKKAYEEALAANTAKN-DQIKAEIEAIQQRSAKA--- 295
 338 AANAAAK---QAYEQALAANSAKNAQITAENEAIQON--AQAKA------DYEAKLAQY 385
 Mingorance J., Tanaka S., Tominaga A., Enomoto M.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCIION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
-!- MISCELLANEOUS: INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE
BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLY TERMED
PHASE-1 AND PHASE-2. BACH SPECIFIED BY SEPRARATE STROUTUREL GENES.
-!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Vanegas R.A., Joys T.M.; "Molecular analyses of the phase-2 antigen complex 1,2,. . of
 Silverman M., Zieg J., Mandel G., Simon M.; "Analysis of the functional components of the phase variation
 457
 386 QKDLAAAQSGNAANEADYQEKLAAYEKELARVQAANAAAKQAYEQQVQQ 434
 -----DYEAKLAQYEKDLAAAQAGNAANEADYQAKKAAYEQELARV-
 QKALEAA-LGKAGQQQGILNALG-----QIASAAVVSAGVLPLQQ
 Cold Spring Harb. Symp. Quant. Biol. 45:17-26(1981)
 Last sequence update)
Last annotation update)
 AA.
 or send an email to license@isb-sib.ch)
 PRT;
 Bacteriol, 177:3863-3864(1995).
 SEQUENCE OF 1-37 FROM N.A.
MEDLINE-82049491; PubMed=6271461;
 Stydene; SG10554; f13B.
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_N.
Pfam; PF00700; Flagellin_C:
Pfam; PF00669; Flagellin_N; 1.
 MEDLINE-95325331; PubMed-7541401;
 E_SALL1
FLJB_SALTY STANDARD,
P52616; P97159;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequent)
 SEQUENCE OF 482-505 FROM N.A.
 EMBL; U17177; AAC43354.1; -.
 V01370; CAA24655.1; -. D26168; BAA05156.1; -.
 Salmonella typhimurium
 SEQUENCE FROM N.A.
 DAYFAGON----
 PHASE-2 FLAGELLIN
 NCBI_TaxID=602;
 STRAIN=SJ2353;
 Salmonella
 Salmonella
 FLJB OR H2
 STRAIN=SL
 REGULT 11

FLD_SALTY

DAD F151E

AC P526IE

DT 01-007

DT 30-MAX-

DE P148E

GN Salmor

OC Bactes

OC SAlmor

RR SAlmor

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20;
 151 DGETIDIDLKQINSQTLGLDSLNVQKAYDVKDTAVTTKAYANNGTTLDVSGLDDAAIKAA 210
 92 RELAVQSANSTNSQSDLDSIQAEI-TQRLNEIDRVSGQTQFNGVKVLAQDNTLTIQVGAN 150
 207
 253 GNAI-----GDAYFAG-QNASGAVENAKSN------NSISNIDSAKAAI 289
 --AKTQIAEAQKKFPDSPILQEAEQMVIQAE---KDLKNIKPA 329
 ----STSLADIQAALVSLQ----DAVTNIKDTAATD------EETAIAAE 159
 211 TGGTNGTASVTGGAV----KFDADNNKYFVTIGGFTGADAAKNGDYEVNVATDGTVTLAA 266
 208 VANNN-----KAAELLKEMQDNPVV---PGKTPAIAQSLVDQTDATAQI-----EKD 252
 GKTIEGGYALKAGDKYYAADYDEATGAIK-AKTTSYTAADGTTKTAANQLGGVD-GKTEV 383
 Gaps
 Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)2-Cys6 binuclear cluster domain and a putative alpha 2-SCB-alpha 2 binding site.";
Yeast 11:681-689(1955).
-i- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
 23 AQGLEASAANKSAEAQRIAG-----AEAKPKESKTDSVERWSILRSAVNALMSLADKL:75
 32 SSGLRINSAKDDAAGQAIANRFTANIKGLTQASRNANDGISIAQTTEGALNEINNNIQRV
 ----TALLOS
 Saccharomycetes;
 76 GIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQ-----TAYDTIFT----
 01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 89-2 KDA PROTEIN IN SCP160-SMC3 INTERGENIC REGION.
 "Sequence analysis of a 33.1 kb fragment from the left arm of
 Length 505;
 Miosga T., Schaaff-Gerstenschlaeger I., Chalwatzis N., Ba
Boles E., Fournier C., Schmitt S., Velten C., Wilhelm N.,
 I -> S (IN REF. 2).
3A5CC404AF7AF88B CRC64;
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 160 WETKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQ----
 6.5%; Score 148; DB 1;
21.0%; Pred. No. 0.5;
iive 59; Mismatches 168
 881 AA.
 BY SIMILARITY
 PRT;
PRINTS; PR00207; FLAGELLIN.
ProDom; PD000316; Flagellin_C; 1.
 MEDLINE=96093911; PubMed=7483841;
 330 DGSDVPNPGTTVGGSKQQGSSI 351
 443 FNSAITNLGNTVNNLSEARSRI 464
 37 I
52404 MW;
 01-FEB-1996 (Rel. 33, Created)
 Conservative
 STANDARD;
 505 AA;
 Similarity
 SEQUENCE FROM N.A.
 YJL078C OR J1027
 NCBI_TaxID=4932;
 Zimmermann F.K.;
 УЈН8_YEAST
P47033;
 93;
 290 AT---
 Flagella.
 INIT_MET
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 19;
 521 SEQSSALATSVPATNCSSIVKTITLENSSTTTITAITKSTTTLATTANN----STRAAT 575
 576 AVTIDPTLDPTDNSASPTDNAKHTSTYGSSSTGASLDSLRTTTSISVSSNTTQLVST--- 632
 SAQTTSSVSASLSSSVAADDIQGSTS--KEATSSVSEHTSIVTSATNA-AQYATRLGSSS 421
 477 ETAQAS-----SSTEKNISNSAATSSSI-----YSNSASVS-GHGVTYAAEYAIT 520
 SNSSSSTSRSA--------DVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFT 123
 STSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYA-- 181
 SAQGLEASAA - - NKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIAS 79
 -SDNQAILDSLGKLTSFDLLQTALLQSVANN-----NKAAELLKEMQDNPVVPGKTPAIA
 236 QSLVDQT-DATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKT
 295 QIAEAQKKFPDSPILQEAEQMVIQAEKDL-KNIKPADGSDVPNPGTTVGGSKQQGSSIGS
 --CTSESDYSDSPSF--AISTATTTESNLITNTITASCSTDSNFPTSAASSTDETAFTRT
 354 IRVS-MLLDDAENETASILMSGFRQMIHMFNT-------ENPDSQAAQQELA
 86;
 Halobacterium salinarium.
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
 73; Mismatches 199; Indels
 ALA/SER/THR-RICH.
37DBAC660CA9D12A CRC64;
 Score 148; DB 1;
Pred. No. 0.99;
 398 AQARAARAAGDDSAAAA-LADAQKALEAALGKAGQQQG 434
 744 VNAATIINPGETSSLASDFATSEKPNEPTSVKSTSNEG 781
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HALOBACTERIAL TRANSDUCER PROTEIN VI.
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 PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1. PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
 EMBL; 249353; CAA89370.1; --
EMBL; X883502; CAA58422.1; --
EMBL; X88881.1; --
HSSP; P04284; ICFE.
SGD; S0003614; VJL078C.
InterPro; IPR001283; SCP.
Pfan; PF00188; SCP.
PRINTS; PR00189; SCP. 1.
 881 AA; 89152 MW;
 / Match 6.5%;
Local Similarity 21.8%;
 Matches 100; Conservative
 Hypothetical protein.
DOMAIN 166 37
 HTR4 OR HTPVI.
 HTR6_HALSA
 SEQUENCE
 Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
 19;
 716
 ADIQAALVSLQDAVTNIKDTAA--TDEETAIAAEWETKNADAIKVGAQITELAKYASDNQ 185
 342 GGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTEN-PDSQAAQQELAAQA 400
 ---ADKLGIASSN-SSSSTSRSADVDSTTATAPPPPTSDDYKTQAQTAYDTFTSTSL 127
 -!- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
 Gaps
 "A family of halobacterial transducer proteins.";
FEMS Microbiol. Lett. 139:161-168(1996).
-!- FUNCTION: POTENTIALLY INVOLVED IN CHEMO- OR PHOTOTACTIC SIGNAL
 DAEAARSEAEAAQADAEAAQ-AEAEAAREESEAQA-RRLETTAEAFSETMRAYAAGDLTV
 AILDSLGKLTSFDLLQTALLQSVANNNKAA----ELLKEMQDNPVVPGKTPAIAQS---
 LVDQTDATATQIEKDGN----AIGDAY--FAGQNASGAVE------NAKSNNSISNIDS
 285 AKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAE---KDLKNIKPADGSDVPNPGTTV
 IQERVSDGVETVSETERS -----LSEIAGRIAEADTGVQEISNAMDDQAASVSDVTTAV
 68;
 Rodewald
 20 DLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSL
 6.5%; Score 147; DB 1; Length 77
22.9%; Pred. No. 0.96;
tive 74; Mismatches 184; Indels
 POTENTIAL.
EXTRACELLULAR (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
134C7D7F0A3334CD CRC64;
 CYTOPLASMIC (POTENTIAL).
 MEDLINE=96275896; PubMed=8674984;
Rudolph J., Nordmann B., Storch K.F., Gruenberg H.,
Oesterhelt D.;
 EMBL; x95590; CAA64843.1; -.
InterPro; IPR000122; Chemotaxis_transducer.
InterPro; IPR000658; DUF5.
InterPro; IPR003660; HAMP.
 POTENTIAL.
 Σ
 Pfam; PF00672; DUF5; 1.
Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
 82077
 Transducer; Transmembrane
 Local Similarity 22.9 tes 97; Conservative
 TRANSDUCTION
NCBI_TaxID=2242;
 TRANSMEM
DOMAIN
SEQUENCE
 DOMAIN
TRANSMEM
 Query Match
 DOMAIN
 378
 128
 401
 Matches
 717
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---ETNARSSETAAERSASAAADAKTAAAGSASTASTKAT-----EAAGSAVSASQS 326

278

QQ Dp

206 QSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQN

224 TAATKASEAATSA----RDAVASKEAAKSSETNASSSAGRAASSATAAENSARAAKTS--

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327 KSAAEAAAIRAKNSAKRAEDIASAVALEDADTTRKGIVQLSSATNSTSETLAATPKAVKV 386

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ΩŽ

EKDLKNIK-PADG---SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGF

387 VMDETNRKAPLDSPALTGTPTAPTALRGT-----

Db

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266 ASGAVENA-KSNNSISNIDSAKAAIA-----TAKTQIAEAQKKFPDSPILQEAEQMVIQA

------ANTQIANTAFVLAAI 430

376 ROMIHMENTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGI 435

431 ADVI----DASPDALNTLNELAA-----ALGND-----PDFATTMTNALAGKQPKNAT 474

436 LNALGQIASA 445 | || :::| LTALAGLSTA 484

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PRT; 1714 AA.

STANDARD;

SYEP\_DROME

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 MISCELLANEOUS: THE COMMON LABORATORY STRAIN OF BACTERIOPHAGE LAMBDA; LAMBDA, THE ORGINAL ISOLATE. THE UR-LAMBDA YIRIONS HAVE THIN, JOINTED TALL FIBERS (SIDE TALL FIBERS) THAT ARE ABSENT FROM LAMBDA WILD TYPE. RELATIVE TO LAMBDA PAPA, UR-LAMBDA HAS EXPANNED RECEPTOR SPECIFICITY AND ADSORBS TO E.COLI CELLS MORE RAPIDLY.
 SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
CORRECTED IN POSITION TO 396 TO RECREATE THE ORIGINAL STF PRIOEIN.
 Haggaard-Ljungquist E., Halling C., Calendar R.;
"DNA sequences of the tail fiber genes of bacteriophage P2: evidence
for horizontal transfer of tail fiber genes among unrelated
 Hendrix R.W., Duda R.L.; "Bacteriophage lambda PaPa: not the mother of all lambda phages."; Science 258:1145-1148(1992).
 no RNA stage; Tailed phages; Siphoviridae;
 MEDLINE-83189071; PubMed-6221115;
Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
"Nucleotide sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
 CDD1DF85E919123B CRC64;
 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) SIDE TAIL FIBER PROTEIN.
 774 AA.
 EMBL; J02459; AAA96555.1; ALT_FRAME.
EMBL; J02459; AAA96557.1; ALT_FRAME.
PIR; A04389; QXBP1L.
PIR; A04370; QXBP2L.
InterPro; IPR00122; Chemotaxis_transducer.
 or send an email to license@isb-sib.ch)
 POA_allergen.
 MEDLINE=92165720; PubMed=1531648;
 MEDLINE=93068310; PubMed=1439823;
 Bacteriol. 174:1462-1477(1992)
 STF_LAMBD STANDARD; F P03764; P03745; 21-JUL-1986 (Rel. 01, Created)
 77527 MW;
 dsDNA viruses,
 InterPro; IPR001778;
Fiber protein.
SEQUENCE 774 AA; 7:
 IDENTIFICATION AS STF
 RECONSTRUCTION OF STF
 Bacteriophage lambda
 Viruses; dsDNA virus
Lambda phage group.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10710;
 bacteriophages.
 LAMBD
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SEQUENCE FROM N.A.
MEDLINE-92097547; PubMed=1756734;
Cerini C., Kerjan P., Astier M., Gratecos D., Mirande M., Semeriva M.;
"A component of the multisynthetase complex is a multifunctional aminoacy1-tRNA synthetase.";
EMBO J. 10:4267-4277(1991).
 Adams M.D., Celnike S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.
 Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Cerini C., Semeriva M., Gratecos D.;
"Evolution of the aminoacyl-tRNA synthetase family and the
organization of the Drosophila glutamyl-prolyl-tRNA synthetase gene.
Intron/exon structure of the gene, control of expression of the two
mRNAs, selective advantage of the multienzyme complex.";
 GLUTAMYL-TRNA
P28668; 09VCF5;
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA
SYNTHETASE (EC 6.1.1.17) (GLUTAMATE-TRNA LIGASE); PROLYL-TRNA
AATS-GLUPRO OR CG5394.
 Eur. J. Biochem. 244:176-185(1997).
 STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
 MEDLINE=97217441; PubMed=9063462;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN=OREGON-R;
 Ephydroidea; Dre
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13;

Gaps

65;

Length 774; Indels

Score 146.5; DB 1; Pred. No. 1; 5; Mismatches 209;

6.5%; Scor 20.9%; Pred tive 66; 1

90; Conservative

Similarity

Query Match Best Local S

Matches

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TSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT1FTSTSLADIQAALVSLQDAVTNIK 145

86

26 LEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSS 85

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Borkows D., Borchan N.R., Bouck J., Brobstin P., Brotler P.,

RA Dodgon K., Dodgolg S., Daller C. M. Develler, Dev J., Dinn P.,

RA Dodgon K., Dodgolg S., Deller C. M. Develler, Dev J., Dinn P.,

RA Dodgon K., Dodgolg L. Donner W., Dev J., Dev J., Dinn P.,

RA Dodgon K., Dodgolg L. Donner W., Dev J., Dev J., Dinn P.,

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RA Durbin K., Dong F., Correll J. M., Gu Z., Guan P., Harris M.,

RA Lidolé M., Andrell B., Karpan G. H., Re' Z. Reminded J. R.,

RA Lidolé M., Anish R., Karpan G. H., Re' Z. Reminded J. R.,

RA Lidall M., Mallah F., Karpan G. H., Re' Z. Reminded J. R.,

RA Lidall M., Mallah E., Karpan G. H., Me' Z. Reminded J. R.,

RA Lidall W., Mallah R., Mallah R., Mallah R., Mallah G.,

RA Lidak D., Lell Y., Lellisky A.A., Li J., Li Z., Linn Y., Lin X.,

RA Lidak D., W. Bitton R., Mallah R., Mallar M., Mallah G.,

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RA Lidak D., W., Bitton R., Mallar M., Mallar M., Mallar M., Mallar M.,

Ra J., Mallar M., R., Mallar M., Mallar M., Mallar M., Mallar M.,

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Ra J., Mallar M., Weers B., Mallar M., Mallar M., Mallar M., Mallar M.,

Radone S., Special M., Mallar M., Mallar M., Mallar M., Mallar M.,

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Radone S., Special M., Mallar M., Mallar M., Mallar M., Mallar M., Mallar M.,

Radone S., Special M.
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1017 QEWKP--GTVAPAPTTVNVIDLTGG--DSGSDVGSVLSKIQAQGDKIRKLKSEKAAKNVI 1072
 1073 DPEVKTLLALKGEYKTLSGKDWTPDAKSEPAVV----KKEASPVSMASPAKDELTQEIN 1127
 701 PSPIVLFSIPDGHTKDVPTSGLKVNAPDAKATKKASSPVSSSGQASELDSQITQQGDLVR 760
 EAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTAT-APTP 102
 103 PPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIA---- 157
 AASSS-----SANDAV----SVNASIVKQGDLVRDLKGKKASKPEIDAAVKTLL 852
 --- AEWETKNADAIKVGAQITELAKYASDNQAI---LDSLGKLTSFDLLQTALLQSVANNN 212
 KAÄELLKEMODNPVVPGKTPAIAOSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVEN 272
 904 KVRELKSAKADKATVDAAVKTLLSLKADYKAATGSD-WKPGTT-----APAPAAAPVKV 956
 273 AKSNN----SISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNI-- 326
 355 --RVSMLL-------DDAENETASILMSGFRQMIHMFNTENPDSQAAQQELA 397
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Multifunctional enzyme; Repeat.
 Gaps
 Indels 142;
 Similarity 19.8%; Score 146; DB 1; Length 1714; Similarity 19.8%; Pred. No. 2.8; Conservative 74; Mismatches 192; Indels 14:
 "KMSKS" REGION.
ATP (BY SIMILARITY).
TSPLP -> DKSIA (IN REF. 3).
VC -> AF (IN REF. 3).
NTACA -> KYCUR (IN REF. 3).
 7 PGPI------DETERTPPADLSAQGLEASAANKSAEAQRIAG------
 6FE8C58045E48A8C CRC64;
 ---KPADGSDVPNPGTT----VGGSKQQGSSIGSI-----
 GLUTAMYL-TRNA SYNTHETASE
 PROLYL-TRNA SYNTHETASE. "HIGH" REGION.
 K -> R (IN REF. 3).

L -> A (IN REF. 3).

T -> S (IN REF. 3).

T -> T (IN REF. 3).

P -> T (IN REF. 3).
 P -> PA (IN REF. 3)
MISSING (IN REF. 3)
G -> V (IN REF. 3).
 WHEP-TRS 4. WHEP-TRS 4. WHEP-TRS 5. WHEP-TRS 5.
 || :|| :|| :|| | || AGGEKVRAAKGNKAAKEVIDAEVAKLLAL 1156
 AQARAAKAAGDDSAAAALADAQKALEAAL 426
 POLY-GLY
 1587 G -
AA; 189197 MW;
 Ouery Match 6.5%
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Matches 101; Conservative
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0910n7 streptomyce 0990k5 streptococc 094x33 streptococc 094x9 streptococc 096x09 oryza sativ p71409 halobacteri 095x13 streptococc 095x13 streptomyce 04525 mycoplasma 095tb0 staphylococ 049545 mycoplasma 099tb0 staphylococ 091803 xenopus lae 096x57 vbrio chol 091803 xenopus lae 090x94 plasmodium 095x9 plectreurys 090x94 oryza sativ 095x19 plectreurys 095x13 oryza sativ 095x13 oryza sativ 095x13 oryza sativ 095x13 oryza sativ 095x13 oryza sativ 095x13 oryza sativ 095x13 oryza sativ 095x183 streptococc 097054 dictyosteli 095x10 persinia pe

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SEQUENCE FROM N.A.

**MEDLINE-94156481; PubMed=7509320;

**Perez-Melgosa M., Kuo C.C., Campbell L.;

**Perez-Melgosa M. Kuo C.C., Campbell L.;

**Factorion and characterization of a gene encoding a Chlamydia pneumoniae 76-kilodalton protein containing a species-specific
 Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
NCBI_TaxID=83558;
 Last sequence update)
Last annotation update)
 ALIGNMENTS
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAY-2000 (TrEMBLrel. 13, Last anno
 Q9KX33
Q9AS09
P71409
 Q9KWR3
Q99MP1
Q99MTQ5
Q925A4
Q49525
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Q91803
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MVNPIGFGPIDETERTPPAD......SAAVVSAGVLPLQQVLWIRA 463
 Search time 172 Seconds
 Description
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 hits satisfying chosen parameters:
 473505 seqs, 146272329 residues
 SUMMARIES
 7, 2002, 21:41:15
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

 BLOSUM62
Gapop 10.0 , Gapext 0.5
 084627
0987M2
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091CH2
085472
0990R6
0990X4
007290
09NDJ0
 sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mc:*
 sp_virus:*
sp_vertebrate:*
sp_unclassified:*
 seq length: 0 seq length: 2000000000
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 sp_rodent:*
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 sp_plant:*
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61 LRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT 120 121 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKY 180 ASTINQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD 240 Gaps 1 MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI ö Length 715; Indels Infect. Immun. 62:880-886(1994). EMBL, L23921; AAA23117.1; -SEQUENCE 715 AA; 76626 MW; 3F01C9A59DE964C5 CRC64; Ouery Match 97.9%; Score 2214; DB 2; Best Local Similarity 98.9%; Pred. No.:3.9e-115; Matches 454; Conservative 2; Mismatches 3; 317 377 181 437 qa o ò ο δί Q

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 62 RSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDY---KTQAQTAY 118
 DIIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELA 178
 109 SGLENATTLAEYETKWADLMAALQDMERLAKQKAEVTRIKEALQEKQEVID---KLNQLV 165
 DDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK 420
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 61 LRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT 120
 2 VNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVEFWSIL
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 "Genome sequence of an obligate intracellular pathogen of humans: Chlamvdia trachomatis.":
1 MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI
 647 AA; 68525 MW; C0D14C2D74473625 CRC64;
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Last annotation update)
 20.0%; Score 451.5; DB 2; 29.6%; Pred. No. 1.6e-17; wiematches 192;
 Chlamydiaceae; Chlamydia
 421 ALEAALGKAGQQQGILNALGQIASAAVVSAGVLP 454
 Created)
 PRT;
 Chlamydia trachomatis.";
Science 282;754-759(1998).
EMBL. AEOUI33; AAC66226.1;
CCOMplete protecome.
SEQUENCE 647 AA; 68525 MW
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 01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
01-NOY-2000 (TrEMBLrel. 1
CHLPN 76 KDA HOMOLOG.
 Query Match 20.0
Best Local Similarity 29.6
Matches 138; Conservative
 Chlamydia trachomatis.
Bacteria; Chlamydiales;
NCBI_TaxID=813;
 PRELIMINARY;
 Davis R.W.;
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 Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
 Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
 MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI
 DDAENETASIIMSGFROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK
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 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL
 MEDLINE-ZULJOJ, FULNET CO. GILL S.R., Heldelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., weidman J., Khouri H., Craven B., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; Kolonay J. McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
 0;
 96.8%; Score 2188; DB 2; Length 651; 98.9%; Pred. No. 9.7e-114; ive 1; Mismatches 4; Indels
 68217 MW; 47AE6C3FF2FF0123 CRC64;
 Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHLPN 76 KDA HOWGLOG.1 (CT622).
CHDN 78 KDA HOWGLOG.1 (CT622).
 421 ALEAALGKAGQQGGILNALGQIASAAVVSAGVLPLQQVL 459
 651 AA
 MEDLINE=20330349; PubMed=10871362;
 STRAIN=CWL029;
MEDLINE=99206606; PubMed=10192388;
 STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
 EMBL; AE001654; AAD18867.1; -.
EMBL; AP002547; BAA98935.1; -.
EMBL; AE002165; AAF37914.1; -.
 Conservative
 PRELIMINARY;
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SEQUENCE 651 AA;
 al Similarity
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 NCBI_TaxID=83558
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1145 NAVTQAN---SNIEAANSQNDVDQAKTTGENSIDQVTPTVNKKAT-----ARNEITAILN 1196
 STRAIN-COL;
MEDLINE-97302526; PubMed-9158773;
Wu S., de Lencastre H., Sali A., Tomasz A.;
Wh S., de Lencastre H., Sali A., Tomasz A.;
A phosphoglucomutase-like gene essential for the optimal expression of methicillin resistance in Staphylococcus aureus: molecular cloning
VENAKSNNSISNI-----DSAKAAIAT----AKTQIAEAQKKFPDSPILQEA--E 313
 QMVIQAEKDLKNIKPADG-SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILM 372
 Gaps
 54
 87
 Jolly L., Wu S.W., Van Heijenoort J., de Lencastre H., Mendin-Lecreulx D., Tomasz A.; "The femR315 gene from Staphlococcus aureus, the interruption of which results in reduced methicillin resistance, encodes a
 PIGPGPIDE----TERTPPADLSAQGLEASAANKSA-EAQRIAGAEAKPKESKTDS---
 ----VERWSILRSAVNALMS-----LADKLG----IASSNSSSSTS
 SGRROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAA-----ALADAQKALEAA
 Indels 144;
 of
 Length 2478;
 expression
 6B9859A02D023C74 CRC64;
 Last sequence update)
Last annotation update)
 8.5%; Score 192; DB 2; Le
Llarity 23.9%; Pred. No. 0.02;
Conservative 86; Mismatches 194;
 Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
 "Mrp-a new auxiliary gene essential for optimal methicillin resistance in Staphylococcus aureus. Microb. Drug Resist. 5:9-18(1999).
 2478 AA
 and DNA sequencing.";
Microb. Drug Resist. 2:277-286(1996)
 Created)
 Bacteriol. 179:5321-5325(1997).
 MEDLINE=99265121; PubMed=10332717;
 MEDLINE=97431478; PubMed=9286983;
 2478 AA; 263029 MW;
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
 1255 TPKVVKKQAAKDEIDQL 1271
 426 LGKAGQQQGILNALGQI 442
 phosphoglucosamine mutase.
 PRELIMINARY;
 Wu S., de Lencastre H.;
 Staphylococcus aureus.
 Query Match
Best Local Similarity
Matches 133; Conserv
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SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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 MRP PROTEIN.
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 -----RVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAK---A 405
 AQKK----FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSI- 354
 Gaps
 4 PIGPGPIDE----TERTPPADLSAQGLEASAANKSA-EAQRIAGAEAKPKESKTDS--- 54
 -----VERWSILRSAVNALMS-----LADKIG-----IASSNSSSSTS 87
 KLEKQNOTLKETLTTDSADQIPAINSQLEINKNSADQIIKDLEGQNI---SYEAVLTNA
 VDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAE
 223 GEVIKASSEAGIKLGQALQSIVDAGDQSQAAVLQAQQNNSPDNIAATKKLIDAAETKVNE
 RSADVDSTTA-TAPTPPPPTSDDYKTQAQTAYDT----IFTSTSLADIQAALVSL---
 ---PAIAQSLVDQTDATATQIEKDGN-------AIGDAYFAGQNASGA
 179 KYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSL
 KMDAYNEVKQAATARKAQNATVSNATNEEVAEADAAVDAAQKQGLHDIQVVKSKQEVADT
 -QDAVTNIKDTAATD-----EETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDS
 LGKLT-----SFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKT------
 of
 8.5%; Score 192; DB 2; Length 1327; 23.9%; Pred. No. 0.0093; ive 86; Mismatches 194; Indels 14
 "Mrp-a new auxiliary gene essential for optimal expression methicullul resistance in Staphylococcus aureus."; Microb. Drug Res. 5:9-18(1999).
EMBL; v(09928; CAA71062.1; -.
 1327 1327
1327 AA; 140516 MW; B90F2085E800586D CRC64;
 401 GADGELPAEIQAIKDALAQAL-KQPSTDGLATAMGQVAFAAAKVGG 445
 406 AGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAG
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
CTORP1365, PARTIAL (FRAGMENT).
 194;
 Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
 1327
 STRAIN=COL;
MEDLINE=99265121; PubMed=10332717;
 Best Local Similarity 23.9
Matches 133; Conservative
 PRELIMINARY;
 Wu S., de Lencastre H.;
 Staphylococcus aureus.
 SEQUENCE FROM N.A.
 NCBI_TaxID=1280
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SEQUENCE
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| B 838 KHDAYNEVRAANARKAONATVEEVAEADAAVDAAOOGGIHDIOVYKSKOEVADF 897 BEADVIDGTTA-TAPTPEPPESTSTYTOAOCTATTA | :   :       Db 898 KSKVLDKINAIQTQAKVKPAADTI | OY 138 -ODAVTNIKDTAATDEETALI                        | OY 191 LGKLTSFDLLQTALLQSVANI :   :   :   :   :   :   :     :                                    | QY 232PAIAQSLVDQTDATATQIEKDGN             | OY 270 VENAKSINISISNIDSA<br>           | QY 314 QMVIQAEKDLKNIKPADG-SDVPNPG<br> | Qy 373 SGFROMIHMENTENPDSQAAQQELAA. : :: :                    | Oy 426 LGKAGOQOGILNALGOI 442   ::  :   :   Db 1294 TPKVVKKQAAKDEIDQL 1310 | RESULT 7 085472 ID 085472 PRELIMINARY; | 085472;<br>085472;<br>01-NOV-1998<br>01-NOV-1998<br>01-MAY-2000<br>EXTRACELLULA | GN EMB.  OS Abiotrophia defectiva.  OC Bacteria; Firmicutes; Bacillus,  OC Abiotrophia.         |                                                                   |                    | SQ SEQUENCE 2055 AA; Z1504U MW: OUEFY MATCh 8.1%; SC                                                  | Best Local Similarity 22.9%; Pr<br>Matches 109; Conservative 76;<br>Qy 19 ADLSAQGLEASAANKSAEAQRIAGAE | 74                                                   | 129                               |
|-------------------------------------------------------------------------------------------------------|---------------------------------------------|-----------------------------------------------------|-------------------------------------------------------------------------------------------------|-------------------------------------------|----------------------------------------|---------------------------------------|--------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------|---------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------|-------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------|------------------------------------------------------|-----------------------------------|
| A B B C                                                                                               |                                             | RSADVDSTTA-TAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSL | -QDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDS<br> :    :     :   :   :   :   :   :   : | LGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKT | PAIAOSLVDGTDATATQIEKDGNAIGDAYFAGQNASGA | DSAKAAIATAKTQIAEAQKKFPDSPILQEAE<br>   | QMVIQAEKDLKNIKPADG-SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILM | NPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAA ::                               |                                        | 6<br>NLCH2 PRELIMINARY; PRT; 2478<br>NLCH2;                                     | (TrEMBLrel. 15, Created)<br>(TrEMBLrel. 15, Last sequence up<br>(TrEMBLrel. 15, Last annotation | nylococcus aur<br>eria; Firmicut<br>Ilus/Staphyloc<br>TaxID=1280; | .A.<br>aureus gene | ;<br>PR-1999) to the EMBL/GenBank/DDBJ dat.<br>16; BAA93438.1;<br>478 AA: 262993 MW: 1C118EBEDDB03B34 | 8.4%; Score 190; DB 2; Length 2478; Similarity 23.9%; Pred. No. 0.026; Indels 144; Gaps              | PIGPGPIDETERTPPADLSAQGLEASAANKSA-EAQRIAGAEAKPKESKTDS | VERWSILRSAVNALMSLADKLGIASSNSSSSTS |

21; | : |: :| |||: :| SAKNAVTQAADAKK-DAIEKDPNLTREEKDAA--KA 1519 : : || : || SIDIDNAA-----ANNDVDNAKTINEATIAAIIPDA 1066 NNGSTTEEKAAAKQQVQTEKTTADAAIDAAHTNAE 1124 OSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLA 128 DEETAIAAEWETKNADAIKVGAQITELAKYASDNQA 186 NNNKAAELLKEMQDNPVVPGKT------ 231 GTTVGGSKQQGSSIGSIRVSMLLDDAENETASILM 372 IAAEWETKNADAIKVGAQITELAKYASDNQAILDS 190 N-----AIGDAYFAGONASGA 269 AKAAIAT----AKTQIAEAQKKFPDSPILQEA--E 313 |: : ||:| TEVENAYNTRKQEIQNSNASTTEEKQAAYTELDTK 954 Score 182.5; DB 2; Length 2055; Pred. No. 0.054; ; Mismatches 189; Indels 101; Gaps AEA----KPKESKTDSVERWSILRSAVNALMSLAD 73 /Clostridium group; Streptococcaceae; of emb, a Gene Encoding the Major stivus."; MBL/GenBank/DDBJ databases. 4; 9699C11DDE93E2FD CRC64; ist sequence update)
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1629 -TSWRTSTSDSQSMSLSTSTSTSMSDS------TSLSDSVSDSTS--DSTSASTSGSMS 1678
 1174 --SNIEAANSONDVDQAKTTGETSIDQVTPTVNKKAT----ARNEITAILNNKLQEIQA 1226
 1516 SASASESDSSSTSLSDSTSASMQSSESDSQSTSASLSDSLSTSTSNRMST----IASLS 1570
 MNDSTTEEQQAAKDKVDQAVVTANADIDNATANTDVDNAKTTNEATIAAITPDANVKPAA 1055
 Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M., Matuyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Tinoue R.I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Gyasawara N., Hayashi H., Hiramatsu K.; Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
 -- IGDAYFAGQNASGAVENAKSNN 277
 82 SSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQT-AYDTIFTSTSLADIQAALVSLQDA 140
 22 SAGGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSN 81
 DLKNIKPADG-SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIH
 TSVSTSESGSTSESTSESDSTSTSLSDSOSTSRSTSASGSASTSTSDSRSTSASSS-
 141 VTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDL-
 381 MFNTENPDSQAAQQELAAQARAAKAAGDDSAAA-----ALADAQKALEAALGKAGQQQ
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 Length 2271;
 7C2A7040D6C8289D CRC64;
 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SA2447 PROTEIN.
 8.0%; Score 180; DB 2; Le
18.9%; Pred. No. 0.084;
tive 96; Mismatches 187;
 Staphylococcus aureus subsp. aureus N315.
Bacteria: Firmicutes; Bacillus/Clostridium grc
Bacillus/Staphylococcus group; Staphylococcus
NCBI_TaxID=158879;
 2271 AA
 PRT;
 Lancet 357:1225-1240(2001).

MBL; ABO03138; BAB43752.1; -.

Complete proteome.

SEQUENCE 2271 AA; 227847 MW;
 AQSLVDQTDATATQIEKDGNA-
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Matches 79; Conservative
 PRELIMINARY;
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 1576 KKDAIEKDPNLTREEKDAAKAKVDAEAKKAKDAIDAATSNADVTAQKDAGKNAINAVPQT 1635
 1696 TAKQNEGTKAINDVPQTPTAKTDAKNAVDQAATDKKSAI------ENDPALTREEKD 1746
 SEQUENCE FROM N.A.

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus

aureus."
187 ILDSLGKLTSFDLLQTALLQS--VANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDA 244
 102 PP------PPTSDDYKTQAQTAYDT-----IFTSTSLADIQAALVSL--- 137
 138 -QDAVTNIKDTAATD-----EETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDS 190
 LGKLT-----SFDLLQTALLQSVANNNKA------AELLKEMQDNPVVPGKT--PAI 234
 Gaps
 55 -----VERWSILRSAVNALMSLADKLGIASSNSSSSTSRSAD-----VDSTTATAPT 101
 PIGPGPIDE----TERTPPADLSAQGLEASAANKSA-EAQRIAGAEAKPKESKTDS--- 54
 283 DSAKAAIATATQIAEAQK-KFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTV
 342 GGSKQQGS-SIGSI-RVSMLLDDAEN---ETASILMSGFRQMIHMFNTEN-----PDSQ
 821 KMDAYKEVRQAATARKAQNATVSNATDEEVAEANAAVDAAQTEGLHDIQVVKSQQEVADT
 391 AAQQELAAQARAAKAAGDDSAAALADAQKALEAALGKAGQQQGILNALGQIASA 445
 8.0%; Score 182; DB 2; Length 2481;
23.3%; Pred. No. 0.072;
ive 91; Mismatches 202; Indels 128;
 2481 AA; 263767 MW; E1EAAB99B81665E8 CRC64;
 Created)
Last sequence update)
Last annotation update)
 Staphylococcus aureus subsp. aureus N315.
Bacteria: Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=158879;
 245 TATQIEKDGNAIGDAYFA-----GQNASGAVENAKSN--
 2481 AA.
 PRT;
 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
 Lancet 357:1225-1240(2001).
EMBL; AP003136; BAB43253.1;
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Matches 128; Conservative
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 D-----SLSDSKSTSGS---TSTSTSGSLSGSESVSESTSLSDSISMSDS 1840
 1201 TEKAKAAELAGEKSLTDTGKEARDAVELAKDKELAKEAIRTEEEEATKIVEKLAEDTRKA 1260
 1261 IEDNPNLSDEDKQAEIKKLTDAVAKTLATI----RDNADKRTQEAEKA-----QALAD 1309
 1310 LEKA-----KETQKIADKAAIDRLTILVKDGELEATKQDAKNKIAKDAAAAKEAIASNPN 1364
 340
 1522 KESAKKAVDADAKAATDAIDASTSPVEAQSAEDKGVGSIAQDVLDAAKQDAKNKIAKEVA 1581
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260 YFAGQNASGAV-----ENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEA 312
 --SIRVSMLLDDA 363
 of
 Gaps
 TERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKES-KTDSVERWSIL-RSAVNALMS 70
 1841 TSTSDSDSLSGSTSLSGSTSLSTSDSLSDSKSLSS---SQSMSGSESTSTSVSDSQSS 1895
 364 ENETASILMSGFROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKA 421
 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 Smith H.E., Reek F.H., Vecht U., Gielkens A.L.J., Smits M.A.;
"Repeats in an extracellular protein of weakly pathogenic strains streptococcus suis type 2 are absent in pathogenic strains.";
Infect. Immun. 61:3318-3326(1993).
EMBL: X71880; CAA507141.:
SEQUENCE 1822 AA; 192631 MW; 3838960C77641D7D CRC64;
 130 IQAALVSLQDAVTNIKDTAATDEETAIA--AEWETKNADAIKVGAQITELAKYASDNQAI
 290 ATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDV-----PNPGTT---
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 188 LDSLGKLTSFDLLQTALLQSVANNNKA-----AELLKEMQDNPVVPGKTPAIAQSLVD
 241 QTDATA-TQIEKDGNAIGDAYFAGQNASGA------VENAKSNNSISNIDSAKAAI
 1415 AAKQDAKNKIAKDAAAAKEAIGSNPNLTDAEKKTFTDAVDAEVAKANDAIS-----
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 77; Mismatches 195; Indels 103;
 Length 1822;
 Last sequence update)
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 EQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIG-
 Score 177.5; DB Pred. No. 0.088;
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 MEDLINE=93328288; PubMed=8335363;
 Query Match
Best Local Similarity 23.6%;
Matches 116; Conservative 77
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SEQUENCE FROM N.A.
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NCBI_TaxID=1307;
 Streptococcus
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01-OCT-2000 (
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 "Plasmodium vivax merozoite surface proteins-3 beta and -3 gamma share structural similarities with Plasmodium vivax MSP-3 alpha and define a new gene family in Plasmodium.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AAF78287.1;
InterPro; IPR000122; Chemotaxis_transducer.
SEQUENCE 697 AA, 75685 MW; OAF2AE9801A956A7 CRC64;
 449
 256
 391
 311
 ETASILMSGFROMIHMFNTE-NPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEA 424
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 143 NIKDTAATDEETAIAAEWETKNADAIKVGAQI-----TELAKYASDNQAILDSLGKLTS 196
 113 AKAAESAKKNTLDALEKVNVPTELNNVKKFAESAATEAQKQENIATEAEKKVAEANGEVV 172
 173 ELOKLKDEVDKAAKKAKOLOLKAEIAEHAVKAQVAKTEAEKAQKDATTAKEVAIKETGTS 232
 -----DLSAQGLEASAANKSAEAQRI 40
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 233 KSENVTKAIDMAKKEEEETKNQASIASENADKAAKAAQEEVKKEIKDENKEISQLENEIT
 197 FDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAI
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Galinski M.R., Al-Khedery B., Ingravallo P., Corredor-Medina C.,
Barnwell J.W.;
 7.8%; Score 177; DB 5; Length 697; 20.9%; Pred. No. 0.029; ive 74; Mismatches 186; Indels 186;
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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 41 AGAEAKPKESKTDSVERWSI---------
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
697
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 ALGKAGQQQGILNALGQIASAAVV 448
 Plasmodium vivax (strain Belem)
 01-JUN-2001 (TrEMBLrel. 17, L
MEROZOITE SURFACE PROTEIN 3B.
 Ouery Match 7.8
Best Local Similarity 20.9
Matches 118; Conservative
 1 MVNPIGPGPIDETERTPPA-
 PRELIMINARY;
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 SASIAAAAAASASSYESQFSDASSSSNAAAAASSQQSSYDTSSDLVSASSAAAAAAASASS 1512
 ---SAAG--RAEGHAEDARDSADAAAL----- 1103
 -----DAEAARSAADTAEQAAEDARDAADHAATEAAAAEEAAKDAQKYAESAQQAAE 1155
 79 SSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQ 138
 ----DAVTNIKDTAATDEETAIAAEWEÎKNADAIKVGAQITELAKYASDNQAILDSLGKL 194
 339 TTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFR-QMIHMFNTENPDSQAAQQE-- 395
 -----LAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQG-----ILNALGQI 442
 HMFNTENPDSQAAQ-----QELAAQAR-AAKAAGDDSAAA--ALADAQKALEAALGKAG 430
 Gaps
 19 ADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIA 78
 TSFDLLQTA-----LLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD-QTDAT
 246 ATQIEKDGNAIGDAY-----FAGQNASGAVENAKSNNSISN--IDSAKAAIATAKTQI
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Spider Silk
 Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Haplogynae; Plectreuridae; Plectreurys.
NCBL_TaxID=33319;
 Length 2016;
 F53A47DB185826F1 CRC64;
 Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R. "Extreme Diversity, Conservation, and Convergence of Fibratic Convergence of
 (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
 AEAQKKFPDSPILQEA-----EQMVIQAEKDLKNIKPADG----
 7.7%; Score 173; DB 5; L
21.5%; Pred. No. 0.18;
ve 83; Mismatches 212;
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 1156 QAEKEANA-EQIDKGTVVDQTGAPIGDVFYV 1185
 431 QQQGILNALGQIASAAVVSAGVLPLQQVLWI 461
 SEQUENCE FROM N.A.
MEDLINE=21179804; Pubmed=11283372;
 2016 AA; 196162 MW;
 Science 291:2603-2605(2001).
EBMBL; AF350283; AAK30612.1; -.
NON_TER 1
SEQUENCE 2016 AA; 196162 MW.
 Plectreurys tristis (Spider)
 Best Local Similarity 21.5%;
Matches 105; Conservative 8
 PRELIMINARY;
 1068 AYDTQATKDAAAAD--
 FIBROIN 3 (FRAGMENT)
 Fibroin Sequences.
Science 291:2603-2
 ASAAVVSA 450
 01-JUN-2001
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 956 APANDAIQLGSPYV---TTDSAAGLAVLTGQSSKTIAEQQQAVAEAH-----AQNAEESA 1007
 1008 AQAQSVANAASGDSKAAYTLAAEALGYAADARNSAKEALGYSAEAASYATQAAQSLIRTI 1067
 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinsshi H., Hopwood D.A.;

"A set of cordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL: AL134423; CAB62715.1;

InterPro; IPR000772; Ricin_B_lectin.

PFam; PR00652; Ricin_B_lectin; 1.

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SEQUENCE 1545 AA; 161519 MW; 81EF325143593AEA CRC64;
 KEMQD-----NPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENA 273
 274 KSNNSISNIDS--AKAAIATAKTQI---AEAQKKFPD-----SPILQEAEQMVIQA 319
 320 EKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMI 379
 741 DAKERAETADTTATEKRKGAEAARDKAKALRDDAWDAEQKANAARAKADAKEAYAQASAS 800
 ----ILRSAVNALMSLADKLGIAS----SNSSSSTSRSADVDSTTATAPTPPPPT---S 107
 108 DDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAI-----AA 158
 EWETKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELL 218
 911 D-AKKEADAAKAEA-VTALA------GANESTGYAYTTAQAAVDAGNSAAQVA 955
 Gaps
 11 DETERTPPADLSA--QGLEASAANKSAEAQRIAGAEAKPK----ESKTDSVERWS----
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
 7.7%; Score 174; DB 2; Length 1545;
25.0%; Pred. No. 0.11;
tive 62; Mismatches 195; Indels 126;
 Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A., Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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 1545 AA
STRAIN=43(2);
MEDLINE=97000351; PubMed=8843436;
 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, PUTATIVE SECRETED PROTEIN.
 Conservative
 PRELIMINARY;
 Streptomyces coelicolor.
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 STRAIN=A3(2);
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AND W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

AND W.V., Kennedy S.P., Hall J., Dahl T.A., Welti R., Goo Y.A.,

B. Wartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

And M., Freitas T., Peck R.F., Krebs M.P., Angewine C.M., Dale H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

B. Behardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

Accome sequence of Halobacterium species NRC-1.",

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

B. Malb., ARG004994, AAG18922.1;

R. InterPro; IPR000122; Chemotaxis_transducer.

R. InterPro; IPR000122; Chemotaxis_transducer.

R. InterPro; DPR00125; Chemotaxis_transducer.

R. InterPro; DPR00125; Chemotaxis_transducer.

R. Rinker PR00125; May P.
 27;
 367 R---IDGIT-ALIEDIAEETNMLALNASIEAARTGSDGD--GFAVVADEVKDLAEETREQ 420
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 276 NNSISNIDSA-----KAAIATAKTQIAEAQKKFPDSP-ILQEAEQMVIQAEKDLKNIKP 328
 || | | | :: | :: | : | :| | 421 AADISEIVDAVIEKAEDASIAIGEVD-AEVERKITKAEGVLRDFEAIV----DEVANVNH 475
 250 QSFSDAVLAVSRTTDERVDAVADRSAAVSESVTEIADGANQQTNQLNNIAAEMDTVSATV 309
 DNPVVPGKTPAIAQSLVDQTDATA--TQIE-----KDGNAIGDAYFAGQNASGAVENAKS 275
 ----GSIRVSMLLDD 362
 TD-------AARAGDL---TATVDAAALDVIDDHRAAVEDFNQLLETLADTISDI 249
 125 TSLADIQAAL------VSLQDAVTNIKDTA--ATDEETAIAAEWETKNADA 167
 72 ADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQA-----QTAYDTIFTS 124
 17 PPADLSAQGLEASAANKSAEAQRIAGAEAKPK----ESKTDSVERWS-ILRSAVNALMSL 71
 168 IKVGAQITELAKYASDNQAIL----DSLGKL-TSFDLLQTALLQSVANNNKAAELLKEMQ
 184; Indels 122;
 7.6%; Score 171; DB 1; Length 627; 23.4%; Pred. No. 0.054;
 Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
 ESF2867FA6CA2A75 CRC64;
 Last sequence update)
Last annotation update)
 627 AA
 87; Mismatches
 329 A--DGSDVPNPG----TTVGGSKQQGSSI----
 Created)
 65655 MW;
 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
 Conservative
 Local Similarity
nes 120; Conserv
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 HTR14 OR VNG0355G.
 SEQUENCE FROM N.A.
1689 AAAASASS 1696
 NCBI_TaxID=64091;
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SEQUENCE FROM N.A.

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Odothi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
 426 NENTQNITDKDVKSMEAALIGSLLSLSNNLDTQAKAAQKDSQALRNISYGILASDKPSDF 485
 FAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAE 320
 374
 653 KNAQANFPKVKSDVAKAANFVRNDLPQ------LEQRLTNATASVNKNLPTLLNG 701
 76 GIAS---SNSSSSTSRSADVDSTTA----TAPTPPPPTSDDYKTQAQTAYDTIFTSTSLA 128
363 AENETASI--LMSGFRQMIHMFNTENPDSQAAQQELAAQARAAK--AAGDDSAAAALADA 418
 LLKEMQDNPVVPGKT-PAIAQSLVDQ---TDATATQ----IEKDGNA-----IGDAY
 600 NKGOTALSNVQ-SKLNTIDQVINSGQAILKNGKTRIDRLQ-----TVLPSIEQQXISAV
 KDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASI - - - - - LLMSG
 Length 993;
 375 FROMIHMENTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAA
 Lancet 357:1225-1240(2001).
EMBL; AP003138; BAB43741.1; -.
Complete proteome.
SEQUENCE 993 AA; 108714 MW; 71C414CF75F84A1F CRC64;
 Last sequence update)
Last annotation update)
 D-----AATDEETA--
 151;
 7.6%; Score 171; DB 2;
24.8%; Pred. No. 0.095;
 Staphylococcus aureus subsp. aureus N315.
Bacteria: Firmicutes; Bacillus/Clostridium gro
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=158879;
 AA.
 Mismatches
 QPASDAE-----DEEGVPDSGGE--SVAVSDGG 613
 419 QKALEAALGKAGQQQGILNALGQIASAAVVSAG 451
 993
 Created)
 24.8%; Fin
 702 YDQAVGLLNKNQPQAKKALSDLA-
 01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
 Query Match 7.65
Best Local Similarity 24.8
Matches 102; Conservative
 PRELIMINARY;
 01-JUN-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
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Search completed: February 7, 2002, 21:41:19 Job time: 4648 sec

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|-------------------------------------------------------|-----------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|---------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| GenCore version 4.5                                   | ceei (a)                                                              | Run on: February 7, 2002, 19:33:50; Search time 12230.8 Seconds (without alignments) 1923.418 Million cell updates/sec     | Title: Perfect score: 1426 Sequence: 1 tgagcagtactcgttgctgctccttgaccctggaaggtgc 1426                                          | Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0                                    | Searched: 1472140 seqs, 8248589755 residues                                            | er of hits sa<br>seq length:                                                           | Maximum DB seq length: 2000000000 Dost-processing: Minimum Match OB | FOSC Processing: Minimum March 0%<br>Maximum Match 100%<br>Listing first 45 summaries                                | Database : GenEmbl:*  1                                                                                                                                                                                                              | 5): em_htg_cher:* 36: em_htg_other:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  \$UMMARIES                                                                                           |

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Hideki Hirakawa, Kyushu University, Graduate School of Genetic Resources Technology; 6-10-1 Hakozski, Higashl'ku, Fukuoka, Fukuoka 812-8581, Japan (E-mail:hirakawa@grt.kyushu-u.ac.jp, URL:http://www.grt.kyushu-u.ac.jp, Tel:81-92-642-3043, Fax:81-92-642-3043)
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Direct Submission
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 Chlamydophila pneumoniae AR39.
Chlamydophila pneumoniae AR39
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Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., White, O., Alcokey, E.K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, K., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
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Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T.
Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA
Nucleic Acids Res. 28 (12), 2311-2314 (2000)
Shirai, M. Direct Submission Submission Construct Submission Shirai, M. Shirai, M. Submitted (04-UDL-2000) to the DDBJ/EMBL/GenBank databases. Mutsunori Shirai, Yamaguchi University School of Medicine, Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi 155-5856, Japan (E-mail:mshirai@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-227, Fax:81-836-22-2415) On Sep 15, 2000 this sequence version replaced gi:6172398 gi:61
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Carter, M.W., Al-Mahdawi, S.A.H., Giles, I.G., Treharne, J.D.,
Mard, M.E. and Clarke, I.M.
Nucleotide sequence and taxonomic value of the major outer membrane protein gene of Chlamydia pneumoniae IOL-207.

J. Gen. Microbiol. 137, 465-475 (1991)
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 Summitted (12-JUN-1993) M. Lavin, Professor of Molecular Oncology, Queensland Institute of Medical Res, The Bancroft Centre, 300 Herston Road, Brisbane QLD 4029, AUSTRALIA updates [2]
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Girjes, A.A., Carrick, F.N. and Lavin, M.F.
Remarkable sequence relatedness in the DNA encoding the major outer membrane protein of Chlamydia psittaci (koala type I) and Chlamydia
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Length 1170; Indels 369

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|---------|----------------------------------------------------------------------|----------------------------------------------------------------------|-----------------------------------------------------------------------|------------------------------------------------------------|-----------------------------------------------------------------------|-----------------------------------------------------------------------|----------------------------------|---------|------------------------------------------------------------------------------------------------------------|----------------------------------|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------|-------------------------|-------------------------|--------------------------------------------------------------------------------------|--------------------------|--------------------------------------------------|---------------------------------------------------------------|-------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------|
| <b></b> | <del>,</del>                                                         | <del></del>                                                          |                                                                       |                                                            |                                                                       |                                                                       |                                  |         |                                                                                                            |                                  |          |                                                                                                                                                                                                     |                                |                         |                         |                                                                                      |                          |                                                  |                                                               |                                                                                     | 3                                                                                                                                                                                      |                              |
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| Db 730  | Qy 849<br>Db 790                                                     | Qy 909<br>Db 850                                                     | Qy 969<br>Db 910                                                      | Oy 1029 o                                                  | Qy 1089<br>Db 1030                                                    | Oy 1149<br>Db 1090                                                    | Oy 1209<br>Db 1150               | # H1080 | CHTOMPAAI<br>LOCUS<br>DEFINITION                                                                           | ACCESSION<br>VERSION<br>KEYWORDS | ORGANISM | KEFEKENCE<br>AUTHORS<br>TITLE                                                                                                                                                                       | JOURNAL                        | FEATURES                | )<br>)                  |                                                                                      | CDS                      |                                                  |                                                               |                                                                                     |                                                                                                                                                                                        | BASE COUNT<br>ORIGIN         |

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 Tharp.A.C., Mitchell,W.M., Stratton,C.W. and Ding,L.-M.
Direct Submission
Submitted (25-FBB-1999) Pathology, Vanderbilt University, C-3321
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Location/Qualifiers
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Tharp, A.C., Mitchell, W.M., Stratton, C.W. and Ding, L.-M.
Presence of viable Chlamydia pneumoniae in fetal calf serum and epithelial-derived cell lines
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Everett,K.D.E., Hambly,W.A. and Andersen,A.A.
Direct Submission
Submitted (22-MAY-2000) Medical Microbiology and Parasitology,
University of Georgia, College of Veterinary Medicine, Athens,
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 Bush, R.M. and Everett, K.D. Molecular evolution of the Chlamydiaceae
Int. J. Syst. Evol. Microbiol. 51 (Pt 1), 203-220 (2001)
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 Salti-Montesanto, V.
 and Loughorton,). In the major identification of protective epitopes by sequencing of the major outer membrane protein gene of a variant strain of Chlamydia
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Submitted (29-MAY-2000) Moredun Research Institute,
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Structures of and allelic diversity and relationships among the major outer membrane protein (ompA) genes of the four chlamydial
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MEDLINE
FEATURES
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Chlamydophila abortus strain B577 major
precursor (ompA) gene, complete cds.
 1206 gtatctggtcagttcagattc 1226
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906

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Gaps

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425 445 485

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LOCUS DEFINITION

RESULT 15 CHTOMPAAD

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 1226 ATGAATGCTCAATTCAGATTC 1246
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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4912 4912 5108 5108

## ALIGNMENTS

AAX25047 standard; DNA; 1261 BP

RESULT AAX25047

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Database

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AAX81562

Plasmid p Plasmid p Plasmid e

Major outer membrane protein; MOMP; psittacosis; infection; vaccine; genetic immunisation; ss. Chlamydia psittaci major outer membrane protein DNA (LOUU ) UNIV LOUISIANA & AGRIC & MECH COLLEGE. Location/Qualifiers 80..1249 /\*tag= a 98WO-US17943 Chlamydia psittaci. W09910005-A1 28-AUG-1998; 28-AUG-1997; 05-JUL-1999 04-MAR-1999 AAX25047; 

Tully TN;

Kousoulas KG,

Baghian A, Chouljenko VN,

WPI; 1999-254214/21. P-PSDB; AAW98188.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description              | Chlamydia psittaci | Chlamydia psittaci | Chlamydia psittaci | C. pneumoniae sero | Chlamydia trachoma | Chlamydia trachoma | DNA encoding Chlam | Chlamydia trachoma | Sequence encoding | Complete genome se | Chlamydia psittaci |
|-----------|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| SUMMARIES | ID                       | AAX25047           | AAX25048           | AAX25046           | AAA64764           | AAH56267           | AAV62447           | AAZ92753           | AAV40646           | AAN60007          | AAZ01425           | AAX25045           |
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|           | Query<br>Match Length DB | 1261               | 1660               | 1209               | 1578               | 1578               | 3133               | 3133               | 3133               | 3133              | 1038602            | 744                |
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|           | Result<br>No.            | 1                  | 7                  | e                  | 4                  | 'n                 | 9                  | 7                  | æ                  | 6                 | 10                 | 11                 |

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FIXEX X DO DO DO DO DO DO X & Q

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This DNA sequence codes for the major outer membrane protein (MOMP, see AAW98187) of Chlamydia psittaci strain 6BC. Claimed MOMP polypeptides (see AAW98183 and AAW98184) comprise regions VD3 and VD4 of an MOMP, i.e. they lack regions VD1 and VD2. Claimed vaccine compositions include such MOMP polypeptides, optionally fused to a maltose binding protein. Also claimed are isolated nucleic acids encoding the polypeptide, a vector, and a method of preventing C.
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 Major outer membrane protein; MOMP; psittacosis; infection; vaccine; genetic immunisation; ss.
 Tully TN;
 psittaci major outer membrane protein
 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE
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 05-JUL-1999
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 for the major outer membrane protein (MOMP,
 This DNA sequence codes for the major outer membrane protein (MOMP see AAW98187) of Chlamydia psittaci strain B577. A claimed MOMP by Orperlide (see AAW98184) comprises regions VD3 and VD4 of MOMP.

i.e. it lacks regions VD1 and VD2. A claimed vaccine composition includes the MOMP polypeptide, optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acide concoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in
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 for Chlamydia psittaci infections
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72.2%;
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 psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking regions VDI and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in
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ilarity 69.5%;
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This DNA sequence codes for the major outer membrane protein (MOMP, see AAW98187) of Chlamydia psittaci strain LSUWTCK, a cockatiel isolate (the MOMP gene sequence of this isolate is identical to that of C. psittaci Avian Type C). A claimed MOMP polypeptide (see AAW98183) comprises regions VD3 and VD4 of MOMP, i.e. it lacks regions VD1 and VD2. A claimed composition includes MOMP colypeptide lacking VD1 and VD2. Optionally fused to a maltose binding protein. Also claimed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing C. Constitution in the polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic vaccination. The vaccines are used to prevent C. psittaci infection, especially in
 ---gattcgttctcagacttcatgcaaattgttcctgtcagatcaacagtttaaatct
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 Major outer membrane protein, MOMP; psittacosis; infection; vaccine; genetic immunisation; ss.
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 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE
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 Disclosure; Page 53-55; 72pp; English
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 36.7%;
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The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is also thought to play a role in the pathogenesis of atherosciencia.
 The present sequence is a nucleic acid sequence
 Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence
 187
 Gaps
EJ;
 infertility;
 Score 514.6; DB 21; Length 1578;
Pred. No. 1.2e-149;
0; Mismatches 314; Indels 42;
 pmp gene Ra12 fusion coding sequence
 Stromberg
 Chlamydial infection; sexually transmitted disease; pelvic inflammatory disease; PID; tubal obstruction; inf trachoma; blindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial;
 Sequence 1578 BP; 414 A; 394 C; 382 G; 388 T; 0 other;
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 invention.
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 Page 205; 256pp; English
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ilarity 68.8%;
Conservative (
 98US-0208277.
99US-0288594.
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99US-0426571.
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 99WO-US29012.
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 coronary heart disease. isolated in the present
 Probst P, Bhatia A,
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 (CORI-) CORIXA CORP.
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08-APR-1999;
01-OCT-1999;
22-OCT-1999;
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 tagaaaagcttgtggagttactgtaggagctactttagttgatgctgataaatggtcact 1165
 1574
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 cggagttaaaaggt-----actactgtaaatgcaaatgaactaccaaacgtttc 580
 975 acgiggagetttaigggaaigiggtigigeaactitaggagetgagiteeaataegetea
 tttaagtaacggagttgttgaactttacacagacacctctttctcttggagcgtaggcgc
 tcgtggagccttatgggaatgcggttgtgcaactttgggagctgaattccaatatgcaca
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 tagoggcatggctgccaactcctacgcaggctataggtaacgcaagtaatactaatcagcc
 ----gccgtagatagacctaacccggcctacaataagcattacacgatgcagagtggtt
 675 agaagcaaatggcagaccgaacatcgcttacggaaggcatatgcaagatgcagagtggtt
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 aggagcttctaatggttacattagaggaaactctacagcgttcaatctcgttggtttatt
 caaacccaagggctataaaggcgtt-----gctttccccttgccaacagacgctggcgt
 ctctctatcttacagactaaactctttagtgccatacattggagtacaatggtctcgagc
 cttaactgcatggaacccttcttactaggaaatgccacagcattgtctactact----
 ---gattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaagtttaaatc
 ttctatgggagccaagcctactggatccgctgctgcaaactatactact--
 c 1575
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Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease
 The present nucleotide sequence is provided in a specification relating to compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of Chlamydia antigens and bank sequences encoding such polypeptides. They are useful for vaccinating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections,
 247
 554
 307
 674
 494
 Gaps
 tgctgcaggagatccttgcgatccttgcgctacttggtgcgacgctattagcttacgtgc
 gttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaagg
 tgcttcaggagatccttgcgatccttgcgctacttggtgtgacgccattagcatccgcgc
 ttctatgggagccaagcctactggatccgctgctgcaaactatactact------
 tagcggcatggctgcaactcctacgcaggctataggtaacgcaagtaatactaatcagcc
 Length 1578;
 42;
 pelvic inflammatory disease; trachoma; atherosclerosis; heart cacute respiratory tract infection; Capl; CT529; OMCB; polymorphic membrane protein; pmp; thiol specific antioxidant;
 ٦,
 Indels
 vaccine; infection; fusion protein; antigen;
 Scholler
 Sequence 1578 BP; 414 A; 394 C; 382 G; 388 T; 0 other;
 Score 514.6; DB 22;
Pred. No. 1.2e-149;
0; Mismatches 314;
 SP,
 Fling
 trachomatis pmp gene sequence.
 Skeiky YAW,
 "Laim 1; Page 211; 295pp; English.
 atherosclerosis and heart disease.
 ВР
 36.1%;
68.8%;
 DNA; 1578
 99US-0454684.
2000US-0556877.
2000US-0598419.
 04-DEC-2000; 2000WO-US32919
 (first entry)
 Query Match 36.1
Best Local Similarity 68.8
Matches 785; Conservative
 Chlamydia trachomatis.
 Bhatia A,
 WPI; 2001-374831/39
 (CORI-) CORIXA CORP
 standard;
 WO200140474-A2
 20-JUN-2000;
 19-APR-2000;
 03-DEC-1999;
 05-SEP-2001
 07-JUN-2001
 Chlamyćia;
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AAH56267
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---gccgtagatagacctaacccggcctacaataagcatttacacgatgcagagtggtt

357

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---gattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaagtttaaatc 1105
 tagaaaagottgtggagttactgtaggagctactttagttgatgctgataaatggtcact 1165
 1166 tactgcagaagctcgtttaattaacgagagctgctcacgtatctggtcagttcagatt 1225 | 1166 tactgcagaagctcgttcagatt 1175 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 | 1177 |
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 1275 aacttttgatgetgatactateegeattgeteaaectaaattaaaateggagattettaa 1334
 1035 atctaatectaagattgagatgeteaacgteactteaageeceageacaatttgtgattea 1094
 caaaccaagaggctataaaggagctagctcgaattttcctttacctataacggctggaac 1154
 934
 cggagttaaaggt-----actactgtaaatgcaaatgaactaccaaacgtttc 580
 855 agggttttcagctgcaagctcaatctctaccgatcttccaatgcaacttcctaacgtagg 914
caaacccaagggctataaaggcgtt-----gctttccccttgccaacagacgctggcgt
 aggagettetaatggttacattagaggaaactetacagegtteaatetegttggtttatt
 701 gtccaaacctaaagttgaagaacttaatgtgatctgtaacgtatcgcaattctctgtaaa
 agcaacagctactggaacaaagtctgcgaccatcaattatcatgaatggcaagtaggagc
 ctctctatcttacagactaaactctttagtgccatacattggagtacaatggtctcgagc
 cttaactgcatggaacccttctttactaggaaatgccacagcattgtctactact-----
 cattactacatggaacccaagccttataggatcaaccactgctttgcccaataatagtgg
 Chlamydia trachomatis major outer membrane protein DNA.
 BP.
 AAV62447 standard; DNA; 3133
 (first entry)
 02-FEB-1999
 1226 c 1226
 1575 c 1575
 AAV62447;
 9
 1095
 875
 935
 1335
 1050
 1106
 1455
 761
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 AAV62447
ID AAV6
XX
AC AAV6
XX
DT 02-F
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DE Chla
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1355 tgcctgtggggaatcctgctgaaccaagccttatgatcgacggaattctatgggaaggtt 1414
 190 ctgcaggagatccttgcgatccttgcgctacttggtgcgacgctattagcttacgtgctg 249
 This DNA sequence codes for a 42 kDa major outer membrane protein (MOMP, see AAW73141) of Chlamydia trachomatis serovar L2. A library of chlamydial genomic DNA was produced in the phage lambda 1059 system. A lambda 1059 recombinant having a 9.2 kD insert was shown to be homologous to lambda gl11/I/L2/33 (see AAW62446) by Southern analysis and was used for endonuclease digestion mapping and additional Southern analyses. 2 Contiguous fragments were identified and these contained sufficient base pairs to encoce the L2 MOMP gene product. These fragments were cloned into M13 for DNA sequencing. Novel recombinant DNA constructs are provided for
 Gaps
 hosts. A claimed probe for detecting C. trachomatis comprises a polynucleotide fragment that specifically hybridises to a DNA or RNA polynucleotide fragment that
 Probe for detecting Chlamydia trachomatis - comprises polynucleotide fragment that hybridises to major outer membrane protein DNA or RNA
 DNA sequencing. Novel recombinant DNA constructs are provided the expression of a polypeptide having immunological activity corresponding to that of a naturally-occurring MOMP of C. trachomatis. Such polypeptides find use as reagents in the detection of C. trachomatis, or antibodies to C. trachomatis, as vaccines against infection by C. trachomatis in susceptible hosts. A claimed probe for detecting C. trachomatis comprises
 DB 19; Length 3133;
 sequence encoding C. trachomatis 38-45 kba MOMP. The probe a sequence which is complementary to at least 12 contiguous of the sequence given in AAV62447.
 Indels
 outer membrane protein; MOMP; diagnosis; vaccine;
 Sequence 3133 BP; 911 A; 667 C; 611 G; 944 T; 0 other;
 33.6%; Score 479.4; DB 19;
llarity 66.5%; Pred. No. 1.6e-138;
Conservative 0; Mismatches 356;
 Stephens R;
 Location/Qualifiers
1288..2472
/*tag= a
1288..1353
/*tag= b
1354..2469
 Agabian N, Kuo C, Mullenbach G,
 Claim 5; Fig 2A-E; 15pp; English.
 Chlamydia trachomatis serovar L2
 86US-0818523.
85US-0692001.
91US-0691639.
93US-0144095.
95US-0468451.
 WASHINGTON RES FOUND
 95US-0468451
 /*tag=
 WPI; 1998-567652/48.
 CORP
 Local Similarity
les 741; Conserv
 P-PSDB; AAW73141
 (CHIR) CHIRON (WASH-) WASHING
 06-JUN-1995;
 L4-JAN-1985;
 25-APR-1991;
28-OCT-1993;
 06-JUN-1995;
 JS5821055-A.
 13-JAN-1986
 sig_peptide
 nat_peptide
 13-OCT-1998
 Query Match
 Matches
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us-09-391-606-12.rng

AAZ92753;

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1954
 2134
 2314
 1131
 2434
 1834
 1894
 955 tccgcattgctcagccaaaactacctacagctgttttaaacttaactgcatggaacctt 1014
 1955 togaagaattaaacgttetetgtaacgeagetgagtttaetateaataageetaaaggat 2014
 1015 ctttactaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgc 1071
 423
 2015 atgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacaggaacta 2074
 540
 774
 363
 594
 654
 714
 834
 894
250 gattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaaacatttt 309
 ttgttgaactttacacagacacctctttctcttggagcgtaggcgctcgtggagccttat
 1895 gggaatgtggatgcgcgactttaggcgcttctttccaatacgctcaatccaagcctaaag
 541 -----aaggtactactgtaaatgcaaatgaactaccaaacgtttctttaagtaacggag
 775 ataaaggcgttgctttccccttgccaacagacgctggcgtagcaacagctactggaacaa
 1072 aaattgtttcctgtcagatcaacaagtttaaatctagaaaagcttgtggagttactgtag

 ctggatccgctgctgcaaactatactactgccgtag

 364 atagacctaacccggcctacaataagcatttacacgatgcagagtggttcactaatgcag
 484 atggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagtta---
 835 agtotgogaccatcaattatcatgaatggcaagtaggagcotototatottacagactaa
 2255 ctattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagataccatgc
 310 ctatgggagccaagccta--
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The present sequence represents DNA encoding the major outer membrane protein (MOMP) of Chlamydia trachomatis serovar L2. DNA obtained from C. trachomatis serovar L2 was partially digested with DNase I and C inserted into the bacteriophage vector lambda-gtll; a lambda-gtll insert (AAZ92752; ATCC #40157, referred to as lambda-gtll/L2/33 in the specification) was obtained which encodes a protein fragment (AAY81267) reactive with a pool of C. trachomatis-specific monoclonal antibodies. The lambda-gtll/L2/33 insert sequence was also used to probe a chlamydial genomic DNA phage lambda 1059 library, and the present sequence which encodes the full-length Chlamydia trachomatis serovar L2 MOMP was identified C. trachomatis is a human pathogen responsible for diseases such as trachoma, inclusion conjunctivitis, pneumonia, inclusion conjunction of antibodies to a MOMP or a fragment thereof is used to elicit the production of antibodies to a MOMP or detecting C. trachomatis or immunoassay reagents (substitutes for native MOMP) for detecting C. trachomatis or inclusion, or as an immunogen for
 tgöctgtagggaaccettetgatecaagettattaattgatggtacaatatgggaaggtg 189
 New synthetic or recombinant polypeptide, useful for diagnosing preventing Chlamydia trachomatis infection, is immunologically equivalent to a major outer membrane protein
 antibody production; immunoassay; detection; vaccine; trachoma; inclusion conjunctivitis; pneumonia; lymphogranuloma venereum; mucous membrane genital tract infections; ds.
 DB 21; Length 3133;
 serovar L2; immunoreactive;
 /product= "Chlamydia trachomatis serovar
 Indels
 Sequence 3133 BP; 911 A; 670 C; 609 G; 943 T; 0 other;
 Score 479.4; DB 21;
Pred. No. 1.6e-138;
0; Mismatches 356;
 Mullenbach G;
 Chlamydia trachomatis major outer
 membrane protein; MOMP;
 Location/Qualifiers
 Kuo C-C,
 2
 Examples; Fig. 2; 17pp; English.
 Chlamydia trachomatis serovar
 (WASH-) WASHINGTON RES FOUND
 93US-0144095.
86US-0818523.
91US-0691639.
85US-0692001.
 Query Match 33.6%;
Best Local Similarity 66.5%;
Matches 741; Conservative
 1288..2472
/*tag= a
 95US-0466152
 (first entry)
 Stephens R,
 WPI; 2000-223163/19.
 P-PSDB; AAY81268
 DNA encoding
 19-JUN-2000
 28-OCT-1993;
13-JAN-1986;
 25-APR-1991;
14-JAN-1985;
 US6030799-A
 06-JUN-1995;
 outer
 29-FEB-2000
 Agabian N,
 130
 Key
ŏ
```

or

L2 MOMP

ä

18; Gaps

1355 tgcctgtggggaatcctgctgaaccaagccttatgatcgacggaattctatgggaaggtt 1414

g

AAZ92753 standard; DNA; 3133 BP

AAZ92753 ID AAZ9

RESULT

BP

DNA; 3133

standard;

AAV40646

RESULT

AAV40646; AAV40646

```
2074
 2134
 1071
 1131
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1475 gitaciatggigacitigitticgaccgigittitgcaaacagaigtgaataaagaaticc 1534
 894
 ctatgggagccaagccta----ctggatccgctgctgcaaactatactactgccgtag 363
 2075 aggatgcctctattgattaccatgaatggcaagcaagttagctctcttacagactga
 tocgcattgctcagccaaaactacctacagctgttttaaacttaactgcatggaaccctt
 ctattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagataccatgc
 1015 ctttactaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgc
 atgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacaggaacta
 ataaaggegttgettteeeettgeeaacagaegetggegtageaacagetaetggaacaa
 364 atagacctaacccggcctacaataagcatttacacgatgcagagtggttcactaatgcag
 getteattgeettaaacatttgggategetttgatgttttetgtaetttaggagetteta
 484 atggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagtta---
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 gggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaag
 agagagetgeteaegtatetggteagtteagatte 1226
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249
 130 tgcctgtagggaaccttctgatccaagcttattaattgatggtacaatatgggaaggtg 189
 Gaps
 DB 19; Length 3133;
 18;
 The sequence is that encoding a major outer membrane protein (MOMP) of Chlamydia trachomatis. This polypeptide can be used in immunoassays, e.g. to detect Chlamydia trachomatis antibodies in blood, or can be used in vaccines. The
 for
 MOMP; major outer membrane protein; immunoassay; diagnosis;
detection; antibody; serovar L2; ds.
 useful
 , Match 33.5%; Score 477.8; DB 19; Length Local Similarity 66.4%; Pred. No. 5e-138; es 740; Conservative 0; Mismatches 357; Indels
 polynucleotide can be labelled and used as a diagnostic
 Sequence 3133 BP; 909 A; 670 C; 610 G; 944 T; 0 other;
 coding region
 coding for Chlamydia trachomatis polypeptide
 χ;
 Stephens
 recombinant polypeptide, etc
 MOMP
 Location/Qualifiers
1288..2472
 တ်
 trachomatis serovar L2
 /*tag= a
/product= MOMP
1287..1353
/*tag= b
 Kuo C, Mullenbach
 Claim 5; Fig 2; 15pp; English
 86US-0818523.
85US-0692001.
91US-0691639.
93US-0144095.
95US-0466814.
 WASHINGTON RES FOUND
 85US-0692001
 (first entry)
 Chlamydia trachomatis
 CORP.
 WPI; 1998-376887/32
 P-PSDB; AAW57775
 (CHIR) CHIRON (WASH-) WASHING
 14-JAN-1985;
 Agabian N,
 27-0CT-1998
 US5770714-A
 06-JUN-1995
 23-JUN-1998
 13-JAN-1986
 14-JAN-1985
 25-APR-1991
 sig_peptide
 18-OCT-1993
 producing
 Chlamydia
 Query Match
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a major outer membrane protein

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Sequence end
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 atggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagtta---
 getteattgeettaaacatttgggategetttgatgttttetgtaetttaggagetteta
 agaaccatgctacagtttcagatagtaagcttgtaccaaatatgagcttagatcaatctq
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 364 atagacctaacccggcctacaataagcatttacacgatgcagagtggttcactaatgcag
 agagagctgctcacgtatctggtcagttcagattc 1226
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1355 tgcctgtggggaatcctgctgaaccaagccttatgatcgacggaattctatgggaaggtt 1414
 1595 caagagagaatcctgcttacggccgacatatgcaggatgctgagatgtttacaaatgctg 1654
 "130 tgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggtg 189
 geiteattgeettaaacatttgggategetttgatgttttetgtaetttaggagetteta 483
 DNAse I and inserted into vector lambda gtll. Clone lambda gt/11/L2/33 (AAN60006) reacted with the pool and was subsequently shown to produce a polypeptide that displays species., subspecies and type-specific epitopes of the chlamydial MOMP. L2 B9-F DNA (AAN60007) is comprised of lambda 1059 recombinants shown to be homologous with
 190 ctgcaggagatccttgcgatccttgcgctacttggtgcgacgctattagcttacgtgctg
 1415 tcggcggacatccttgcgatccttgcaccacttggtgtgtgacgctatcagcatgcgtatgg
 310 ctatgggagccaagccta----ctggatccgctgctgcaaactatactactgccgtag
 atagacctaacccggcctacaataagcatttacacgatgcagagtggttcactaatgcag
 New DNA constructs and polypeptide(s) - displaying antigenicity of major outer membrane protein of Chlamydia trachomatis
 Length 3133;
 Sequence 3133 BP; 911 A; 673 C; 606 G; 943 T; 0 other
 33.3%; Score 474.6; DB 7; 66.2%; Pred. No. 4.9e-137;
 0; Mismatches 359;
 GT;
cervicitis;
 Mullenbach
 in AAN60006'
 Location/Qualifiers
|1288..1348
|1289..1348
|*tag= a /roduct= leader
|1349..2472
|*tag= b |
trachoma; conjunctivitis;
 Example; Appendix B; 31pp; English
 Kuo CC,
 /*tag= c /
/note= "AGA
 86EP-0100279
 85US-0692001
 Conservative
 ĸ,
 Chlamydia trachomatis
 Stephens
 WPI; 1986-226702/35
 (CHIR-) CHIRON CORP
 Best Local Similarity.
Matches 738; Conserv
 ambda gt11/L2/33.
 P-PSDB; AAP60004
 misc_difference
 10-JAN-1986;
 14-JAN-1985;
 27-AUG-1986
 Agabian N,
Vaccine;
 Query Match
 424
 qq
 q
 Qγ
 οy
```

3;

BP 3133

standard;

AAN60007

(first entry)

30-JUL-1991

W09928475-A2

```
Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
 1131
 2254
 etttactaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgc 1071
 2314
 gagotactttagttgatgotgataaatggtcacttactgcagaagctcgtttaattaacg 1191
 2434
 2134
 2014
 2074
 1014
 cttacatggcattgaatatttgggatcgttttgatgtattctgtacattaggacccacca 1714
 954
 atggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagtta--- 540
 1835 ttgttgagttgtatacagatactacttttgcttggagtgctggagctcgtgcagctttgt
 tecgeattgeteagecaaaactacetacagetgttttaaacttaactgeatggaaceett
 ctattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagataccatgc
 1775 agaaccatgctacagtttcagatagtaagcttgtaccaaatatgagcttagatcaatctg
 ttgttgaactttacacagacacctctttctcttggagcgtaggcgctcgtggagccttat
 gggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaag
 ataaaggcgttgctttccccttgccaacagacgctggcgtagcaacagctactggaacaa
 atgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacaggaacta
 agtetgegaceateaattateatgaatggeaagtaggageetetetatettaeagaetaa
 895 actetttagtgecatacattggagtacaatggtetegageaacttttgatgetgataaca
 aaattgtttcctgtcagatcaacaagtttaaatctagaaaagcttgtggagttactgtag
 ----aaggtactactgtaaatgcaaatgaactaccaaacgtttctttaagtaacggag
Chlamydia trachomatis
 agagagetgeteaegtatetggteagtteagatte
 DNA; 1038602
 Complete genome sequence of
 (first entry)
 Chlamydia trachomatis
 standard;
 07-0CT-1999
 AAZ01425
 AAZ01425;
 RESULT 10
 2435
 2015
 835
 2135
 2195
 1015
 2255
 1072
 1132
 2375
 1192
 715
 1955
 955
 1715
 1655
 595
 655
 484
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parise chiamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chiamydia trachomatis is responsible for a large number of diseases. e.g. e.g. eg diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 ţ
 733307 tgcctgtggggaatcctgctgaaccaagccttatgatcgacggaattctatgggaaggtt 733366
 other;
 trachomatis. Open reading frames (ORFs) of the genome encode polypeptides AAY36754-Y37949. The polypeptides can be used as vaccines
 540
 249
 tgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggtg 189
 363
 595 tigitigaacittacacagacacctctttctcttiggagcgtaggcgctcgiggagccttat 654
 Gaps
 conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpinguitis, perihapatutis, bartholinitis; penemopathy in breast feeding infants; and veneral lymphogranulomatosis. The polypeptides of the invention may be of the invention may b
 agaaccatgctacagtttcagatagtaagcttgtaccaaatatgagcttagatcaatctg
 Length 1038602;
 ctgcaggagatccttgcgatccttgcgctacttggtgcgacgctattagcttacgtgctg
 gattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaaacatttt
 atagacctaacccggcctacaataagcatttacacgatgcagagtggttcactaatgcag
 733547 caagagagaatcctgcttacggccgacatatgcaggatgctgagatgtttacaaatgctg
 getteattgeettaaaacatttgggategetttgatgttttetgtactttaggagetteta
 ----aaggtactactgtaaatgcaaatgaactaccaaacgtttctttaagtaacggag
 ctatgggagccaagccta----ctggatccgctgctgcaaactatactactgccgtag
 atggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagtta---
 Sequence 1038602 BP; 304265 A; 214645 C; 214259 G; 305001 T; 432
 genome of Chlamydia
 Indels
 Score 397.2; DB 20;
Pred. No. 1.3e-111;
); Mismatches 357;
 present sequence represents the complete
 0; Mismatches
 Genome sequence of Chlamydia trachomatis
 English.
 Claim 1; Page 373-656; 1755pp;
 98US-0107077.
97FR-0015041.
97FR-0016034.
 / Match 27.9%;
Local Similarity 66.4%;
nes 740; Conservative
 treating these diseases
 WPI; 1999-371125/31
 (GEST) GENSET
 27-NOV-1998;
 28-NOV-1997;
17-DEC-1997;
 04 - NOV - 1998;
 10-JUN-1999
 Query Match
Best Local Si
Matches 740;
 130
 190
 250
 310
 424
 484
 733727
 733427
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WPI; 1999-254214/21. P-PSDB; AAW98184.

733846

733787 tigtigagitigtatacagatactactittigcitiggagigciggigggctcgtgcagcttitgt

g

733847 gggaatatggatgcgcgactttaggcgcntctttccaatacgctcaatccaagcctaaag

gggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaag

A new vaccine for Chlamydia psittaci infections

Example 2; Page 47-48; 72pp; English

This DNA sequence codes for a major outer membrane protein (MOMP) polypeptide (see AAW98183) of Chlamydia psittaci strain B577. The MOMP polypeptide comprises regions VD3 and VD4 of native MOMP (see also AAW98188), i.e. it lacks regions VD1 and VD2 of MOMP. DNA encoding the MOMP polypeptide was obtained by PCR amplification (see also AAX25049 and AAX25052) of C psittaci B577 DNA. A claimed fused to a maltose binding protein. Also claimed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing c. psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic (naked nucleic acid vaccination and vaccines are used to prevent C. psittaci infection, especially in birds. 

Sequence 744 BP; 213 A; 164 C; 157 G; 210 T; 0 other;

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tcgaagaattaaacgttctctgtaacgcagctgagtttactatcaataagcctaaaggat 733966

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734026

ataaaggcgttgctttccccttgccaacagacgctggcgtagcaacagctactggaacaa

775 733907

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835

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Db 734027 aggatgcctctattgattaccatgaatggcaagcaagtttagctctatcttacagactga

agtetgcgaccateaattateatgaatggcaagtaggageetetetatettacagaetaa

617 Gaps 75 gcaaatgaactaccaaacgtttctttaagtaacggagttgttgaactttacacagacacc 16 getgatcagettcccaatgtaggcatcactcaaggaatcgttgaattttatacagataca ó Length 744; Indels DB 20; Score 352.2; DB 20; Pred. No. 2.8e-99; 0; Mismatches 198; Query Match
Best Local Similarity 70.4%;
Matches 471; Conservative 558 δ qq

677 tctttctcttggagcgtaggcgctcgtggagccttatgggaatgcggttgtgcaactttg 618 δ

678

797 aacgtatcgcaattctctgtaaacaaacccaagggctataaaggcgttgctttccccttg 738 196 δ

857 ccaacagacgetggcgtagcaacagetactggaacaaagtetgcgaccatcaattatcat 798 256 g.. ₹ q

oy do oy

cctacagctgttttaaacttaactgcatggaacccttctttactaggaaatgccacagca 436 978 g

1037

435

977

ttgtctactactgattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaag 1097 1038 ŏ pp

496

tttaaatctagaaaagcttgtggagttactgtaggagctactttagttgatgatgtaaa 1157 615 1098 556 ŏ q

tggtcacttactgcagaagctcgtttaattaacgagagagctgctcacgtatctggtcag 1217 1158 δ

136 С οŽ Db gaacaactattgtggatgcagacaaatacgcagttacagttgagactcgcttgatcgatg 734386 734147 ttcgtattgctcagccgaagtcagctacaactgtctttgatgttaccactctgaacccaa 734206 734266 tccgcattgctcagccaaaactacctacagctgttttaaacttaactgcatggaaccctt 1014 1191 734207 ctattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagataccatgc 1015 ctttactaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgc aaattgtttcctgtcagatcaacaagtttaaatctagaaaagcttgtggagttactgtag 734327

Db 734387 agagagctgctcacgtaaatgcacaattccgcttc 734421 1192 agagagetgeteacgtatetggteagtteagatte 1226

RESULT 11 

ВÞ 744 DNA; AAX25045 standard;

AAX25045;

Chlamydia psittaci MOMP (minus VD1 and VD2 region) DNA

(first entry)

05-JUL-1999

ter membrane protein; MOMP; psittacosis; infection; genetic immunisation; ss. outer membrane vaccine; Major

Chlamydia psittaci

Location/Qualifiers

1..687 /\*tag= WO9910005-A1

04-MAR-1999

98WO-US17943 28-AUG-1998;

97US-0057147 28-AUG-1997; LOUISIANA & AGRIC & MECH COLLEGE. (LOUU ) UNIV

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27-JUN-2000

AAA08124;

12

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RESULT 1 AAA08124 ID AAA0

919

음 ŏ Synthetic

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598
 006
 718
 096
 778
 838
 868
 1137
 928
 1197
 840
 181
 301
 480
 540
 421
 900
 099
 306
 420
 g.
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 qq
 g
 δy
 Db
 g
 QY
 ρp
 Qγ
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 οy
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 qa. A
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 \Omega Y
 Dp
 δy
 g
 QΥ
 qa.
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 . . Q
 ÓΣ
 qq
 òγ
 5,
 The present invention describes fusion proteins (I) comprising at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis, at least one hydrophilic polypeptide having no immunoreactivity to human serum and their connected part. AAA08120 to AAA08125 encode specifically claimed examples of the fusion proteins given in AAY82388 to AAY82393. Also described is a method (A) for the detection of Chlamydia trachomatis antibody using (I) as the antigen. (I) is used for the diagnosis of Chlamydia trachomatis infectious diseases. The method can diagnose Chlamydia trachomatis infectious diseases specifically in a
 "Fusion protein containing at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis; no stop codon given"
 126 atgitgcctgtagggaaccttctgatccaagcttattaattgatggtacaatatgggaa 185
675
 Gaps
 C. trachomatis MOMP containing fusion protein nucleotide sequence #5.
 Chlamydia trachomatis; fusion protein; major outer membrane protein; MOMP; hydrophilic polypeptide; antibody; detection; diagnosis; infections infectious disease; ds.
 A soluble fused protein useful for diagnosis of Chlamydia infection, comprises at least part of major outer membrane protein (MOMP) of
tggtcaatcactggtgaagcacgcttaatcaatgaaagagccgctcacatgaatgctcaa
 Length 1047;
 72;
 Score 328.8; DB 21; Length
Pred. No. 6.5e-92;
0; Mismatches 367; Indels
 Sequence 1047 BP; 315 A; 209 C; 233 G; 290 T; 0 other;
 Claim 20; Page 29-30; 37pp; Japanese
 Location/Qualifiers
1..1047
 BP.
 MOMP; hydrophilic polypeptide;
infection; infectious disease;
 (ELED) DENKI KAGAKU KOGYO KK.
 23.1%;
60.5%;
 AAA08124 standard; DNA; 1047
 98JP-0213212.
 98JP-0213212
 (first entry)
 Conservative
 Chlamydia trachomatis
 Chlamydia trachomatis.
 2000-295780/26.
 1218 ttcagattc 1226
 Similarity
 WPI; 2000-295780,
P-PSDB; AAY82392
 high sensitivity
 JP2000041678-A
 28-JUL-1998;
 28-JUL-1998;
```

15-FEB-2000.

```
1020 ctaggaaatgccacagcattgtctactactga---ttcgttctcagacttcatgcaaatt 1076
 ttagtgccatacattggagtacaatggtctcgagcaacttttgatgctgataacatccgc 959
 839
 657
 gegaceateaattateatgaatggcaagtaggageetetetetatacagaetaaaetet 899
 420
 462
 629
 719
 539
 597
 240
 479
gctggagctggcgatgtgaaagctagcgcagagggtcagctcggagataccatgcaaatc
 gtttccttgcaattgaacaagatgaaatctagaaaatcttgcggtattgcagtaggaaca
 gggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacaggaactaaggat
 aatg-----agaaccatgctacagtttcagatagtaagctgtacca
 540 caa--taacaataacaataacaatgctgagtttactatcaataagcctaaaggatatgta
 780 ggcgttgctttccccttgccaacagacgctggcgtagcaacagctactggaacaaagtct
 121 atgggttactatggtgactttgttttcgaccgtgttttgcaaacagatgtgaataaagaa
 ttttctatgggagccaagccta----ctggatccgctgctgcaaactatactactgcc
 gtagatagacctaacccggcctacaataagcatttacacgatgcagagtggttcactaat
 gcaggettcattgccttaaacatttgggatcgctttgatgttttctgtactttaggagct
 tctaatggttacattagaggaaactctacagcgttcaatctgttggtttattcggagtt
 aaaggtactactgtaaatgcaaatgaactaccaaacgtttctttaagtaacggagttgtt
 qaactttacacagacacctctttctcttggagcgtaggcgctcgtggagccttatgggaa
 tgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaagttgaa
 246 gctggattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaaaca
 gctgctcacgtatctggtcagttcagattc 1226
 463 aatatgagcttagatcaatct------
 g
```

13

RESULT

ggtgctgcaggagatccttgcgatccttgcgctacttggtgcgacgctattagcttacgt 245

186

1 atgetgeetgtgggtaaceetgetgaaceaageettatgategaegggateetatgggaa

Matches 671;

ŏ q δy

Local

Query Match

Fri

```
aacaaacccaagggctataaaaggcgtt-----gctttccccttgccaacagacgctggc 812
 Chlamydia trachomatis.
 JP2000041678-A.
 ttc 1226
 28-JUL-1998;
 28-JUL-1998;
 27-JUN-2000
 15-FEB-2000
 |||
| 664 ttc
 Synthetic
 AAA08122;
 RESULT 14
 866
 1104
 1164
 1224
 484
 873
 933
 Key
 AAA08122
 . qq
 qq
QX
Opp
 qa
Ö
 da y
 5
 totttaagtaacggagttgttgaactttacacagacacctctttctctttggagcgtaggc 638
 Gaps
 optionally fused to a mailtose binding protein. Also failmed are an isolated nucleic acid encoding the polypeptide, a vector, and a method of preventing C. psittaci infection by administering the vaccine containing the MOMP polypeptide. Vectors encoding MOMP polypeptides lacking regions VD1 and VD2 are useful for genetic (naked nucleic acid) vaccination. The vaccines are used to prevent C. psittaci infection, especially in birds.
 This DNA sequence codes for a major outer membrane protein (MOMP) polypeptide (see AAW98183) of Chlamydia psittaci strain LSUWTCK, cockatiel isolate (the MOMP gene sequence of this isolate is identical to that of C. psittaci Avian Type C). The MOMP polypeptide comprises regions VD3 and VD4 of native MOMP (see also AAW98187), i.e. it lacks regions VD1 and VD2 of MOMP. DNA encoding the MOMP polypeptide was obtained by PCR amplification (see also AAX25049 and AAX25051) of C. psittaci LSUWTCK DNA. A claimed vaccine composition includes this MOMP polypeptide.
 15;
 Length 726;
 Major outer membrane protein; MOMP; psittacosis; infection; vaccine; genetic immunisation; ss.
 0; Mismatches 182; Indels
 Chlamydia psittaci MOMP (minus VD1 and VD2 region) DNA
 Sequence 726 BP; 221 A; 153 C; 144 G; 208 T; 0 other;
 Baghian A, Chouljenko VN, Kousoulas KG, Tully TN;
 DB 20;
 A new vaccine for Chlamydia psittaci infections
 (LOUU) UNIV LOUISIANA & AGRIC & MECH COLLEGE.
 Score 321.8; DE
Pred. No. 8e-90;
 Example 2; Page 43-45; 72pp; English
 Location/Qualifiers
1..669
/*tag= a
 BP.
 22.6%;
70.3%;
 AAX25044 standard; DNA; 726
 98WO-US17943.
 97US-0057147
 (first entry)
 Best Local Similarity 70.3
Matches 466; Conservative
 WPI; 1999-254214/21.
P-PSDB; AAW98183.
 Chlamydia psittaci.
 05-JUL-1999
 WO9910005-A1
 28-AUG-1998;
 28-AUG-1997;
 04-MAR-1999
 AAX25044;
 Query Match
 579
 4
 639
 64
 124
 669
 Key
AAX25044
```

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```
"Fussion protein containing at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis; no stop codon given"
 1163
 aacttaactgcatggaacccttctttactaggaaatgccacagcattgtctactact--- 1049
 1050 -----gattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaagtttaaa 1103
 244 acaacagaagetacagacaccaaatcagetacaattaaataccatgaatggcaagtagge 303
 304 ctcgccctgtcttacagattgaatatgcttgttccatatattggcgtaaactggtcaaga 363
 Č. trachomatis MOMP containing fusion protein nucleotide sequence #3.
 Chlamydia trachomatis; fusion protein; major outer membrane protein; MOMP; hydrophilic polypeptide; antibody; detection; diagnosis; infections disease; ds.
 gtagcaacagctactggaacaaagtctgcgaccatcaattatcatgaatggcaagtagga
 tctagaaaagcttgtggagttactgtaggagctactttagttgatgctgataaatggtca
 goctototatottacagactaaactotttagtgocatacattggagtacaatggtotoga
 544 tctagaaaagcttgtggtgtagctgttggtgcaacgttaatcgacgctgacaaatggtca
 Location/Qualifiers
 AAA08122 standard; DNA; 1362 BP
 (ELED) DENKI KAGAKU KOGYO KK.
 98JP-0213212
 98JP-0213212
 (first entry)
 .1362
 /*tag=
 /note=
 WPI; 2000-295780/26.
P-PSDB; AAY82390.
```

#1.

(first entry)

27-JUN-2000

AAA08120;

```
1;
 The present invention describes fusion proteins (I) comprising at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis, at least one hydrophilic polypeptide having no immunoreactivity to human serum and their connected part. AAA08120 to AAA08125 encode specifically claimed examples of the fusion proteins given in AAY82388 to AAY82393. Also described is a method (A) for the detection of chlamydia trachomatis antibody using (I) as the antigen. (I) is used for the diagnosis of Chlamydia trachomatis infectious diseases. The method can diagnose Chlamydia trachomatis infectious diseases specifically in a high sensitivity.
 1141
 1065
 1185
 ataacatccgcattgctcagccaaaactacctacagctgttttaaacttaactgcatgga 1008
 acccaactattgctggagctggcgatgtgaaagctagcgcagagggtcagctcggagata 1201
 1262 cagtaggaacaactattgtggatgcagacaaatacgcagttacagttgagactcgcttga 1321
 1022 gactgaatatgttcactccctacattggagttaaatggtctcgagcaagttttgatgcag 1081
 948
 acggagttgttgaactttacacagacactcttttctcttggagcgtaggcgctcgtggag 648
 901
 Gaps
 A soluble fused protein useful for diagnosis of Chlamydia infection, comprises at least part of major outer membrane protein (MOMP) of Chlamydia trachomatis -
 accettetttactaggaaatgecacagcattgtetactactga---ttegtteteagaet
 ctgtaggagctactttagttgatgctgataaatggtcacttactgcagaagctcgtttaa
 cettatgggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaac
 gactaaactctttagtgccatacattggagtacaatggtctcgagcaacttttgatgctg
 agggctataaaggcgttgctttccccttgccaacagacgctggcgtagcaacagctactg
 aaggatatgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacag
 gaacaaagtetgcgaccatcaattatcatgaatggcaagtaggagcetetetatettaca
 Score 287.4; DB 21; Length 1362; Pred. No. 5.7e-79;
 3;
 211; Indels
 Sequence 1362 BP; 383 A; 283 C; 324 G; 372 T; 0 other;
 ttaacgagagagctgctcacgtatctggtcagttcagattc 1226
 0; Mismatches
 37pp; Japanese
 20.2%;
66.6%;
 al Similarity 66.6
427; Conservative
 Page 28;
 claim 16;
 Query Match
Best Local 3
 1126
 1186
 1322
 589
 1009
 Matches
 649
 782
 209
 842
 169
 902
 829
 962
 889
 949
 1142
 Q
 q
 Q
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 δλ
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The present invention describes fusion proteins (I) comprising at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis, at least one hydrophilic polypeptide having no immunoreactivity to human serum and their connected part. AAAA08125 on AAAA08125 encode specifically claimed examples of the fusion proteins given in AAX82388 to AXX82393. Also described is a method (A) for the detection of chlamydia trachomatis antibody using (I) as the antigen. (I) is used for the diagnosis of Chlamydia trachomatis infectious diseases. The method can diagnose Chlamydia trachomatis infectious diseases specifically in a
 Pasion protein containing at least part of a major outer membrane protein (MOMP) of Chlamydia trachomatis; no stop codon given"
 708
 790
 911 aaggatatgtagggcaagaattccctcttgatcttaaagcaggaacagatggtgtgacag 970
 Gaps
 A soluble fused protein useful for diagnosis of Chlamydia infection, comprises at least part of major outer membrane protein (MOMP) of Chlamydia trachomatis -
 Chlamydia trachomatis; fusion protein; major outer membrane protein; MOMP; hydrophilic polypeptide; antibody; detection; diagnosis: infection; infections disease; ds.
 agggetataaaggegttgettteeeettgeeaacagaegetggegtageaacagetaetg
 cettatgggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaac
 851 ctaaagtcgaagaattaaacgttctctgtaacgcagctgagtttactatcaataagccta
 589 acggagttgttgaactttacacagacacctctttctctttggagcgtaggcgctcgtggag
 C. trachomatis MOMP containing fusion protein nucleotide sequence
 DB 21; Length 1371;
 ..
..,
 Indels
 Sequence 1371 BP; 390 A; 276 C; 324 G; 381 T; 0 other;
 20.2%; Score 287.4; DB 21;
66.6%; Pred. No. 5.7e-79;
ive 0; Mismatches 211;
 Claim 12; Page 26-27; 37pp; Japanese.
 Location/Qualifiers
 98JP-0213212.
 98JP-0213212
 al Similarity 66.6
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|            | *                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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Sequence 3
 Sequence
 Sequence
 |APPLICANT: Hobat, Peter

APPLICANT: Parker, Suzanne

APPLICANT: Margalith, Michal

APPLICANT: Khatibi, Shirin

TITLE OF INVENTION: PLASMIDS SUITABLE FOR IL-2 EXPRESSION

NUMBER |OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
 US-08-343-401A-3
US-08-445-265A-1
US-08-990-4313-1
US-08-564-313-1
US-08-073-836-3
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US-08-645-38-5
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 US-08-893-327-17
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US-08-776-511-3
US-08-470-299-2
 ALIGNMENTS
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/345,913
 REFERENCE/DOCKET NUMBER: VICAL.043A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEPHOX: 619-235-0176
 Sequence 1, Application US/08345913
Patent No. 5641665
 NAME: Ways Vensko, Nancy
REGISTRATION NUMBER: 36,298
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LINGTH: 4928 base pairs TYPE: nucleic acid STRANDEDNESS: single
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4249
42283
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5555
5555
62238
62238
62238
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62238
62238
62238
 STRANDEDNESS: Sir
TOPOLOGY: linear
 GENERAL INFORMATION:
 MOLECULE TYPE: CI
USA
 ORIGINAL SOURCE
 92660
 FRAGMENT TYPE:
 CA
 CITY: New STATE: CA COUNTRY:
 RESULT 1
US-08-345-913-1
 FEATURE:
 (without alignments)
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4, Appli
1, Appli
2, Appli
57, Appl
156, Appl
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Sequence 7
Sequence 5
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US-08-910-647-3

US-08-910-647-3

US-08-910-647-1

US-08-910-647-1

US-08-63-998-3

US-08-63-998-3

US-08-63-998-1

US-08-63-998-1

US-08-663-998-2

US-08-85-156

US-08-976-161-57

US-08-976-161-57

US-08-976-161-57

US-08-99-575-156

US-08-899-575-170

US-08-899-575-170
 -US95-08743-156
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-08-801-092-5
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Listing first 45 summaries
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1426
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Maximum DB seq length: 2000000000
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 Score 118; DB 3; Length 4928;
Pred. No. 7e-28;
0; Mismatches 5; Indels
 8.3%; Score 118; DB 1; Length 4928; 96.0%; Pred. No. 7e-28;
 APPLICANT: Harrian Michal
APPLICANT: Margalith, Michal
APPLICANT: Margalith, Michal
APPLICANT: Parker, Suezanne E.
APPLICANT: Margalith, Shirin
TITLE OF INVENTION: Plasmids Suitable for IL-2 Expression
FILE REFERENCE: 1530.0080001
CURRENT APPLICATION NUMBER: US/08/818,562
CURRENT FILING DATE: 1997-03-14
FARLIER APPLICATION NUMBER: US 08/345,913
FARLIER FILING DATE: 1994-11-28
NUMBER OF SEQ ID NOS: 3
SOGTWARE: Patentin Ver. 2.0
SEQ ID NO :
SEQ ID NO :
LENGTH: 4928
 0; Mismatches
 APPLICANT: Ronald Zuckermann et al.
 Sequence 1, Application US/09132808 Patent No. 6197332 GENERAL INFORMATION:
 RESULT 2
US-08-818-562-1
Sequence 1, Application US/08818562
; Patent No. 6147055
; GENERAL INFORMATION:
 8.3%;
96.0%;
; NAME/KEY: Coding Sequence; LOCATION: 1689...2159 CTHER INFORMATION: US-08-345-913-1
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Best Local Similarity 96.0
Matches 121; Conservative
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Best Local Similarity 96.0
Matches 121; Conservative
 ; LOCATION: (1689)..(2159) US-08-818-562-1
 ORGANISM: Homo sapiens
 1651 gcctca 1656
 121 ccacca 126
 1651 GCCTCA 1656
 121 ccacca 126
 NAME/KEY: CDS
 US-09-132-808-1
 TYPE: DNA
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TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related IITLE OF INVENTION: Compositions and Methods Thereof
 Gaps
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 Length 4328;
 Indels
 Sequence 2, Application US/08910647
Fatent No. 6251433
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
FILING DATE:
 SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/132,808 FILING DATE:
 Query Match 7.3%; Score 104.8; DB 4; Best Local Similarity 94.0%; Pred. No. 1.2e-23; Matches 109; Conservative 0; Mismatches 7;
 FILING DAYE:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: FUJITA, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1387.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEPHONE: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER.FICS:
LENGTH: 4328 base pairs
TYPE: nucleic acid
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
 ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITX: Emeryville
STATE: California
 ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-09-132-808-1
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
 COUNTRY: U.S.A. ZIP: 94608-2916
 N: U.S.A. 94608-2916
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 Length 5107;
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 Indels
Score 104.8; DB 4; I Pred. No. 1.3e-23;
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 Score 104.8; DB 4;
 Pred. No. 1.4e-23;
 GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
ITILE OF INVENTION: Compositions and Method
TITLE OF INVENTION: Polynucleotide Delivery
 0; Mismatches
 0; Mismatches
 REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEFANK: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
 APPLICATION NUMBER: US/08/910,647
 OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 1, Application US/08910647; Patent No. 6251433; GENERAL INFORMATION:
 Sequence 3, Application US/08910647; Patent No. 6251433
 Chiron Corporation
 E: Floppy disk
IBM PC compatible
 NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
 STREET: 4560 Horton Street
 DNA (genomic)
 7.3%;
 7.3%;
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 5107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Conservative
 Conservative
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron CO:
 ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 FILING DATE:
CLASSIFICATION: 514
 CITY: Emeryville
STATE: California
 linear
 Best Local Similarity
Matches 109; Conserv
 Best Local Similarity
 MOLECULE TYPE:
 COMPUTER:
 STATE: Ca
 Matches 109;
 RESULT 6
US-08-910-647-3
 US-08-910-647-3
 US-08-910-647-1
 Query Match
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 1546 TGAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGA 1605
 Gaps
 1 tgagcagtactcgttgctgccgcgcgccaccagacataatagctgacagactaacaga
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 Length 4328;
 Indels
 GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
 Score 104.8; DB 4;
Pred. No. 1.2e-23;
0; Mismatches 7;
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
 REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 ATTORNEY AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGIGSRATTON NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEPHONE: (510) 655-3542
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENTH: 4328 base pairs
 Sequence 4, Application US/08910647
Patent No. 6251433
 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
 MOLECULE TYPE: DNA (genomic) US-08-910-647-2
 MOLECULE TYPE: DNA (genomic) US-08-910-647-4
 7.3%;
94.0%;
 LENGTH: 4818 base pairs
 Query Match 7.35
Best Local Similarity 94.05
Matches 109; Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
 TYPE: nucleic acid STRANDEDNESS: single
 CITY: Emeryville
STATE: California
 linear
 linear
 COUNTRY: U.S.A.
ZIP: 94608-2916
 CLASSIFICATION:
 FILING DATE:
 RESULT 5
US-08-910-647-4
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GENERAL INFORMATION:

APPLICANT: Hasel, Karl W.

APPLICANT: Hasel, Karl W.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: HIV-1 VACCINES, ANTIBODY COMPOSITIONS RELATED TITLE OF INVENTION: THERETO, AND THERAPEUTIC AND PROPHYLACTIC USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
 Score 104.2; DB 2; Length 3125; Pred. No. 1.6e-23; 0; Mismatches 8; Indels 0;
 ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41190/JFW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 677-9550
TELEFAX: (212) 664-0525
TELETS: 42253 COOPUI
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARCTERISTICS:
 NAME: White, John P. REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 41190/JPW/AJM
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/037,816
FILING DATE: 26-WAR-1993
ATTORNEY/AGENT INFORMATION:
 US/08/530,146
 UMBER: US/08/037,816A
26-MAR-1993
 SOFTWARE: Patentin Release #1.24
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,14(
FILING DATE:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 US-08-530-146-13; Sequence 13, Application US/08530146; Patent No. 5886163
 MOLECULE TYPE: DNA (genomic) FEATURE:
 7.3%;
 Floppy disk
 LENGTH: 3125 base pairs
 Query Match 7.3
Best Local Similarity 93.2
Matches 109; Conservative
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 single
 APPLICATION NUMBER:
 nucleic acid
 linear
 CITY: New York STATE: New York
 CLASSIFICATION:
 USA
 STRANDEDNESS:
 FILING DATE:
 10112
 COUNTRY:
 TOPOLOGY:
 RESULT
 g
 δλ
 0
 1 tgagcagtactcgttgctgccgcgcgcgccaccagacataatagctgacagactaacaga 60
 Sequence 13, Application US/08037816A
Patent No. 5869624
GENERAL INFORMATION:
APPLICANT: Hasel, Karl W.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: HIV-1 VACCINES, ANTIBODY COMPOSITIONS RELATED
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
 Query Match 7.3%; Score 104.8; DB 4; Length 9600; Best Local Similarity 94.0%; Pred. No. 2e-23; Matches 109; Conservative 0; Mismatches 7; Indels 0;
 COMPUTER: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,647
 TITLE OF INVENTION: Compositions and Methods for IIILE OF INVENTION: Polynucleotide Delivery
 1218.002
 MEDIUM TYPE: Floppy disk
Compurer: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS.
ADDRESSE: Chiron Corporation
STREET: 4560 Horron Street
 ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9600 base pairs
 ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 121
 MOLECULE TYPE: DNA (genomic)
 Zuckermann et al.
 TYPE: nucleic acid
STRANDEDNESS: single
 ZIP: 10112
COMPUTER READABLE FORM:
 CLASSIFICATION: 514
 linear
 USA
 STATE: New COUNTRY: US. ZIP: 10112
 FILING DATE:
 US-08-037-816A-13
 TOPOLOGY:
 US-08-910-647-1
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Gaps

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1584 TGAGCAGTACTCGTTGCTGCCGCGCGCCCACAGACATAATAGCTGACAGACTAACAGA 1643
 61 ctgttcctttccatgggtcttttctgcagtcaccgtcgtcgacacgtgtgatcagatatc 120
 1 tgagcagtactcgttgctgccgcgcgccccagacataatagctgacagactaacaga 60
 tgagcagtactcgttgctgccgcgcgcgccaccagacataatagctgacagactaacaga 60
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 Length 5676;
 Length 5682;
 Indels
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/663,998 FILING DATE: 06-JUN-1996 CLASSIFICATION: 424
 APPLICANT: NORMAN, JON A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kistin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.
TITLE CF INVENTION: COMPOSITIONS AND METHODS FOR
 Score 103.6; DB 2;
Pred. No. 3.6e-23;
0; Mismatches 29;
 7.3%; Score 103.6; DB 2;
80.7%; Pred. No. 3.6e-23;
Live 0; Mismatches 29;
 E: Curtis, Morris & Safford, P.C.
530 Fifth Avenue
 ATTORNEY/AGENT INFORMATION:
NAME: KOWAISKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-333
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 1704 AGGAGTCCAGGGCTGGAGAGAAACCTCTG 1733
 121 ccaccatgttgcctgtagggaacccttctg 150
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 4, Application US/08663998
Patent No. 5846946
GENERAL INFORMATION:
 APPLICANT: HUEBNER, Robert C.
 DNA (genomic)
 DNA (genomic)
 7.3%;
 5682 base pairs
 Query Match 7.35
Best Local Similarity 80.75
Matches 121; Conservative
 Query Match 7.39
Best Local Similarity 80.79
Matches 121; Conservative
 nucleic acid
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES
 linear
 New York
 USA
 TYPE: nucleic
STRANDEDNESS:
) MOLECULE TYPE:
US-08-663-998-3
 TOPOLOGY: 11
 10036
 ADDRESSEE:
 RESULT 11
JS-08-663-998-4
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 1449 TGAGCAGTACTCGTTGCTGCCGCGCGCGCCACAGAATAGCTGACAGACTAACAGA 1508
 1 tgagcagtactcgttgctgccgcgcgcgccaccagacataatagctgacagactaacaga 60
 Gaps
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 DB 2; Length 3125;
 Score 104.2; DB 2; Length Pred. No. 1.6e-23; 0; Mismatches 8; Indels
 COUNTK:.

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PATEN: PatentIn Release #1.0, Version #1.30
 APPLICANT: HUEBNER, Robert C.
APPLICANT: NORMAN, JON A.
APPLICANT: LIANG, Xiaowu
APPLICANT: LARGE, Kristin R.
APPLICANT: CARNER, Kristin R.
APPLICANT: LUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ADMINISTERING BORRELIA DNA NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis ...
 ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue CITY: New York
 NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32.147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 Sequence 3, Application US/08663998
Patent No. 5846946
 TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUI
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3125 base pairs
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 7.38;
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 5676 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 Query Match 7.3 Best Local Similarity 93.2 Matches 109; Conservative
 single
 NAME/KEY: CDS
LOCATION: 1555..3115
OTHER INFORMATION:
 TYPE: nucleic acid
 STRANDEDNESS:
 STRANDEDNESS
TOPOLOGY: 1
 US-08-530-146-13
 RESULT 10
US-08-663-998-3
 STATE:
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1 tgagcagtactcgttgctgccgcgcgcgccaccagacataatagctgacagactaacaga 60
 APPLICANT: Kondo, Kazuhiro
APPLICANT: Mooarski, Edward S. Jr.
TITLE OF INVENTION: LATENT TRANSCRIPTS AND PROMOTERS
TITLE OF INVENTION: OF CYTOMEGALOVIRUS
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,998 FILING DATE: US/01V1996 CLASSIFICATION: 424
 7.3%; Score 103.6; DB 2;
80.7%; Pred. No. 3.7e-23;
 GENERAL INFORMATION:
APPLICANT: HUEBNER, Robert C.
APPLICANT: NORMAN, Jon A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine G.
TITLE OF INVENTION: ADMINISTERING BORRELIA DNA
 E: Curtis, Morris & Safford, P.C. 530 Fifth Avenue
 Pred. No. 3.7e
0; Mismatches
 1707 AGGAGTCCAGGGCTGGAGAAAACCTCTG 1736
 121 ccaccatgttgcctgtagggaacccttctg 150
 FILING DATE: 06-JUN-1996
CLASSIFICATION: 424
ATTORNEY/AGRWT INFORMATION:
NAME: KOWALSKI, THOMAS J. 7
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECOMMUNICATION INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 RESULT 14
US-08-450-945-57/c
; Sequence 57, Application US/08450945
; Patent No. 5783383
; GENERAL INFORMATION:
 Sequence 2, Application US/08663998 Patent No. 5846946
 MOLECULE TYPE: DNA (genomic) US-08-663-998-2
 Kazuhiro
 TELEPHONE: 212-840-3333 INFORMATION FOR SEQ ID NO:
 5952 base pairs
 Query Match 7.3'
Best Local Similarity 80.7'
Matches 121; Conservative
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 linear
 New York
 STRANDEDNESS:
 USA
 10036
 ADDRESSEE:
 COUNTRY:
 US-08-663-998-2
 STREET:
 STATE:
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 1588 TGAGCAGTACTCGTTGCTGCCGCGCGCCCACCAGACATAATAGCTGACAGACTAACAGA 1647
 61 ctgttcctttccatgggtctttctgcagtcaccgtcgtcgacacgtgtgatcagatatc 120
1584 TGAGCAGTACTCGTTGCTGCCGCGCGCGCCACACATAATAGCTGACAGACTAACAGA 1643
 1 tgagcagtactcgttgctgccgcgcgccaccagacataatagctgacagactaacaga 60\,
 Gaps
 61 ctgttcctttccatgggtcttttctgcagtcaccgtcgtcgacacgtgtgatcagatatc 120
 Length 5900;
 Indels
 APPLICANT: CARNER, KISSTIN R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: BUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: ADMINISTERING BORRELIA DNA
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 7.3%; Score 103.6; DB 2;
80.7%; Pred. No. 3.7e-23;
tive 0; Mismatches 29;
 SSEE: Curtis, Morris & Safford, P.C. F: 530 Fifth Avenue New York
 ATTORNEY/ACENT INFORMATION:
NAME: KOWAISKI, Thomas J.
REGISFRATION NUBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 5900 base pairs
 1708 AGGAGTCCAGGGCTGGAGAGAAACCTCTG 1737
 121 ccaccatgttgcctgtagggaacccttctg 150
 1704 AGGAGTCCAGGGCTGGAGAGAAACCTCTG 1733
 121 ccaccatgttgcctgtagggaacccttctg 150
 APPLICATION NUMBER: US/08/663,998
FILING DATE: 06-JUN-1996
CLASSIFICATION: 424
 Sequence 1, Application US/08663998
Patent No. 5846946
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 , MOLECULE TYPE: DNA (genomic) US-08-663-998-1
 HUEBNER, Robert C.
 NORMAN, Jon A.
LIANG, Xiaowu
 Query Match 7.3°
Best Local Similarity 80.7°
Matches 121; Conservative
 single
 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 nucleic acid
 linear
 GENERAL INFORMATION:
 STRANDEDNESS:
 ΝŽ
 ADDRESSEE:
 APPLICANT:
APPLICANT:
APPLICANT:
 STATE: N'
COUNTRY:
 STREET:
 RESULT 12
US-08-663-998-1
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Length 5952; Indels

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1597 TGAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGA 1538
 1 tgagcagtactcgttgctgccgcgcgcgccaccagacataatagctgacagactaacaga 60
 ö
 region of AD169 strain HCMV (antisense) containing antisense transcript ORFs
 1537 CIGTICCTTTCCATGGGTCTTTTCTGCAGTCACCGTCCTTGACACGATGGA 1487
 Length 2057;
 61 ctgttcctttccatgggtctttctgcagtcaccgtcgtcgacacgtgtga 111
PatentIn Release #1.0, Version #1.30
 7.2%; Score 103; DB 4; L
ilarity 95.5%; Pred. No. 3.1e-23;
Conservative 0; Mismatches 5;
 Search completed: February 7, 2002, 15:54:39 Job time: 393 sec
 8600-0157
 US/08/976,161
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,945
 RAGES Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600.
TELECOMMUNICATION INPORMATION:
TELEFAX: (415) 324-0860
INFORMATION FOR SED ID NO: 57:
SEDUENCE CHARATERISTICS:
 CDNA to mRNA
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
 2057 base pairs
 CURRENT APPLICATION DATA
APPLICATION NUMBER: U
 TYPE: nucleic acid
STRANDEDNESS: double
 INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
 unknown
 Query Match
Best Local Similarity
Matches 106; Conserv
 ORIGINAL SOURCE
 MOLECULE TYPE:
 ANTI-SENSE:
 US-08-976-161-57
 LENGTH:
 qu
 ö
 1538 TGAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGA 1538
 Gaps
 1 tgagcagtactcgttgctgccgcgcgcgccaccagacataatagctgacagactaacaga 60
 ó
 region of AD169 strain HCMV (antisense) containing antisense transcript ORFs
 61 ctgttcctttccatgggtctttctgcagtcaccgtcgtcgacacgtgtga 111
 Score 103; DB 1; Length 2057;
Pred. No. 3.1e-23;
0; Mismatches 5; Indels
 APPLICANT: Kondo, Kazuhiro
APPLICANT: Mocarski, Edward S. Jr.
TITLE OF INVENTION: LATENT TRANSCRIPTS AND PROMOTERS
TITLE OF INVENTION: OF CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
 SOFTWARE PATENTIAN STATES AND STATES AND STATES APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,945
FILING DATE: 23-MAY 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
 E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 57, Application US/08976161
Patent No. 6194542
 CDNA to mRNA
 2057 base pairs
 Query Match
Best Local Similarity 95.55
Matches 106; Conservative
 double
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-450-945-57
 TYPE: nucleic acid
STRANDEDNESS: doub
 unknown
 GENERAL INFORMATION:
 Palo Alto
 CITY: Palo Alto
 ANTI-SENSE: YES ORIGINAL SOURCE:
 USA
 USA
 TOPOLOGY: un
MOLECULE TYPE:
 HYPOTHETICAL:
 94306
 RESULT 15
US-08-976-161-57/c
 ZIP: .94306
 COUNTRY:
 COUNTRY:
 STREET:
 STATE:
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|                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                 |

```
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
 249243 MA
249243 MA
MI-P-A1-a
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Smith, T.P.L., Gross, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Sasas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 MI-P-Al-a
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 MI-P-A3-a
 MI-P-Al-a
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 MI-P-A1-a
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 25-APR-2001
 AZ840016 2
AU034107 P
BG490965 6
 AW359614
BF199164
BF199165
 BF711604
BF703303
 BF702121
BF711339
BF712300
BG894486
 AW669676 149 bp mRNA EST 2
131373 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW669676.1 GI:7526190
 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, USA
TED: 402 762 4360
Fax: 402 762 4390
 BF702314
BF711501
BF712292
BF712400
 BF711339
BF712300
 BF712372
BF198279
 AW359614
BF199164
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Plate: 107 row: D column: 22
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 BG894486
 BF712448
 BF712424
 BF702026
 BF702127
 CNS0039G
 AZ840016
 BF199165
 and minmatch 12 options.
PCR PRimers
PORWARD: AGGAAACAGCTATGACCAT
 Bos taurus
 Keele, J.W.
21180013
 39.8
39.2
38.4
 RESULT 1
AW669676
LOCUS
DEFINITION
 VERSION
KEYWORDS
SOURCE
ORGANISM
 JOURNAL
MEDLINE
COMMENT
 ACCESSION
 REFERENCE
 AUTHORS
 TITLE
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AW785253 116166 MA
AW785251 116166 MA
AW785901 117399 MA
AW666914 111105 MA
AW666934 113105 MA
AW669633 113105 MA
BF074689 222166 MA
BG355021 100689 MA
AQ778622 HS_2235_A
BF712368 MT-P-A3-a
BF711512 MI-P-A2-a
 Search time 7419.31 Seconds (without alignments) 2065.351 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 tgagcagtactcgttgctgc......tccttgaccctggaaggtgc 1426
 Description
 22703874
 . GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 11351937 seqs, 5372889281 residues
 lotal number of hits satisfying chosen parameters:
 ٠.
 SUMMARIES
 7, 2002, 21:32:29
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 AW669522
AW785253
AW669518
AW669634
AW669633
BF074689
BG365021
AQ778622
BF712368
 - nucleic search, using sw model
 AW669676
 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-391-606-12
1426
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em_gss_rod:*
 em_gss_fun:*
em_gss_hum:*
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 em_gss_inv:*
 em_gss_vrt:*
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 DB
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em_eston:
em_estpl:
em_estba:
em_estro:
em_estro:
em_estro:
 gb_est1:*
gb_est2:*
gb_htc:*
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Query
Match Length D
 *:ssb_dp
 149
1162
1162
1243
328
334
503
503
3337
359
 February
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EST:\*

Database

Perfect score:

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Scoring table:

Searched:

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70 70 70 70 70 70 70 70 84 84 41.6

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6 8 8 10 11 12

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Score

Result Š.

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1417 tggaaggtgc 1426
fat,
 1417 tggaaggtgc 1426
 109 TGGAAGGTGC 118
 Sus scrofa
 ď
 28
 28
 source
 BASE COUNT
 DEFINITION
 ORGANISM
 REFERENCE
AUTHORS
 BASE COUNT
 JOURNAL
 ACCESSION
 KEYWORDS
 FEATURES
 AW785253
 TITLE
 VERSION
 COMMENT
 ORIGIN
 RESULT
 ÖΛ
 δŏ
 g
 qq
 Qγ
 Pb
 [(bases 1 to 162) Smith, Treking, B.A., Roberts, A.J., Stone, R.T., Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Way, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904 e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 ;
 Bos taurus
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
 /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
48 c 38 g 39 t
 Gaps
 25-APR-2001
 ö
 Length 149;
 AW669522 162 bp mRNA EST 2
112928 WARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW669522
 0; Indels
 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
T=1: 402 762 4366
Fax: 402 762 4390
 Query Match

4.9%; Score 70; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.5e-10;
Matches: 70; Conservative 0; Mismatches 0;
 Email: smith@email.marc.usda.gov
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 Plate: 106 row: K column: 23
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 BACKWARD: GITITCCCAGICACGACG
 Location/Qualifiers
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 1417 tggaaggtgc 1426
 96 TGGAAGGTGC 105
 PCR PRimers
 21180013
 24
 EST
 DEFINITION
 ORGANISM
 BASE COUNT
ORIGIN
 ACCESSION
VERSION
KEYWORDS
SOURCE
 MEDLINE
 REFERENCE
 AUTHORS
 JOURNAL
 RESULT
AW669522
 FEATURES
 FEATURES
 TITLE
 LOCUS
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 ö
 ö
 Casas, E.,
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 162)

Stabrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.

Design and use of two pooled tissue normalized cDNA libraries for
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20,
 0; Gaps
 09-JUL-2000
 Gaps
 ö
 Length 162;
 Length 162;
 AW785253 162 bp mRNA EST 09
116166 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW785253
 Indels
 Indels
 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TPL: 402 762 4366
Fax: 402 762 4390
pituitary."
41 t
 Query Match

4.9%; Score 70; DB 10; L
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 70; Conservative 0; Mismatches 0;
 4.9%; Score 70; DB 10; 100.0%; Pred. No. 7.8e-10; Live 0; Mismatches 0;
 41
 Email: smith@email.marc.usda.gov
 1. .162
/organism="Sus scrofa"
 hypothalamus, and
51 c 42 g
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 Location/Qualifiers
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 and 30 embryos.
 EST discovery in swine Unpublished (2000)
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Best Local Similarity 100.0
Matches 70; Conservative
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Sns

ORGANISM

AUTHORS

REFERENCE

JOURNAL

COMMENT

TITLE

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AW785901

RESULT LOCUS

g

```
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

1 (bases 1 to 243)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 1 (bases 1 to 328)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.E., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary." 67 c 59 g 61 t
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 25-APR-2001
 ;
0
 Length 243;
 AW669634 328 bp mRNA EST 2
113105 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW669634
 Indels
 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402,762 4366
Fax: 402.762 4390
 DB 10; Le
9e-10;
hes 0;
 4.9%; Score 70; DB 100.0%; Pred. No. 9e-live 0; Mismatches
 /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"

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 /organism="Bos taurus"

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 /tissue_type="pooled"
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 GI:7526148
 Bovidae; Bovinae; Bos.
 Contact: Smith TPL
 Conservative
 1417 tggaaggtgc 1426
 109 TGGAAGGTGC 118
 Local Similarity
nes 70; Conserv
 AW669634.1
EST.
 Bos taurus
 Keele, J.W.
 Keele, J.W.
 21180013
 26
 COV
 Query Match
 source
 BASE COUNT
ORIGIN
 AW669634/c
LOCUS
 DEFINITION
 ORGANISM
 Best Loca
Matches
 JOURNAL
MEDLINE
 REFERENCE
AUTHORS
 REFERENCE
 AUTHORS
 ACCESSION
 FEATURES
 KEYWORDS
 TITLE
 TITLE
 COMMENT
 VERSION
 RESULT
 SOURCE
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 g
 Email: Smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
 .;
0
 Casas, E.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1a (bases 1 to 162)
1a Therenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
 Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
 Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 /note-"Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
 09-JUL-2000
 Gaps
 25-APR-2001
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AW785901
 AW669518 243 bp mRNA EST
112921 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
 Indels
 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 48390
Fax: 402 762 4390
 DB 10; L
7.8e-10;
 Query Match 4.9%; Score 70; DB Best Local Similarity 100.0%; Pred. No. 7.8 Matches 70; Conservative 0; Mismatches
 41
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 Smith TPL
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109 TGGAAGGTGC 118
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 AW785901.1
 PCR PRimers
 AW669518.1
 scrofa
 contact:
```

28

BASE COUNT ORIGIN

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Source

FEATURES

AW669518

ACCESSION VERSION

LOCUS DEFINITION

RESULT AW669518

COM

KEYWORDS SOURCE ORGANISM

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Gaps

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Contact: Smith TPL
 Tel: 402 762 4366
Fax: 402 762 4390
 Query Match
Best Local Similarity 100.
Matches 70; Conservative
 1417 tggaaggtgc 1426
 TGGAAGGTGC 40
 Bos taurus
 ๗
 BF074689
 84
 source
 source
 DEFINITION
 ORGANISM
 JOURNAL
MEDLINE
 REFERENCE
AUTHORS
 BASE COUNT
 49
 ACCESSION
 VERSION
KEYWORDS
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 BF074689
 FEATURES
 TITLE
 COMMENT
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 ORIGIN
 LOCUS
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 Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Peccra; Bovidea; Bovide
 ;
0
 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 /organism="Bos taurus"
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/lab_host="PoH10B"
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 25-APR-2001
 ;
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113104 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW669633
AW669633.1 GI:7526147
 USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
 Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4390
Res. 11 (4), 626-630 (2001)
 FORWARD: AGGAAACAGCTATGACCAT
BACKKARD: GTTTTCCCAGTCACGACG
Plate: 107 row: I column: 14
Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
 Contact: Smith TPL
 Conservative
 1417 tggaaggtgc 1426
 50 TGGAAGGTGC 41
 Best Local Similarity
 Bos taurus
 Keele, J.W.
 Genome Re
21180013
 71
 Query Match
 ORGANISM
 MEDLINE
COMMENT
 AW669633/c
 DEFINITION
 ACCESSION
VERSION
KEYWORDS
 REFERENCE
 JOURNAL
MEDLINE
COMMENT
 AUTHORS
 JOURNAL
 Matches
 TITLE
 FEATURES
 RESULT
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οy a

```
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.908004.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
 1 (bases 1 to 503)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Sasas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett,
G.L., Heaton, M.P., Lagereid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pitultary."
 25-APR-2001
 ö
 Length 374;
 BF074689 503 bp mRNA EST 222166 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
 4.9%; Score 70; DB 10;
100.0%; Pred. No. 1e-09;
tive 0; Mismatches 0;
and -minmatch 12 options.

PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT,
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 107 row: I column: 13
Seq primer: ATTTAGGTGACGTATAGG
 /organism="Bos taurus"
/db_xref="taxon:9913"
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/clone_lib="MARC 1BOV"
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Plate: 82 row: E column: 4
 Location/Qualifiers
 Location/Qualifiers
 BF074689.1 GI:10868200
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```
human.
 Query Match
 Query Match
 source
 RESULT 10
AQ778622/C
 DEFINITION
 ORGANISM
 Best Loca
Matches
 BASE COUNT
ORIGIN
 REFERENCE
AUTHORS
 ACCESSION
 MEDLINE
 KEYWORDS
SOURCE
 JOURNAL
 FEATURES
 VERSION
 TITLE
 COMMENT
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 ò
 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 ó
 Bovidae; Bovinae; Bos.

1 (bases 1 to 98)

Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 Gaps
 25-APR-2001
 ö
 Length 503;
 BG365021 98 bp mRNA EST '2
100689 MARC 1BOV Bos taurus cDNA 5', mRNA sequence
16365021
 Indels
 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
T=1: 402 762 4336
Eax: 402 762 4390
Email: smith@email.marc.usda.gov
 1.2e-09;
 4.9%; Score 70; DB 11;
100.0%; Pred. No. 1.2e-09
tive 0; Mismatches 0
 adrenal, and endometrium."
146 c 130 g 105 t
 Seq primer: ATTTAGGTGACACTATAG. Location/Qualifiers
 /organism="Bos taurus"
/clone_lib="MARC 2BOV"
 /tissue_type="pooled"
/lab_host="DH10B"
 FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 72 row: L column: 16
 BG365021.1 GI:13254118
 Ouery Match
Best Local Similarity 100.0
 1417 tggaaggtgc 1426
 427 TGGAAGGTGC 436
 Bos taurus
 Ø
 21180013
 800
 source
 BASE COUNT
ORIGIN
 DEFINITION
 BASE COUNT
ORIGIN
 ACCESSION
VERSION
KEYWORDS
SOURCE
 ORGANISM
 REFERENCE
AUTHORS
 JOURNAL
 RESULT
BG365021
 FEATURES
 TITLE
 COMMENT
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Adams, M.D. and
 העייטני 566 bp DNA GSS 02-AUG-1999 HS_2235_A2_B08_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=16 Row=C, DNA sequence. AQ778622. GI:5681582
 ö
 ö
 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2235 _row: C _column: 16
 Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
 1. .566
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/slone=lib="CIT Approved Human Genomic Sperm Library D"
 Holzman,T.,
 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108" $101\ {\rm c}\ 101\ {\rm g}\ 201\ {\rm t}\ 3 others
 596 tgitgaacittacacagacacctctttctcttggagcgtaggcgctcgtggagccttatg 655
 248 ITTTAAAATATTCAGAATCACAATTTTTTTTCTCAAAAGTAATATCTTATGGAGGTTAAG 189
 656 ggaatgcggttgtgcaactttgggagctgaattccaatatgcacagtccaaacctaaagt 715
 188 AGTATGTGAAGATGAAACTAAGCTGTATATGTACTAACAAGCACAAGATCAGACATAGTT 129
 Gaps
 Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
 1426
 0;
 54
 Length 566;
 1373 ccagccatctgtttgtccctcccccgtgccttccttgaccctggaaggtgc
 Mahairas, G.G., Waljace, J.C., Smith, K., Swartzell, S., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S.,
Length 98;
 Indels
 Match 3.0%; Score 42.2; DB 13;
Local Similarity 51.6%; Pred. No. 0.21;
les 95; Conservative 0; Mismatches 89;
3.8%; Score 54; DB 11;
100.0%; Pred. No. 3.6e-05;
tive 0; Mismatches 0;
 High quality sequence stop: 566.
Location/Qualifiers
 101 g
 Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 566)
 Best Local Similarity 100.0
Matches 54; Conservative
 Seq primer: T7
Class: BAC ends
 160
 Hood, L.
 776 tada 779
 g
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RESULT

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/klastef="texon:9823"
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/clone_lib="MI-P-A3" def-d-06-1-UM"
/clone_lib="MI-P-A3" def-d-06-1-UM"
/clone_lib="MI-P-A3" def-d-06-1-UM"
/clone_lib="Vector: pT7130-Pec (Pharmacia) with a modified
/note="Vector: pT7130-Pec (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-A3
plibrary is derived from anterior pituitary at estrus day
12. For a detailed description of the library from which
this clone was derived, please visit our web site at
 The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A strand cDNA and therefore this may represent a bonafide poly A rail. The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to verify it as a clone from the non-normalized anterior pituitary at estrus day 12 library cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. (thases 1 to 37)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
 133 CTGTGCCTTCTAGTTGCTGGGCATCTCT--GTTGCCCCTCCCCAGTACCTCGCTTGACCC 76
 02-JAN-2001
 Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
 http://pigest.genome.iastate.edu/.
TAG_LIB=MI-P-A3
TAG_ISSUB-anterior pituitary at estrus day 12
TAG_SEQ-TGACAG"
 Length 337;
 BF712368 337 bp mRNA EST 02-JP
MI-P-A3-adf-d-06-1-UM.S1 MI-P-A3 Sus scrofa cDNA clone
MI-P-A3-adf-d-06-1-UM 3', mRNA sequence.
 Indels
 Score 41.6; DB 11;
Pred. No. 0.27;
0; Mismatches 9;
 Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
 80
 Genome Res. 6 (9), 791-806 (1996)
 /organism="Sus scrofa"
 Location/Qualifiers
 106 g
 Email: cktuggle@lastate.edu
 BF712368.1 GI:12011843
 2.9%;
 Conservative
 Tel: 5152944252
Fax: 5152942401
 1417 tggaaggtgc 1426
 Similarity
 75 TGGAAAGTGC 66
 Sus scrofa
 discovery
 97044477
 BF712368
 59;
68 TAAA 65
 pig.
 EST
 Query Match
Best Local
 source
 BASE COUNT
 BF712368/c
LOCUS
 DEFINITION
 Matches
 ORGANISM
 AUTHORS
TITLE
 JOURNAL
MEDLINE
COMMENT
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 REFERENCE
 VERSION
KEYWORDS
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.,
 /note="vector: pryT3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-A2 library is derived from anterior pituitary at estrus day 5. For a detailed description of the library from which this clone was derived, please visit our web site at
 Email: cktuggle@leastate.edu
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dr track served to verify it as a clone from the non-normalized anterior pituitary at estrus day 5 library cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science Research Conter, Department of Animal Science Hough Research Genetics (www.resgen.com)
 Sus scrofa
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eureleostomi,
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 359)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
 02-JAN-2001
 Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
 .;
?i
 TAG_TISSUE-anterior pituitary at estrus day 5
 BF711512 359 bp mRNA EST 02-JA
MI-P-A2-acq-e-09-11-UM.s1 MI-P-A2 Sus scrofa cDNA clone
MI-P-A2-acq-e-09-11-UM 3', mRNA sequence.
 Length 359;
 /lab_host-"DH10B (Life Technologies)"
 Score 41.6; DB 11;
Pred. No. 0.27;
0; Mismatches 9;
 http://pigest.genome.iastate.edu/
TAG_LIB=MI-P-A2
 Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
 /strain="crossbreed"
/db_xref="taxon:982"
/clone="MI-P-A2-aq-e-09-1-UM"
/clone_lib="MI-P-A2"
 Genome Res. 6 (9), 791-806 (1996)
 1. 359
/organism="Sus scrofa"
 Location/Qualifiers
 108 g
 primer: M13 Forward
 BF711512
BF711512.1 GI:12010987
 2.9%;
 Query Match
Best Local Similarity 84.33
Matches 59; Conservative
 1417 tggaaggtgc 1426
 discovery
 68
 97044477
 source
 BASE COUNT
 DEFINITION
 ORGANISM
BF711512/c
 REFERENCE
AUTHORS
TITLE
 · MEDLINE
COMMENT
 ACCESSION
 VERSION
KEYWORDS
 JOURNAL
 FEATURES
 ORIGIN
 SOURCE
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75 TGGAAAGTGC

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Gaps

; ;

Sus scrofa

ORGANISM

LOCUS

ACCESSION

VERSION KEYWORDS SOURCE

BF712352/c

discovery

MEDLINE COMMENT

JOURNAL

AUTHORS TITLE

REFERENCE

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/clone_lib="MI-P-A3"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: ECORI; The MI-P-A3
library is derived from anterior pituitary at estrus day
12. For a detailed description of the library from which
this clone was derived, please visit our web site at
http://pigest.genome.lastate.edu/.
 The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NoII site and the oligo-dr track served to verify it as a clone from the non-normalized anterior pituitary at estrus day 12 library cDNA Library Preparation: RV Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 396)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
 133 CTSTGCCTTCTAGTTGCTGGGCATCTCT--GTTGCCCCTCCCCAGTACCTCCCTTGACC 76
 22-DEC-2000
02-JAN-2001
 Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
 ;
;
 TAG_TISSUB-anterior pituitary at estrus day 12
TAG_SEQ=TGACAG"
 3F702314 403 bp mRNA EST 22-DE
MI-P-A2-aar-f-03-1-UM.s1 MI-P-A2 Sus scrofa cDNA clone
 MI-P-A3-ade-h-04-1-UM.s1 MI-P-A3 Sus scrofa cDNA clone MI-P-A3-ade-h-04-1-UM 3', mRNA sequence.
 2.9%; Score 41.6; DB 11; Length 396; 84.3%; Pred. No. 0.28;
 Indels
 6
 98 t
 0; Mismatches
 Genome Res. 6 (9), 791-806 (1996)
97044477
 /organism="Sus scrofa"
 Location/Qualifiers
1. .396
 /strain="crossbreed
 118 g
 Email: cktuggle@iastate.edu
 BF712329.1 GI:12011804
 Seq primer: M13 Forward
 Local Similarity 84.3
nes 59; Conservative
 Tel: 5152944252
Fax: 5152942401
 1417 tggaaggtgc 1426
 75 TGGAAAGTGC 66
 Sus scrofa
 discovery
 11
 EST.
 Query Match
 source
 LOCUS
 ORGANISM
 BASE COUNT
ORIGIN
 BF702314/c
 DEFINITION
 JOURNAL
MEDLINE
COMMENT
 REFERENCE
AUTHORS
TITLE
 Matches
 ACCESSION
 VERSION
KEYWORDS
 FEATURES
 RESULT
 SOURCE
 q
 ò
 g
 δ
 /Clone="MI-P-A3:adf-b-07-1-UM"
/Clone_lib="MI-P-A3"
/Clone_lib="MI-P-A3"
/Clone_lib="Mi-P-A3"
/Obje="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: EcoR; The MI-P-A3
Ilprary Is derived from anterior pituliary at estrus day
12. For a detailed description of the library from which
this clone was derived, please visit our web site at
 The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NoII site and the oligo-dr track served to verify it as a clone from the non-normalized anterior pituitary at estrus day 12 library cDNA Library Preparation: N Woods, JA Green, RS Prather 3142 Animal Science Research Center, Department of Animal Science, University available through Research Genetics (www.resgen.com)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. I (bases 1 to 359), Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Gaps
 133 CTGTGCCTTCTAGTTGCTGGGCATCTCT--GTTGCCCCTCCCCAGTACCTCCCTTGACCC 76
 02-JAN-2001
 Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
 5
 http://pigest.genome.iastate.edu/.
TAG_LIB-MI-P-A3
TAG_TISSUE=anterior pituitary at estrus day 12
 MI-P-A3-adf-b-07-1-UM.s1 MI-P-A3 Sus scrofa cDNA clone
MI-P-A3-adf-b-07-1-UM 3', mRNA sequence.
 Length 359;
 Indels
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84.3%; Pred. No. 0.27;
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 Genome Res. 6 (9), 791-806 (1996) 97044477
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 /strain="crossbreed"
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 Location/Qualifiers
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 Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
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91 c 10
 BF712352.1 GI:12011827
 359 bp
 Contact: Tuggle CK
 Conservative
 1417 tggaaggtgc 1426
 Best Local Similarity
Matches 59; Conserva
 TGGAAAGTGC 66
```

POLYA-Yes

source

FEATURES

71

BASE COUNT ORIGIN

Query Match

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RESULT 14 BF712329/c

75

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us-09-391-606-12.rst

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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. CDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.resgen.com)
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polylinker; Site_I: Not I; Site_3: EcoRI; The MI-P-A2
For a detailed description of pituitary at estrus day
this clone was derived, please visit our web site at
http://pjeet.genome.iastate.edu/.
TAG_SEQ=None found" 100 t
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 403)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
 Gaps
 Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
 5;
 Query Match

2.9%; Score 41.6; DB 11; Length 403;
Best Local Similarity 84.3%; Pred. No. 0.28;
Matches 59; Conservative 0; Mismatches 9; Indels 2
 Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
MI-P-A2-aar-f-03-1-UM 3', mRNA sequence.
BF702314
BF702314.1 GI:11987722
 /clone="MI-P-A2-aar-f-03-1-UM"
 Genome Rês. 6 (9), 791-806 (1996)
97044477
 /organism="Sus scrofa"
 /strain="crossbreed"
/db_xref="taxon:9823"
 Location/Qualifiers
 Tel: 5152944252
Fax: 5152942401
 1417 tggaaggtgc 1426
||||| ||||
 pig.
Sus scrofa
 POLYA=Yes
 discovery
 79
 source
 BASE COUNT
ORIGIN
 ORGANISM
 AUTHORS
TITLE
 ACCESSION
 MEDLINE
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 JOURNAL
 FEATURES
 COMMENT
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 Dp
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Search completed: February 7, 2002, 21:32:32 Job time: 20666 sec

73 TGGAAAGTGC 64

QQ

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Human LYST1 longer isoform.

RESULT 14

AAW31950

```
(17571) Polypeptide (Compissors a tysowomen tential required.)

(17571) Polypeptide (Compissors a tysowomen tential required.)

(17571) In mutated in several chediak-Higashi syndrome (CHS) patients.

(17571 long isoform can be expressed in host cells using an isolated tysomomen (See AAP74201) for use in various pharmacological and munological applicatins. A shorter LYST1 isoform (see AAW23597).

(17571 long isoform can alternative splicing, has also been identified.

(17571 regulates degranulation of lysosomes, late endosomes and acidic secretory granules, primarily in leukocytes. Inhibition of such degranulation using dominant negatively acting truncated LYST1 peptides may be used to treat inflammatory bowel disease, systemic lupus of asthma, urticaria, inflammatory bowel disease, systemic lupus carthmanatous, rheumatoria arthritis, psoriasis, systemic vasculitis, concernosis, while LYST1 peptides that mimic or augment LYST1 function may be used to treat neoplasia.
 LVST1; human; lysosomal trafficking regulator; chediak-Higashi syndrome; CH syndrome; autoimmune disease; tumour; asthma. urticaria; inflammatory bowel disease; psoriasis; systemic lupus erythematosus; rheumatoid arthritis; systemic vasculitis; glomerulonephritis; multiple sclerosis; post-angioplasty restenosis; vaccine; therapy; diagnosis.
 Mammalian lysosomal trafficking regulators LYST1, Lyst1, LYST2 and
Lyst2 – useful to diagnose Chediak-Higashi syndrome
 protein sequence comprises a lysosomal trafficking regulator
 Claim 3; Page 108-109; 237pp; English.
 Kingsmore SF;
 97WO-US01748.
 96US-0034346.
 96US-0011146.
 Barbosa-Alleyne MDFS,
 (UYFL) UNIV FLORIDA.
 WPI; 1997-402616/37.
 2001 AA;
 N-PSDB; AAT74201
 WO9728262-A1
 Homo sapiens
 31-JAN-1997;
 01-FEB-1996;
20-DEC-1996;
 07-AUG-1997
 Sequence
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7; 1585 niflpsk------wqhlvltylqqpqgkrrihgkisiwvsgqrkpdvt 1626 ----eafylyacgpnhtsvmpckyg 1702 79 YGAFLMNPLAKATKTTLNGKENLAW-FIGGTLGG----LRKAGDWSATVRYEYVEALSVP 133 EIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLSFRAYGAYS 193 ----WINGOKKPLYL 78 27 ldfml-----prktslssdsnktfcmighclssqeeflqlagkwdl------79; 6.6%; Score 77.5; DB 18; Length 2001; 22.2%; Pred. No. 56; Live 15; Mismatches 50; Indels 79; 31 NTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVP-----gnlllfngakvgsq----Query Match
Best Local Similarity 22.27

Conservative 41; Conservative g ò δ

TD 198

7.

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This polypeptide is encoded by an alternatively spliced transcript of the human beige (bg) gene (see AAT89257). The amino acid sequence of the human beige (bg) gene (see AAT89257). The amino acid sequence of the predicted by gene product indicates that the protein is covel. A longer, putatively full-length by transcript (see AAT89256) encodes, a 3801-amino acid protein (see AAW3144). The by gene product is involved in the normal differentiation and/or function of intracellular vesicles. Mutation of the human by gene is responsible for human Chediak Higashi syndrome (CHS). An intracellular vesicle disorder, specifically CHS, can be diagnosed by measyring by gene expression in a patient sample, e.g. by measyring by gene expression in a patient sample, e.g. by gene[mutation contained in the genome of the mammal, specifically in a splice site of the by gene (claimed). Genetically sepecifically in a splice site of the by gene (claimed). Genetically contained in the compounds useful contained in the send for compounds useful.

Che the treatment of intracellular vestcle disorders, specifically contained in a mammal (claimed).
 || || || :| |
-----wqhlvltylqqpqkrrihgkisiwvsgqrkpdvt 1626
 Murine and human long and short form beige genes - useful to screen for compounds to treat, or to diagnose intracellular vesicle disorders, specifically Chediak-Higashi syndrome
 ----WINGOKKPLYL 78
 syndrome; beige; bg gene; intracelullar vesicle;
 3565..3579
/note= "WD40 or G protein-beta subunit repeat
motif"
 Length 3672;
 Human bg protein associated with Chediak-Higashi syndrome.
 6.6%; Score 77.5; DB 18; 22.2%; Pred. No. 1.3e+02;
 15; Mismatches
 31 NTEVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVP-
AAW31950 standard; Protein; 3672 AA.
 Location/Qualifiers
 Claim 94 Fig 8; 133pp; English.
 96US-0021064.
96US-0013883.
96US-0015673.
 MILL-) MILLENNIUM PHARM INC
UTAH) UNIV UTAH.
 97WO-US05068
 human; therapy; diagnosis.
 41; Conservative
 Kaplan J, Moore KJ,
 WPI; 1997-502728/46.
N-PSDB; AAT89257.
 Local Similarity
 3672 AA;
 Chediak-Higashi
 1585 niflpsk---
 Homo sapiens.
 109734914-A1
 14-APR-1998
 21-MAR-1997;
 01-JUL-1996;
 2-MAR-11996;
 9-APR-1996;
 35-SEP-1997
 AAW31950;
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 Peptide
 Query Match
 Matches
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(first entry)
 Arabidopsis thaliana.
 WPI; 2000-587311/55.
 753 AA;
 WO200052162-A2
 10-FEB-1998
 01-MAR-1999;
 08-SEP-2000
 Becker JM,
 Obtaining
 AAW23596;
 Sequence
 UYTE-)
 RESULT 13
 AAW23596
qq
 Ω
 17;
 by Holicobacter pylori. The vaccine contains at least one isolated H. pylori polypeptide, or its fragments, in a carrier, where the carrier is a Salmonella, vibrio cholerae or Shigalla vector containing a nucleic acid encoding the H. pylori polypeptide. The vaccines induce humoral and cellular immune responses. The vaccines are used to treat or prevent infections by H. pylori. Sequences AAX75779 to AAX75837 represent nucleic acid sequences encoding H. pylori outer membrane polypeptides (OMPs) AAX17160 to AAX17218.
 relates to a vaccine for preventing or treating infections
 Outer membrane polypeptide; OMP; vaccine; H. pylori infection; humoral;
 230 kfwwfssfgrgfaynewlynfyspktytlkngqtinpgvhafyiiwnykgfs----ig 283
 48 AMKYKYC-VWQWLVGKHSQVPWIN-GQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFI 105
 106 GGTLG-----GLRKAGDWSATVRYEYVEALSV-----PEIDVSGIGRG-----NL--L 146
 Gaps
 Oligopeptide transporter; OPT; isp4-like protein; OPT1; enkephalin; opiold.
 74;
 Score 79; DB 20; Length 327; Pred. No. 3;
 71; Indels
 182 DSLSFRAYGAY-----SKPANDKLGSDFTFR-KFDLGIISAF 217
 284 pfvyfspfneydpnftltydsnptftglg---frsqtdvtvlnpf 325
 Arabidopsis thaliana OPT family member emb CAB43855.1.
 Smith D;
 6.8%; Scor.
25.7%; Pred. No. 3,
''ve 23; Mismatches
 Cellular vaccine against Helicobacter pylori
 Ellis RW, Guild BC, Noonan BM,
 147 KFW----FAQAIAAN----YDPKE---ANSFT-
 Claim 7; Page 311-312; 352pp; English.
 H. pylori outer membrane polypeptide
 AAY96159 standard; Protein; 753 AA
 (GENO-) GENOME THERAPEUTICS CORP.
 98WO-US22883.
 97US-0993001.
 (first entry)
 58; Conservative
 cellular immune response
 1999-326698/27
 Query Match
Best Local Similarity
 Helicobacter pylori
 327 AA;
 N-PSDB; AAX75836
 The invention
 19-DEC-2000
 W09921959-A2
 28-OCT-1998;
 17-DEC-1997;
 06-MAY-1999
 AAY96159;
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 RESULT 12
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Matches

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102 AWFIGGTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPK 161
 54 CVWQWLVGKHSQVP-----WINGQKKPLYLYGAFLMNPLAKATKTTLNGKENL 101
 Gaps
 --FFVKCSVVDWNTFVPSETSTTEKAATNAMKYKY 53
 family member (isp4-like protein) from Arabidopsis thaliana, designated emb (AB43855.1. Members of the OPT family have been identified in yeasts and plants. The invention relates to a novel OPT of Saccharomycose cerevisiae, designated opr1 (see AAY96149). OPT is the first example of a genetically defined eukaryotic transport protein which can transport enkephalins across the cell membrane. Vectors allowing expression of the OPT1 gene, transgenic plants, and treatment of OPT1 with toxic enkephalins as an antifungal method are claimed. Also claimed is a method for obtaining mammalian enkephalin transporters by functional complementation of OPT1 deficient yeast.
 564 wllssvenicntdmlpksspwtcpgdvvfynasii-wgiigpgrmftskgi----rypg
 enkephalin across cell membrane, comprises transforming OPT1 gene
deleted yeast strain with mammalian gene library and selecting the
 mammalian enkephalin transport proteins for transporting
 present sequence is that of an oligopeptide transporter (OPT)
 65
 Length 753;
 Indels
 50;
 6.7%; Score 78; DB 21;
22.2%; Pred. No. 12;
trive 16; Mismatches 50
 Ω
 Barnes
 AAW23596 standard; Protein; 2001 AA
 Donhardt A,
 | |||: | : | : |
680 --yifrrykgwwarhnyilsaal 700
 Disclosure; Fig 5; 59pp; English
 EANSFINYKGFSALYMYGITDSL 184
 UNIV TENNESSEE RES CORP
01-MAR-2000; 2000WO-US05158
 99US-0122312
 Conservative
 8 WV---VEGILN--RLPKQ--
 Hauser M,
 Query Match
Best Local Similarity
Matches 45; Conserva
 (BECK/) BECKER J M.
(HAUS/) HAUSER M.
(DONH/) DONHARDT A.
(BARN/) BARNES D.
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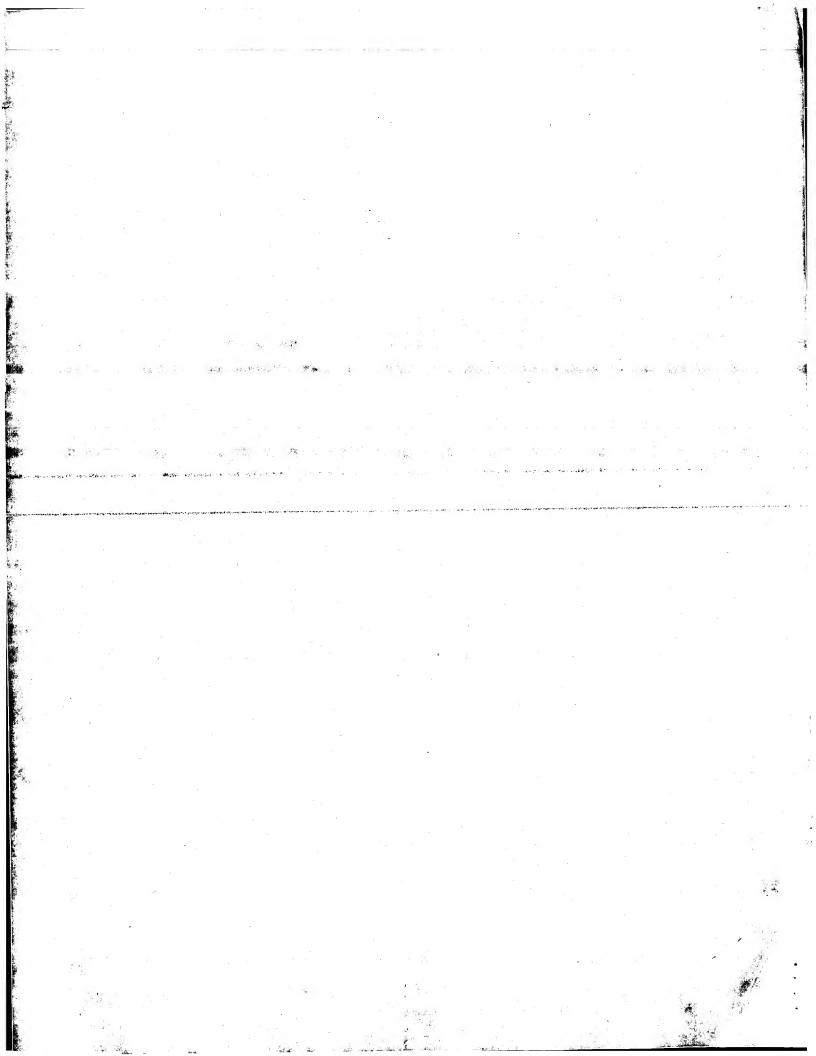
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667

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 134 EIDVSGIGRGNILKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLSFRAYGAYS 193
 31 NTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVP------WINGQKKPLYL 78
 Indels 79; Gaps
compounds useful for the treatment of intracellular vesicle disorders, specifically CHS, e.g. a molecule that modulates the expression of the bg gene in a mammal (claimed).
 Length 3801;
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6.6%; Score 77.5; DB 18;
Best Local Similarity 22.2%; Pred. No. 1.4e+02;
Matches 41; Conservative 15; Mismatches 50;
 Search completed: February 7, 2002, 21:34:34 Job time: 20753 sec
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GENERAL INFORMATION:
APPLICANT: Charles W. Stratton
APPLICANT: Charles W. Stratton
APPLICANT: Charles W. Miltonell
TITLE OF INVENTION: Methods for in vitro and in vivo
TITLE OF INVENTION: Susceptibility testing of Chlamydia species
FILE REFRENCE: 50150/00603
CURRENT FILE OF INVENTION NUMBER: US/09/025,176
PRIOR APPLICATION NUMBER: US/09/025,176
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 2
SOFTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 40
 Length 40;
 DB 4; Leuy
 APPLICANT: Burczak, John
APPLICANT: Burczak, John
APPLICANT: Carrino, J.J.
APPLICANT: Salituro, J.A.
APPLICANT: Rabich, E.K.
APPLICANT: Honowski, P.A.
APPLICANT: Manlove, M.T.
APPLICANT: Marshall, R.L.
APPLICANT: C. E. INVENTION: Materials and Methods for the TITLE OF INVENTION: Of Chlamydia Trachomatis
 US-08-867-030B-6

US-08-867-030B-6

US-08-233-813-5

US-09-233-813-5

US-08-233-813-5

US-08-233-47-1

US-08-277-231A-1

US-08-277-231A-1

US-08-477-326-4

US-08-229-515A-12

US-08-645-865-12

US-08-645-865-12

US-08-645-865-12

US-08-611-928-42

US-08-611-928-42

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US-09-173-891-42

US-09-009-44-5

US-09-010-232-5
 Score 37; DB 4; Pred. No. 0.000; Mismatches
 ALIGNMENTS
 3.4%; Scor.
100.0%; Pre
 RESULT 2
US-08-116-389-6
Sequence 6, Application US/08116389
Patent No. 5601978
GENERAL INFORMATION:
APPLICANT: Burczak, John
APPLICANT: Carrino, J.J.
 Sequence 2, Application US/09025176 Patent No. 6258532
 TYPE: DNA
CREANISM: Chlamydia pneumoniae
US-09-025-176-2
 Query Match 3.41
Best Local Similarity 100.
Matches 37; Conservative
 1307
2359
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 Search time 243.49 Seconds (without alignments) 1024.076 Million cell updates/sec
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 6,
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Sequence 6
Sequence 4
Sequence 4
 Sequence 1
Sequence 4
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 SUMMARIES
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Listing first 45 summaries
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: ABBOTT LABORATORIES One Abbott Park Road

CORRESPONDENCE ADDRESS: ADDRESSEE: ABBOTT LA STREET: One Abbott P

Sequence s Sequence

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Abbott Park

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 TITLE OF INVENTION: Materials and Methods for the Detection TITLE OF INVENTION: of Chlamydia Trachomatis NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: ABDOTT LABORATORIES STREET: One Abbott Park Road CITY: Abbott Park
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 Query Match
3.2%; Score 35.2; D
Best Local Similarity 83.3%; Pred. No. 0.02
Matches 40; Conservative 0; Mismatches
 APPLICATION NUMBER: 08/116,389
FILING DATE: 03 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: Brainard, Thomas D.
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5372.US.O1
TELECOMMUNICATION INFORMATION:
 REGISTRATION NUMBER: 32,459
REGISTRATION NUMBER: 372.05.01
REPERENCE/DOCKET NUMBER: 5372.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708 937-4884
 SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,830
FILING DATE:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/449,863
 Chlamydia trachomatis
US-08-708-431-6
 COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PCDOS/MSDOS
SOFTWARE: WordPerfeat
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,389
FILING DATE: 03 SEPTEMBER 1993
ATTORNEY/AGENT INFORMATION:
NAME: Brainard, Thomas D.
 Sequence 6, Application US/08880830 Patent No. 5846785
 MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
 APPLICANT: Klonowski, P.A.
APPLICANT: Manlove, M.T.
APPLICANT: Marshall, R.L.
 APPLICANT: Carrino, J.J. APPLICANT: Salituro, J.A. APPLICANT: Pabich, E.K.
 GENERAL INFORMATION:
APPLICANT: Burczak, John
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
 TELEPHONE: 708 937-488 TELEFAX: 708 938-2623
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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EDNESS: double
 COUNTRY: USA
 ZIP: 60064-3500
 CLASSIFICATION:
 linear
 FILING DATE:
 TYPE: nucleic
STRANDEDNESS:
 TOPOLOGY:
 02-08-880-830-6
 TELEX:
 ;
0
 Gaps
 APPLICANT: Salituro, J.A.
APPLICANT: Pabich, E.K.
APPLICANT: Manlove, M.T.
APPLICANT: Manlove, M.T.
APPLICANT: Marshall, R.L.
TITLE OF INVENTION: Materials and Methods for the Detection TITLE OF ENVENTION: Of Chlamydia Trachomatis
where of Sequences: 25
 Length 48;
 8; Indels
 Score 35.2; DB 1;
Pred. No. 0.028;
0; Mismatches 8;
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brainard, Thomas D.
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5372.US.OI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708 938-2623
 MORDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PCDOS/MSDOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,389
PILING DATE: 03 SEPTEMBER 1993
CLASSIFFICATION: 435
 APPLICATION NUMBER: US/08/708,431
FILING DATE: 05-SEP-1996
CLASSIFICATION: 435
 STREET: One Abbott Park Road CITY: Abbott Park
 Chlamydia trachomatis
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PCOS/MSDOS SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
 Sequence 6, Application US/08708431 Patent No. 5756298
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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Best Local Similarity 83.33
Matches 40; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
 Carrino, J.J
 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LA
 COMPUTER READABLE FORM:
 TYPE: nucleic acid
STRANDEDNESS: double
 COMPUTER READABLE FORM:
 ZIP: 60064-3500
 GENERAL INFORMATION:
 X: USA
60064-3500
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 COUNTRY: USA
 ORGANISM:
US-08-116-389-6
 US-08-708-431-6
 COUNTRY:
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Gaps

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ö
 APPLICANT: BARBOUR, Alan G.
APPLICANT: BEGSTROEM, Sven
APPLICANT: HANSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
MINMER OF SEQUENCES: 22
ICORRESPONDENCE ADDRESS:
 Length 48;
 Swedish isolate, pt. acrodermatitis chronicum migrans
 318 ttgggatcgctttgatgttttctgtactttaggagcttctaatggtta 365
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 Patentin Release #1.0, Version #1.25
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Pred. No. 0.028;
 ADDRŽSSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
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 OTHER INFORMATION: /function= "Primer
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,175A
FILING DATE: 26-OCT-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 4, Application US/08137175A Patent No. 5777095
 Borrelia burgdorferi
 LOCATION: 111..130
OTHER INFORMATION: /function-
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 TELEFAX: Zv.
TELEFAX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1978 base pairs
"YPE: nucleic acid
 REFERENCE/DOCKET NUMBER: BY
TELECOMMUNICATION INFORMATION
TELEFHONE: 202-628-5197
 Floppy disk
 NAME/KEY: misc_feature
LOCATION: 111..130
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OTHER INFORMATION: /fur
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 NAME/XEY: misc_feature LOCATION: 85..104
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 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 INDIVIDUAL ISOLATE:
 CDNA
 INFORMATION:
 TOPOLOGY: line
MOLECULE TYPE: c
ORIGINAL SOURCE:
 3Y: USA
20004
 ACA1
 D.C.
 SOFTWARE:
 ORGANI SM:
 RESULT 6
US-08-137-175A-4
 COUNTRY:
 LOCAT ION:
 Query Match
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 TITLE OF INVENTION: Materials and Methods for the Detection TITLE OF INVENTION: of Chlamydia Trachomatis UNDBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS:
 Length 48;
 318 ttgggatcgctttgatgttttctgtactttaggagcttctaatggtta 365
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Pred. No. 0.028;
0; Mismatches 8;
 ATTORNEY/AGENT INFORMATION:
NAME: Brainard, Thomas D.
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5372.US.O1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708 937-4884
TELEFAX: 708 938-2623
 APPLICATION NUMBER: PCT/US94/13895
FILING DATE: 03 SEPTEMBER 1993
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PCDOS/MSDOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
 ; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
ORGANISM: Chlamydia trachomatis
PCT-US94-13895-6
 ORGANISM: Chlamydia trachomatis
US-08-880-830-6
 Sequence 6, Application PC/TUS9413895 GENERAL INFORMATION:
 SSEE: ABBOTT LABORATORIES
T: One Abbott Park Road
Abbott Park
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
 3.2%;
nilarity 83.3%;
Conservative
 APPLICANT: Klonowski, P.A.
APPLICANT: Manlove, M.T.
APPLICANT: Marshall, R.L.
 Carrino, J.J.
Salituro, J.A.
Pabich, E.K.
TELEPHONE: 708 937-4884
TELEFAX: 708 938-2623
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
 Burczak, John
 TYPE: nucleic acid
STRANDEDNESS: double
 Query Match
Best Local Similarity
Matches 40; Conserva
 linear
 Illinois
 60064-3500
 CLASSIFICATION:
 STATE: Illing
COUNTRY: USA
 ADDRESSEE:
 RESULT 5
PCT-US94-13895-6
 APPLICANT:
 STREET:
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 955 toctgtcagatcaacaagtttaaatctagaaaagcttgtggagttactgtaggagctact 1014
 1715 AGTGCTGACAGTAAAAAAACTAAAGATTTTGTGTTCTTAACAGATGGTACCATTACAGTA 1774
 1775 CAAGCATATGACACAGCAGGTACTAAACTTGAGGGCAACTCAAGTGAAATTAAAGATCTT 1834
 1835 GCAGCACTTAAAAGCTGCTTTAAAATAACATAAAAGTAAAACATCCTACATCGGCTAATACC 1894
 895 ctaggaaatgccacagcattgtctactactgattcgttctcagacttcatgcaaattgtt 954
 835 attgetcagecaaaactacetacagetgttttaaaettaactgeatggaaceettettta 894
 Gaps
 0;
 Sequence 4, Application US/08479017
Patent No. 6143872
GENERAL INFORMATION:
APPLICANT: BARBOUR, Alan G.
APPLICANT: BERGSTROEM, Sven
APPLICANT: HENSSON, Lennart
TITLE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
 Length 1978;
 Score 34.2; DB 1; Length 1 Pred. No. 0.47; 0; Mismatches 103; Indels
 ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PAPELIFORM:
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEHLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,017
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,175
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 22-OCT-1992
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
 LOCATION: 127..948
OTHER INFORMATION: /product= "Ospa"
 NAME/KEY: CDS

LOCATION: 962..1861

OTHER INFORMATION: /product= "OspB"

US-08-137-175A-4
 NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFLECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-628-5197
TELEX: 248633
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 1895 TTTGTAGGTGTTGTTATT 1913
 1015 ttagttgatgctgataaat 1033
 Query Match
Best Local Similarity 48.2%;
Matches 96; Conservative
NAME/KEY:
 RESULT 7
US-08-479-017-4
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955 tectgteagateaacaagtttaaatetagaaaagettgtggagttaetgtaggagetaet 1014
 1715 AGTGCTGACAGTAAAAAACTAAAGATTTTGTGTTCTTAACAGATGGTACCATTACAGTA 1774
 835 attgctcagccaaaactacctacagctgttttaaacttaactgcatggaacccttcttta 894
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 Gaps
 Length 1978;
 Swedish isolate, pt. acrodermatitis chronicum migrans
 Indels
 APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Martin, Senis
APPLICANT: STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
 Score 34.2; DB 3;
Pred. No. 0.47;
0; Mismatches 103;
 "Primer
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
 LOCATION: 962..1861
COTHER INFORMATION: /product= "OspB" US-08-479-017-4
 New York
United States of America
 ORIGINAL SOURCE:
ORGANISM: Borrelia burgdorferi
STRAIN: ACAl
 NAME/KEY: misc_feature
LOCATION: 948..965.
OTHER INFORMATION: /function=.
 Sequence 1, Application US/08472534; Patent No. 5919620; GENERAL INFORMATION:
 NAME/KEY: misc_feature
LOCATION: 111..130
OTHER INFORMATION: /function=
 NAME/KEY: misc_feature
LOCATION: 85.104
OTHER INFORMATION: /function=
 1015 ttagttgatgctgataaat 1033
 1895 Trigradgrerrerrarr 1913
 Query Match 3.1%;
Best Local Similarity 48.2%;
Matches 96; Conservative
LENGTH: 1978 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 COUNTRY: United State ZIP: 10020 COMPUTER READABLE FORM:
 INDIVIDUAL ISOLATE:
 LOCATION: 127..948 OTHER INFORMATION:
 linear
 NAME/KEY: CDS
 MOLECULE TYPE:
 NAME/KEY:
 US-08-472-534-1
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United States of America

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pp
 Db
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 2914 AAGATGAGTGTATTGGATGAAGAGTATCTAAAAATACACGAAAAGTTTATAATGATTT 2973
 3034 TATTTAGCTAGATATAGAGAAATTATTAGCTGAGCATGATAGTTGTGTCAAAAATGAT 3093
 319 tgggatcgctttgatgttttctgtactttaggagcttctaatggttacattagaggaaac 378
 379 tctacagcgttcaatctcgttggtttattcggagttaaaggtactactgtaaatgcaaat 438
 259 aataagcatttacacgatgcagagtggttcactaatgcaggcttcattgccttaaacatt 318
 Length 3167;
 Score 34.2; DB 2; Length 3
Pred. No. 0.61;
0; Mismatches 93; Indels
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KENURAL INCORMATION:

APPLICANT: Hamel, Josee

APPLICANT: Barbard R

APPLICANT: Martin, Denis

TITLE OF INVENTION: BETT SHOCK PROTEIN HSP72 FROM

TITLE OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

KIREET: 1251 Avenue of the Americas

CITT: New York
 ; LOCATION: 771..2912
; OTHER INFORMATION: /product= "Fuci/HSP72 (C-169)"
US-08-472-534-1
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFENCE/DOCKET NUMBER: BLOVAC-2
TELEPHONE: 212-596-9000
TELEPHONE: 212-596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3167 base pairs
TYPE: nucleic acid
STRANDENESS: Gouble
 ORGANISM: Streptococcus pneumoniae
 APPLICATION NUMBER: US/08/472,534
FILING DATE:
CLASSIFICATION: 424
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
 Query Match
Best Local Similarity 49.2%;
Matches 90; Conservative
 30..755
 ORIGINAL SOURCE:
 NAME/KEY: CDS
 HYPOTHETICAL: NAMI-SENSE: NO
 3094 GAA 3096
 439 gaa 441
 LOCATION:
FEATURE:
 NAME/KEY:
 FEATURE
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2564 TGTAATCAAGCTGATAACTATAGAACATCAAAAGATTTTATTGTTGATAATATTCCAATAGAA 2623
 2504 AAGATGAGTGTATTGGATGAAGAGTATCTAAAAATACACGAAAAGTTTATAATGATTT 2563
 319 tgggatcgctttgatgttttctgtactttaggagcttctaatggttacattagaggaaac 378
 259 aataagcatttacacgatgcagagtggttcactaatgcaggcttcattgccttaaacatt 318
 379 totacagogitcaaictcgitggittaitcggagitaaaggiactacigiaaaigcaaai 438
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 Length 4320;
 Indels
 /product= "NH2-terminal portion of DNA J"
 LOCATION: 682..2502
OTHER INFORMATION: /product= "Heat-Shock Protein 72"
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,534
 93;
 DB 2;
 Score 34.2; DB
Pred. No. 0.73;
0; Mismatches
 NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFRENCE/CDOCKET NUMBER: Blovac-2
TELECCOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELER AX: 212-596-9000
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 ORGANISM: Streptococcus pneumoniae
 ; Sequence 1, Application US/08245511
; Patent No. 5928900
; GENERAL INFORMATION:
APPLICANT: Masure, H Robert
 3.18;
 DNA (genomic)
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
 LENGTH: 4320 base pairs
 Ouery Match 3.1%
Best Local Similarity 49.2%
Matches 90, Conservative
 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
 3265..4320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 OTHER INFORMATION:
OTHER INFORMATION:
 0
N
 NAME, KEY: CDS
 MOLECULE TYPE:
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 ORIGINAL SOURCE
 FILING DATE:
 HYPOTHETICAL:
 2684 GAA 2686
 439 gaa 441
 ANTI-SENSE:
 NAME/KEY:
 NAME/KEY:
 ; LOCATION:
US-08-472-534-4
 LOCA'TION:
 US-08-245-511-1
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795 acaatggtctcgagcaacttttgatgctgataacatccgcattgctcagccaaaactacc 854
 Score 33.2; DB 2; Length 490;
Pred. No. 0.45;
0; Mismatches 33; Indels
BACTERIAL EXPORTED PROTEINS AND ACELLULAR VACCINES BASED THEREON
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 600-1-069 US
 CURRENT APPLICATION NUMBER: US/08/600,993A
PILING DATE: 1-MAR-1996
CLASSPETCATION : 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
PILING DATE: 18-MAY-1994
CLASSIFICATION NUMBER: US 08/116,541
PRIOR APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
APTORNEY/AGENT INFORMATION:
RESISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
RELEPHONE: 201487-5800
TELECHANNINGATION:
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TELECHANNINGATION:
TELECHANNINGATION:
TELECHANNINGATI
 ORGANISM: Streptococcus pneumoniae
 855 tacagctgttttaaacttaactgcat 880
 390 AAAAGACGAAGTAAACAATATTACAT 415
 RESULT 12
19-08-245-511-46
US-08-245-511-46
Sequence 46, Application US/08245511
Patent No. 592890
GENERAL INFORMATION:
APPLICANT: MASURE, H ROBERT
 E: Klauber & Jackson
411 Hackensack Avenue
 3.0%;
 TOPOLGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
 LENGTH: 490 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
 Conservative
 TELEX: 133521
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
 TITLE OF INVENTION: BACT
TITLE OF INVENTION: ACEI
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & J
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Ouery Match
Best Local Similarity
Matches 53; Conserve
 1..490
 STREET: 411 Hacker
CITY: Hackensack
STATE: New Jersey
 NAME/KEY: CDS
 MOLECULA - HYPOTHETICAL: N
 ANTI-SENSE: NO ORIGINAL SOURCE:
 ;
US-08-600-993A-1
 07601
 COUNTRY:
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 795 acaatggtctcgagcaacttttgatgctgataacatccgcattgctcagccaaaactacc 854
 330 ACAATCCTTGGAAGCAACTTTAGGAGCTGATAATGTCATTATTGATATTGAACAACTACA 389
 0;
 Length 490;
 33; Indels
 APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
UMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
 Score 33.2; DB 2;
Pred. No. 0.45;
0; Mismatches 33;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
 600-1-069 CIP
 CLASSIFICATION: 424
PRIOR APPLICATION: 424
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 (TELECHONE: 201 487-5800
TELECHONE: 201 343-1684
 Streptococcus pneumoniae
 855 tacagctgttttaaacttaactgcat 880
 390 AAAAGACGAAGTAAACAATATTACAT 415
 Sequence 1, Application US/08600993A
Patent No. 5981229
GENERAL INFORMATION:
APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
 LUCULOGY: UNTROWN
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORIGINAL
 ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 490 base pairs TYPE: nucleic acid STRANDEDNESS: both
 Ouery Match 3.0%;
Best Local Similarity 61.6%;
Matches 53; Conservative
 ; NAME/KEY: CDS
; LOCATION: 1..490
US-08-245-511-1
 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
 SPRU98
 STRAIN: R6
 RESULT 11
US-08-600-993A-1
 ZIP: 07601
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1317 ACAATCCTTGGAAGCAACTTTAGGAGCTGATAATGTCATTATTGATATTCAACAACTACA 1376
 795 acaatggtctcgagcaacttttgatgctgataacatccgcattgctcagccaaaactacc 854
 ó
 Length 2019;
 Indels
 BACTERIAL EXPORTED PROTEINS AND ACELLULAR VACCINES BASED THEREON
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 Score 33.2; DB 2;
Pred. No. 1;
0; Mismatches 33;
 PRILING DATE: 1-MAR-1996
CLASSIFICATION NUMBER: 05/08/600,993A
FILING DATE: 1-MAR-1996
CLASSIFICATION DATA:
(A APPLICATION DATA: 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION NUMBER: US 08/245,511
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION: 08/116,541
FILING DATE: 01-88-1994
ATTELEPHAN: 26.742
TELEPHAN: 201343-1684
 Streptococcus pneumoniae
 1377 AAAAGACGAAGTAAACAATATTACAT 1402
 855 tacagctgttttaaacttaactgcat 880
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 US-08-680-726A-57
Sequence 57, Application US/08680726A
Patent No. 5804197
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
 411 Hackensack Avenue
 Klauber & Jackson
 3.0%;
 TELEX: 133521
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2019 base pairs
 Query Match 3.0°
Best Local Similarity 61.6°
Matches 53; Conservative
 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
 1..1932
 New Jersey
USA
 Hackensack
 IMMEDIATE SOURCE
 SPRU98
 NAME/KEY: CDS
 ORIGINAL SOURCE
 HYPOTHETICAL:
 COUNTRY: U
 ADDRESSEE:
 US-08-600-993A-46
 ORGANISM:
STRAIN: R
 LOCATION:
 TELEFAX:
TELEX: 1
 CLONE:
 RESULT 14
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 795 acaatggtctcgagcaacttttgatgctgataacatccgcattgctcagccaaaactacc 854
 .
0
 Length 2019;
 33; Indels
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS: ADDRESSEE: Klanker Appressee: Kl
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
 Score 33.2; DB 2;
Pred. No. 1;
0; Mismatches 33;
 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 CIP
TELECOMMUNICATION INFORMATION:
TELEFHONE: 201 487-5800
TELEFAX: 201 343-1684
 Streptococcus pneumoniae
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
 1377 AAAAGACGAAGTAAACAATATACAT 1402
 855 tacagctgttttaaacttaactgcat 880
 US-08-600-993A-46
Sequence 46, Application US/08600993A
Patent No. 5981229
GENERAL INFORMATION:
 ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
 APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
 3.0%;
 TELEX: 13351
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 2019 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
 Query Match
Best Local Similarity 61.64
Matches 53; Conservative
 NAME/KEY: CDS
LOCATION: 1..1932
 FOPOLOGY: linear
 IMMEDIATE SOURCE:
CLONE: SPRU98
 ANTI-SENSE: NO ORIGINAL SOURCE:
 MOLECULE TYPE:
 R6
 HYPOTHETICAL:
 ZIP: 07601
 ;
US-08-245-511-46
 RESULT 13
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 380 ctacagcgitcaaictcgitggittaitcggagitaaaggiactacigtaaaigcaaaig 439
 347 ATGITIATITIGITAATGATAGIGITITITCCAATAATAACTACAAATAAAAGTGGTATCC 406
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 260 ataagcatttacacgatgcagagtggttcactaatgcaggcttcattgccttaaacattt 319
 227 AACGTAATATTGGGAAGAAGATATTTTTGAATAAACGATGTACAATTAAAACTATTA 286
 140 atgttttcgaccgtatcttaaaagtagatgcacctaaaacattttctatgggagccaagc 199
 107 ATGGTTATAGTACTAACCCACCATTTAATGAGACTAAAAAATTTACTAGAGGATGGGTAT 166
 167 TITTACAAACCCCCCTTCTTATTGTAAAGATGGGATATCAATATCTAATATATGCATTG 226
 Length 1569;
 Score 32.2; DB 1; Length 1
Pred. No. 1.8;
0; Mismatches 183; Indels
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-JUL-1996
 ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
 FILING DATE: 12-JUL-1996
CLASSIFICATION: 44
ATONEY AGENT INFORMATION:
NAME: Connell, Gary J.
REGIESTATION UNDBER: 2618-46-C1
REPERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPANE: (303) 863-970
TELEPAN: (303) 863-023
INFORMATION FOR SEQ ID NO: 57:
 440 aactaccaaacgtttctttaagtaa 464
 Sequence 57, Application US/09092409
Patent No. 6159478
GENERAL INFORMATION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1569 base pairs
 Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
 TITLE OF INVENTION: REC
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
 1..1566
 Query Match
Best Local Similarity
Matches 142; Conserva
 MOLECULE TYPE: CDNA
 CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
 NAME/KEY: CDS
 ; LOCATION:
US-08-680-726A-57
 RESULT 15
US-09-092-409-57
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287 ATTATCCCTTAGCTGTAGCAGATTTGAGATTAGTAATAATACTATTAAAAAAATG 346
 380 ctacagogitcaaictogitggittaitcggagitaaaggiaciacigiaaaigcaaaig 439
 260 ataagcatttacacgatgcagagtggttcactaatgcaggcttcattgccttaaacattt 319
 227 AACGTAATATTTGTGAAGAAGATATTTTTGAATAAACGATGTACAATTAAAACTATTA 286
 320 gggatcgctttgatgttttctgtactttaggagcttctaatggttacattagaggaaact 379
 140 atgitticgaccgtatcitaaaagtagatgcacctaaaacatttictatgggagccaage 199
 107 AIGGITAIAGIACIAACCCACCALITAAIGAGACIAAAAAITIACIAGAGGAIGGGIAI 166
 167 TITIACAAACCCCCCTICTTATIGTAAAGAIGGGATATCAATAICTAATATATGCATIG 226
 Length 1569;
 Indels
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 DB 3;
 Score 32.2; DB 3;
Pred. No. 1.8;
0; Mismatches 183;
 E: Sheridan Ross & McIntosh
1700 Lincoln Street, Suite 3500
 APPLICATION NUMBER: US/09/092,409 FILING DATE:
 440 aactaccaaacgtttctttaagtaa 464
 407 ATATCACAAATGTGACTATAAATAA 431
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
 E: Floppy disk
IBM PC compatible
 32,020
 REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
TELEPHONE: (303) 863-9700
 Query Match 2.9%;
Best Local Similarity 43.7%;
Matches 142; Conservative
 TELEFAX: (303) 863-023
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 LENGTH: 1569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 NAME: Connell, Gary J. REGISTRATION NUMBER:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: CDNA
 OPERATING SYSTEM:
 linear
 CLASSIFICATION:
 Denver
 ADDRESSEE:
STREET: 17
 NAME/KEY:
 LOCATION:
US-09-092-409-57
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Search completed: February 7, 2002, 15:54:46 Job time: 400 sec

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 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 566)
Mahairas, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Xeller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 AL503431 AL503431
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BG218650 RST38431
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AL503431
 AQ778622 566 bp DNA GSS 02-AUG-1999 HS_22335_A2_B08_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=16 Row=C, DNA sequence.
 High Throughput Sequencing Center University of Washington University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA fel: (206) 616-3618 Fax: (206) 616-3618 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (206) 616-3887 Fax: (201) Sequence-tagged connectors: A sequence approach to mapping scanning the \operatorname{human}\ \operatorname{genome}
 AL434143
AL068607
BG153882
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
 AZ686763
 Contact: Mahairas GG, Wallace JC, Hood L
 ALIGNMENTS
 High quality sequence stop: 566.
Location/Qualifiers
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 AZ538399
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AA431622 Zw72D04.r
BF263367 HV_CEa000
BH131620 EWTWAX35TR
AQ955118 RPCI-23-3
AZ671757 ENTKH65TR
 Search time 7419.31 Seconds
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/db_xref="taxon:9606"
/clone="Plate=2235 Col=16 Row=C"
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 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K10"
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 /sex="male"
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 1 (bases 1 to 675)
Dunn,D., Aoyadi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 AZ840016 675 bp DNA GSS 20-FEB-2001
2M0136D20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 675)
 tgtcagatcaacaagtttaaatctagaaaagcttgtggagttactgtaggagctacttta 1017
 957
 897
 967
 717
 accatcaattatcatgaatggcaagtaggagcctctctatcttacagactaaactcttta 777
 778 gtgccatacattggagtacaatggtctcgagcaacttttgatgctgataacatccgcatt 837
 618
 597
 674
 675 YHWATYHYYYWWCAMMCMCTHTCHHCYYYYHHYTAHHTHHWYAHYYWWYYMWAYWM 734
 735 УСТАСТУНУННННҮНWAYHTTWY------АWAНAMWMHHAHYAAAAAAAAATTHHY 787
 Gaps
 908 CHEHNHCTCHHHHTMYHMTCHWMNHHWHHHWMATWMTTMMMCCMMHHHCHMYH
 getcagecaaaactacetacagetgttttaaacttaactgeatggaaceettetttacta
 ggaaatgccacagcattgtctactactgattcgttctcagacttcatgcaaattgtttcc
 ggttgtgcaactttggggagctgaattccaatatgcacagtccaaacctaaagttgaagaa
 658 gttgctttccccttgccaacagacgctggcgtagcaacagctactggaacaaagtctgcg
 358 aatggttacattagaggaaactctacagcgttcaatctcgttggtttattcggagttaaa
 ggtactactgtaaatgcaaatgaactaccaaacgtttctttaagtaacggagttgttgaa
 ctttacacagacacctctttctcttggagcgtaggcgctcgtggagccttatgggaatgc
 11;
 Length 1101;
 Indels
 276;
 DB 13;
 Best Local Similarity 18.0%; Pred. No. 1.8;
Matches 121; Conservative 265; Mismatches
 clone UUGC2M0136D20 F, DNA sequence
 Score 39.8;
Pred. No. 1.
 AZ840016.1 GI:13009924
 3.6%;
 1088 HYHWAHHCWYYTM 1100
 1018 gttgatgctgata 1030
 house mouse.
Mus musculus
 AZ840016
 Query Match
 SOURCE . ORGANISM
 DEFINITION
 928
 1028
 718
 838
 868
BASE COUNT
 ACCESSION
 REFERENCE
 VERSION
KEYWORDS
 AUTHORS
 AZ840016
 RESULT
 qq
 g
 QΫ́
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Dp
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AU034107.1 GI:3799531
 225
 human.
 EST
 source
 LOCUS
DEFINITION
 ORGANISM
 BASE COUNT
ORIGIN
 ORGÄNISM
 JOURNAL
 ACCESSION
 REFERENCE
 AUTHORS
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 VERSION
KEYWÖRDS
SOURCE
 BG490965
 FEATURES
 TITLE
 COMMENT
 RESULT
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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114) iplah29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
 U
 ;
0
 AU034107 690 bp mRNA EST 28-APR-1999
M0034107 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLB750, mRNA sequence.
AU034107
.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
 SIC,
 Mouse whole genome scaffolding with paired end reads from 10kb
 284 ggttcactaatgcaggcttcattgccttaaacatttgggatcgctttgatgttttctgta 343
 224 atactactgccgtagatagacctaacccggcctacaataagcatttacacgatgcagagt 283
 483 AAACCGAACCAGAAGAGCCAACTGCCCAGACAATCCAATGAGATCTCCGACATTCACATA 542
 164 tagatgcacctaaaacattttctatgggagccaagcctactggatccgctgctgcaaact 223
 Gaps
 Э
,
 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
 ö
 /db_xrefe"taxon:10090"
/clone="UUGC2M0136D20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
 Length 675;
 88; Indels
 Score 39.2; DB 13;
Pred. No. 2.2;
0; Mismatches 88;
 0.00
 Laboratory Mouse DNA Resource
 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0136 row: D column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
 /organism="Mus musculus"/strain="C57BL/6J"
 High quality sequence stop: 675.
Location/Qualifiers
 3.6%;
ilarity 51.1%;
Conservative
 /sex="Male"
 Class: plasmid ends
 plasmid inserts
Unpublished (2000)
 Tel: 801 585 5606
Fax: 801 585 7177
 .675
 l Similarity
92; Conserva
 USA
 201
 Query Match
Best Local
 source
 LOCUS
DEFINITION
 BASE COUNT
ORIGIN
 AU034107/C
 Matches
 JOURNAL
 ACCESSION
 FEATURES
 TITLE
 COMMENT
 RESULT
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 /db_xref="taxon:44689"
/clone="SLB750"
/clone=1.lb="Dictyostelium discoideum SL (H.Urushihara)"
 BG490965 1321 bp mRNA EST 27-MAR-2001 602519759F1 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:4638326 5',
 1 (bases 1 to 1321)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
 567 atatgcacagtccaaacctaaagttgaagaacttaatgtgatctgtaacgtatcgcaatt 626
 627 ctctgtaaacaaacccaagggctataaaggcgttgctttcccttgccaacagacgctgg 686
 746
 293 AGCTTTAGTGGCTTGGGCAACAGATTTTGCAGCAGAGTTAAACCTTCAGCCCAAGTTGG 234
 747 agcetetetatettacagaetaaaetetttagtgeeataeattggagtaeaatggteteg 806
 233 ATCCTTTCTATAGAGTGGACCACCATCACTTGTTCTACCCTTTTCGACACGTTCTTTG 174
 413 ACAAGCAGAGACCAATTGAGAAGTTGCAGCAGTTACAGCCATCGAAGTTGCAATGAGAGC 354
 687 cgitagcaacagctactggaacaaagtctgcgaccatcaattatcatgaatggcaagtagg
 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
 ö
 Indels
 /organism="Dictyostelium discoideum"
 Pred. No. 2.6;
0; Mismatches 140;
 DB 10;
 u
 176
 Institute of Biological Sciences University of Tsukuba
 Score 39;
 DNA Res. 5 (6), 335-340 (1998) 99156227
 Location/Qualifiers
1. .690
 b
 Contact: Hideko Urushihara
 /dev_stage="slug"
141 c 148
 807 agcaacttttgatgctgataaca 829
 173 TGCTAAAGTGGCGGCACCAACCA 151
Dictyostelium discoideum.
Dictyostelium discoideum
 BG490965.1 GI:13452462
 /strain="AX4"
 Query Match 3.5%;
Best Local Similarity 46.8%;
Matches 123; Conservative
 mRNA sequence.
BG490965
 Homo sapiens
 development
 POLYA=No.
 AUTHORS
TITLE
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83 t
 Query Match
3.5%; Score 38.2; Di
Best Local Similarity 53.9%; Pred. No. 3.3;
Matches 76; Conservative 0; Mismatches
 δ
 9
 ccttatgggaatgcggttgtg 544
 CTTTCTGGTTTGANAGTTGTG 151
 AW675282.1 GI:7540517
 Contact: Kerlavage, AR
 57 c
 AW675282
 96026280
 human.
 EST
 DEFINITION
 ORGANISM
 AUTHORS
TITLE
JOURNAL
 BASE COUNT
 464
 524
 171
 ACCESSION
 RESULT
AW675282
LOCUS
 REFERENCE
 VERSION
KEYWORDS
 JOURNAL
 FEATURES
 COMMENT
 SOURCE
 ORIGIN
 dC
 qq
 δy
 δλ
 δ
 Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 296)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White,
O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
J.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A.,
Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 /tissue_type="large_cell carcinoma"
//tasue_type="large_cell carcinoma"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: lung; Vector: pornB; site_l: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGGG(). Library constructed by Ling Hong in the
laboratory of Garald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Supersority II RT (Life Technologies). Note: this is a
NTH MGC Library."
 ;
0
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurament: DCTD/DTP/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1400 row: e column: 15
 139 tatgitticgaccgiatctiaaaagtagatgcacctaaaacattitctatgggagccaag 198
 259 aataagcatttacacgatgcagagtggttcactaatgcaggcttcattgccttaaacatt 318
 Gaps
 AA381424 296 bp. mRNA EST 21-APR-1997
EST94500 Activated T-cells I Homo sapiens CDNA 5' end, mRNA
 0;
 Length 1321;
 Indels
 3.5%; Score 38.4; DB 11; 47.8%; Pred. No. 4.7;
 0; Mismatches 121;
 339 t
 /organism="Homo sapiens"
 /clone_lib="NIH_MGC_18"
 /db_xref="taxon:9606"
/clone="IMAGE:4638326"
 High quality sequence stop: 3. Location/Qualifiers
 342 g
 NIĤ_MGC Lîbrary.
327 c 342
 AA381424
AA381424.1 GI:2033743
 Conservative
Inpublished (1999)
 1. .1321
 Similarity
 sequence.
 313
 human.
 111;
 Query Match
 Best_Local
Matches 11
 source
 LOCUS
 ORGANISM
 AA381424/C
 BASE COUNT
 ACCESSION
 VERSION
KEYWORDS
 REFERENCE
 JOURNAL
 FEATURES
 COMMENT
 ORIGIN
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Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bediarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,W.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
 ő
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 517)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
 Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 404 tattcggagttaaaaggtactactgtaaatgcaaatgaactaccaaacgtttctttaagta 463
 acggagttgttgaactttacacagacacctctttctcttggagcgtaggcgctcgtggag 523
 AW675282 517 bp mRNA EST 11-APR-2000 ba61h08.yl NIH_MGC_12 Homo sapiens cDNA clone IMAGE:2901087 5' similar to gb:MZ3115 CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE, SLOW (HUMAN);, mRNA sequence.
 291 TATTTGTTTTTACTTGAATTACAGTAGAGGGGAAANAATTACCTAACTTATCTAAATGCA 232
 Gaps
 ::
 Length 296;
 Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
1971: 3018699056
Fax: 3018699423
 6 others
 Indels
 /organism="Homo sapiens"
/db_xref="ATCC (inhost):185782"
/db_xref="taxon:9606"
/colone_lib="Activated T-cells I"
/cell_type="T-lymphocyte"
/dev_stage="adult"
 65;
 DB 10;
```

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barley.

Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; Pooideae;

Triticeae; Hordeum.

1 (bases 1 to 593)

Ming, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, Y., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories
 BF263367 593 bp mRNA EST 09-MAR-2001
HV-CE80006124f Hordeum vulgare seedling green leaf EST library
HV-CDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV-CE80006124f, mRNA sequence.
 211 CTAAAGACATAGTTCCTGGTGATATTGTAGAAATTGCTGTTGGTGACAAAGTTCCTGCTG 270
 863 ttttaaaacttaactgcatggaacccttctttactaggaaatgccacagcattgtctacta 922
 On Nov 17, 2000 this sequence version replaced gi:11194361
 Score 38.2; DB 10;
Pred. No. 4;
0; Mismatches 73;
 Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 460.
Location/Qualifiers
 /clone="IMAGE:781711"
/clone_lib="Soares_testis_NHT"
 SC 29634, USA
 Contact: Wing RA
Clemson University Genomics Institute
 1. .534
/organism="Homo sapiens"
/db_xref="taxon:9606"
 Seq primer: AATTAACCCTCACTAAAGGG
 High quality sequence stop: 503
 /sex="male"
/lab_host="DH10B"
 100 Jordan Hall, Člemson,
Tel: 864 656 7288
Fax: 864 656 4293
 Email: rwing@clemson.edu
 BF263367.2 GI:13260766
 3.5%;
 for barley genomics
Unpublished (2000)
 Clemson University
 82; Conservative
 Best Local Similarity
 BF263367
 164
 Query Match
 source
 6
 LOCUS ||
DEFINITION
 BASE COUNT
ORIGIN
 SOURCE
 Matches
 ACCESSION
 REFERENCE
 JOURNAL
 AUTHORS
 VERSION
KEYWORDS
 BF263367
 FEATURES
 TITLE
 COMMENT
 RESULT
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 1 (bases 1 to 534)
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
Washu-Merck EST Project 1997
 ö
 Center
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
 AA431622 534 bp mRNA EST 22-MAY-1997 zw/2b04.rl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781711 5' similar to gb:M23115 CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM TYPE, SLOW (HUMAN);, mRNA sequence.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 863 ttttaaacttaactgcatggaacccttctttactaggaaatgccacagcattgtctacta 922
 263 ATATAAGGTTAACTTCCATCAAATCTACCACACTAAGAGTTGACCAGTCAATTCTCACAG 322
 Gaps
 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/thml/lresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 425.
 ô
 63108
 3.5%; Score 38.2; DB 10; Length 517;
llarity 52.9%; Pred. No. 4;
Conservative 0; Mismatches 73; Indels 0.
 /tissue_type="cervical carcinoma cell line"
/lab_host="DH108"
 2 others
 õ
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
 323 GTGAATCTGTCTCTGTCAACCACACTGATCCC 357
 923 ctgattcgttctcagacttcatgcaaattgtttcc 957
 128 t
 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2901087"
 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
 /clone_lib="NIH_MGC_12"
 Location/Qualifiers
 127 g
 Tissue Procurement: ATCC
 AA431622.1 GI:2115330
 rechnologies.
94 c
 Contact: Wilson RK
 Tel: 314 286 1800
Fax: 314 286 1810
 Homo sapiens
 Query Match
Best Local Similarity
Matches 82; Conserv
 ๙
 human.
 source
 BASE COUNT
ORIGIN
 LOCUS
DEFINITION
 ORGANISM
 803
 TITLE
JOURNAL
COMMENT
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 RESULT
AA431622
 REFERENCE
 AUTHORS
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COMMENT
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Gaps

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Indels

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, DNA sequence.
AQ925118
 house mouse.
 301
 GSS.
 Query Match
Best Local
 source
 DEFINITION
 ORGANISM
 TITLE
JOURNAL
 BASE COUNT
ORIGIN
 REFERENCE
AUTHORS
 Matches
 ACCESSION
 VERSION
KEYWORDS
 RESULT 1
AQ925118
 FEATURES
 COMMENT
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 QΥ
 QY
 /db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Textamoeba histolytica Sheared DNA"
/clone="Vector: pHOSI: Site_l: Bat I; constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
 .;
0
 Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
 /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For
 more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 174 c 168 g 130 t 2 others
 b DNA GSS 07-AUG-2001 histolytica Sheared DNA Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 869)

Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HMI:IMSS sheared DNA library (2001)
 64 golgoaggagatectigegatectigegetactiggigegegetattagettaegiget 123
 328 TIGGCICTIGGAAAAGCIGGCIGCAAGGICCIAGIGAATTAIGCACGAICCICGAAAGAG 387
 388 GCTGAAGCAGTCTCTGAAGAGCTGAAGCATCTTGTGGTCAGGCTATTACCTTTGGAGGA 447
 Gaps
 4 ttgcctgtagggaacccttctgatccaagcttattaattgatggtacaatatgggaaggt 63
 green leaf EST
 /clone_INP_EGG0006124f"
/clone_Ilb="Hordeum vulgare seedling green leaf ES
library HYCDNA0004 (Erysiphe infected & control)"
//issue_type="seedling green leaf"
/lab_host="TUC121"
 124 ggattttacggagactatgttttcgaccgtatcttaaaagtagatgcacctaaa 177
 ;
 3.5%; Score 38; DB 11; Length 593; ilarity 51.1%; Pred. No. 4.7; Conservative 0; Mismatches 85; Indels
 MD 20850, USA
 /organism="Entamoeba histolytica"
 Unpublished (2001)
Contact: Brendan J Loftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
 /organism="Hordeum vulgare"
/cultivar="C116155 (Mla13)"
/db_xref="taxon:4513"
 High quality sequence start: 45
High quality sequence stop: 817,
Location/Qualifiers
Location/Qualifiers
 /strain="HM1:IMSS"
 Seq primer: M13-Reverse
 BH131620.1 GI:15090089
 Entamoeba histolytica.
 genomic, DNA sequence.
BH131620
 Entamoeba histolytica
 dq 698
 ENTMX35TR Entamoeba
 Class: shotgun
 Best Local Similarity
 BH131620
 119
 89;
 Query Match
 source
 source
 DEFINITION
 RESULT 10
BH131620
 BASE COUNT
 ORGANISM
 Matches
 ACCESSION
 REFERENCE
 AUTHORS
 JOURNAL
 VERSION
KEYWORDS
SOURCE
 FEATURES
 FEATURES
 TITLE
 LOCUS
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using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
 NA . GSS 21\text{-DEC}-1999 Mus musculus genomic clone RPCI-23-302M22
 Judacs, Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, Jaho, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other, GSSs: RPCI-23-302M22.TJ
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fex: 301 838 0200
 ö
 Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/coderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: 77
Class: BAC ends.
 Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; 1 (bases 1 to 602)
 861 tgitttaaacttaactgcatggaacccttctttactaggaaatgccacagcattgtctac 920
 921 tactgattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaagtttaaatc 980
 Gaps
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 981 tagaaaagcttgtggagttactgtaggagctactttagttgatg 1024
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 Location/Qualifiers
 AQ925118 682 bp DNA
RPCI-23-302M22.TV RPCI-23 M
 AQ925118.1 GI:6614121
 3.4%;
51.8%;
 l Similarity 51.8
85; Conservative
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Feb

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mRNA 'sequence.
 Ouery Match
Best Local Similarity
Las 79; Conservē
 Homo sapiens
 BE544037
 194
 human.
 source
 LOCUS
 ORGANISM
 COUNT
 TITLE
JOURNAL
COMMENT
 COUNT
 ACCESSION
 AUTHORS
 RESULT 1
BE544037
 VERSIÓN
KEYWORDS
SOURCE
 REFERÊNCE
 FEATURES
 ORIGIN
 ORIGIN
 BASE
 BASE
 g
 δ
 Anote—"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BH10B electrocompetent cells (BRL Life Technologies). "
121 c 117 g 172 t 2 others
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/note="Vector: PHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (FIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark,
 SM Entamoba histolytica

Eukaryota; Entamoeblae; Entamoeba.

Eukaryota; Entamoeblae; Entamoeba.

E 1 (bases 1 to 877)

E 5 (butus, b., van Aker, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1:IMSS sheared DNA library

L Unpublished (2000)

LOCATOCT: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208
 ó;
 Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
 A2671757 877 bp DNA GSS 14-DEC-2000
ENTKH65TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
 678
 gaattccaatatgcacagtccaaacctaaagttgaagaacttaatgtgatctgtaacgta 618
 447 GTATACTTACATGATCCCAAAAATTGTACCGGGGAACTCCTACAGCTGATAAACAGCTTC 506
 507 AGCAAAGTGGCTGAATACAAAATTAACTTAAATAAATCACTAGCCTTCCTCTATACAACA 566
 679 gacgctggcgtagcaacagctactggaacaagtctgcgaccatcaattatcatgaatgg 738
 Gaps
 619 tcgcaattctctgtaaacaaacccaagggctataaaggcgttgctttccccttgccaaca
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Pred. No. 9.6;
0; Mismatches 92; Indels
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 Seq primer: M13-Reverse
Class: shotgun
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AZ671757
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 Entamoeba histolytica.
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1 Similarity 49.7%;
91; Conservative
 Query Match
Best Local Similarity
 739 caa 741
 627 GAA 629
 BASE COUNT
ORIGIN
 DEFINITION
 259
 RESULT 12
 ACCESSION
VERSION
 ORGANISM
 AUTHORS
TITLE
 Matches
 KEYWORDS
SOURCE
 JOURNAL
 REFERENCE
 AZ671757
 FEATURES
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C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a mathod for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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/Ab_host="DHIOB"
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 584)
 BE544037 584 bp mRNA EST 09-AUG-2000 601069987F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3456213 5',
 295 gcaggettcattgccttaaacatttgggatcgctttgatgtttctgtactttaggagct 354
 355 tetaatggttacattagaggaaactetacagegtteaatetegttggtttatteggagtt 414
 NIT.MCC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
 585 GTATTCTTATTTTCATCAACTTTTGAGTTTGTTGTTCATTTTGTTTTAAGAGTT 644
 Gaps
 645 GTTAAAGGTTCAACTTTAGAGAAATTATCAGTGTTAGATGGTATTTCTTCTTTTTGA 704
 .;
0
 Length 877;
 Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
 others
 Indels
 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAN6443 row: n column: 22
High quality sequence stop: 577.
Location/Qualifiers
1. 584
 10;
 Score 37; DB 13;
Pred. No. 10;
0; Mismatches 70
 200 t
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/db_xref="taxon:9606"
/clone="IMAGE:3456213"
/clone_lib="NIH_MGC_12"
 Contact: Robert Strausberg, Ph.D.
 415 aaaggtactactgtaaatgcaaatgaact 443
 95 9
 BE544037.1 GI:9772682
 Technologies.
 3.4%;
ilarity 53.0%;
Conservative
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/clone_lib="Estamoba histolytica Sheared DNA"
/clone_lib="Estamoba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
 /db_xref="taxon:5759"
 3.38;
 Similarity 49.27
95; Conservative
 1. .1015
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 CAGATAGAGCTGA 308
 Class: shotgun
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 139
 Query Match
 Best Local
 source
 DEFINITION
 ORGANISM
 REFERENCE
AUTHORS
 BASE COUNT
 216
 1037
 296
 Matches
 RESULT 1
AZ686763
 ACCESSION
 VERSION
KEYWORDS
 JOURNAL
 FEATURES
 TITLE
 COMMENT
 SOURCE
 DRIGIN
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 /note="Vector: pBaCe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 53)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 ä
 Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 590 row: A column: 4
class.row.
 AQ818532 539 bp DNA GSS 26-AUG-1999 HS_5014_A2_A02_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=590 Col=4 Row=A, DNA sequence.
 543 tgcaactttgggagctgaattccaatatgcacagtccaaacctaaagttgaagaacttaa 602
 cacagacacctctttctcttggagcgtaggcgctcgtggagccttatgggaatgcggttg 542
 363 ttacattagaggaaactctacagcgttcaatctcgttggtttattcggagttaaaggtac 422
 49 TTATATTTGTAAATACTGTATACCATGTATTATGTGTATTGTTCATACTTGAGAGGTA 108
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 109 TATTATAGITIGITATGAAAGTATGTATTTTGCCCT-GCCCACATTGCAGGTGTTTTGTA 167
 168 TATATACAATGGATAAATTTTAAGTGTGTGCTAAGGCACATGGAAGACCGATTTTATTTG 227
 Gaps
 Sequence-tagged connectors: A sequence approach to mapping
 scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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 University of Washington
Onlouen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
 Indels
Score 36.4; DB 10;
Pred. No. 14;
0; Mismatches 136;
 Hood L
 Contact: Mahairas GG, Wallace JC,
 High Throughput Sequencing Center
 High quality sequence stop: 539.
Location/Qualifiers
 603 tgtgatctgtaacgtatcgcaattct 628
 288 IGTGAACAGITIACIAATGCACIACI 313
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1.38;
al Similarity 48.58;
129; Conservative
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 Class: BAC ends
 Homo sapiens
 Hood, L.
 human.
 Query Match
Best Local S:
Matches 129
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 RESULT 14
AQ818532
 ORGANISM
 DEFINITION
 423
 483
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 AUTHORS
 REFERENCE
 JOURNAL
 FEATURES
```

TITLE

COMMENT

```
Entanceba histolytica

Eukaryota; Entamoebidae; Entamoeba.

E 1 (bases 1 to 1015)

S Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1: MSS sheared DNA library
L Unpublished (2000)

Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
 ô
 Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
 AZ686763 1015 bp DNA GSS 14-DEC-2000
ENTIS68TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
 aatotagaaaagottgtggagttactgtaggagotactttagttgatgctgataaaiggt 1036
 857 cagetgittitaaacitaactgeatggaaceetteittactaggaaatgeeacageaitgi 916
 116 CAGTIGGCGIGACTCTATITGGCAGGAGCATAAAAGCCCTGGTCAATTCTTCAGGGTCAA 175
 236 AATCTAAAGATTCCTGCTGCCTTCCTGTAACTGCCCAATGGGTTCATCTTGCCCACTGCC 295
 Gaps
 917 ctactgattcgttctcagacttcatgcaaattgtttcctgtcagatcaacaagitta
 Ö
 Length 539;
 Indels
 10
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 98;
 DB 13;
pBACe3.6 vector at EcoRI sites"
115 c 131 g 144 t
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High quality sequence stop: 556.
Location/Qualifiers
 DNA library
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 AZ686763.1 GI:11823909
 genomic, DNA sequence.
AZ686763
 Entamoeba histolytica
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Barell, Oxford University Press, 1999)."
342 a 109 c 215 g 349 t
 BASE COUNT
ORIGIN
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| 0;                                                                                                                                                             |                                                                      |    |     |                                                                  |                                                                  |                                                               |                                                                      |                                                                  |                                                             |                                                           |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|----|-----|------------------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------------------------|-------------------------------------------------------------|-----------------------------------------------------------|
| Query Match 3.3%; Score 36.2; DB 13; Length 1015;<br>Best Local Similarity 45.3%; Pred. No. 18;<br>Matches 131; Conservative 0; Mismatches 158; Indels 0; Gaps | 765 actaaactotttagtgccatacattggagtacaatggtctcgagcaacttttgatgctga 824 |    |     | 136 AGGAAAAGAATTAGGACATACAAAAGAATTTTAGGTAAAATGTCAACTACAGAAGA 195 | ccettetttactaggaaatgccacagcattgtetactactgattggttetcagacttcat 944 | TATATATTATGTGGAAATACATATGCATTTGATTCATGGATATCATAATGAATCATT 255 | 945 gcaaattgtttcctgtcagatcaacaagtttaaatctagaaagcttgtggagttactgt 1004 | 256 TGATATTTTTGATGCAACTAAATTAAAAGAAATAAAAGAAATAAAAGAAATATTAT 315 | 1005 aggagetaetttagttgatgetgataaatggteaettaetgeagaaget 1053 | 316 TGGAACTCAATTAAATAGTCGTCAAGAATATTATATTTGTGGTGATGGT 364 |
| ery Ma<br>est Loc<br>atches                                                                                                                                    | 765                                                                  | 16 | 825 | 136                                                              | 882                                                              | 196                                                           | 945                                                                  | 256                                                              | 1005                                                        | 316                                                       |
| ÕĂŸ                                                                                                                                                            | Οy                                                                   | qq | ογ  | QQ                                                               | ογ                                                               | qq                                                            | ò                                                                    | qq                                                               | οy                                                          | qq                                                        |

Search completed: February 7, 2002, 21:32:39 Job time: 20673 sec

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| 4                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| *.                                                                           | e de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del companya de la companya de la companya del companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya del la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la companya de la c   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| <b>3</b>                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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- protein search, using sw model OM protein

February 7, 2002, 20:23:51; Search time 172 Seconds (without alignments) 184.541 Million cell updates/sec Run on:

US-09-391-606-7 1166

1 MTKKHYAWVVEGILNRLPKQ......DKLGSDFTFRKFDLGIISAF 217 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL\_17:\* Database :

sp\_vertebrate:\*
sp\_unclassified:\* sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\* sp\_organelle:\* sp\_rodent:\* sp\_plant:\* sp\_virus:\* sp\_phage:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description                   | 0927h6 chlamydia p | 091sb3 chlamydia p | 046166 chlamydia p | 084628 chlamydia t | 046380 chlamydia t | 09q3f9 bovine aden | 084501 paramecium | 091za7 bovine aden | 0911f8 streptomyce | 09wax4 chlorella v | 044021 plasmodium | 091121 streptomyce | 087696 chimpanzee | 058900 pyrococcus | 09kqu0 streptococc | 0915n0 pseudomonas | 098587 paramecium | 026913 trypanosoma | 000819 trypanosoma |
|-------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| ID                            | 94226              | Q9JSB3             | 046166             | 084628             | Q46380             | 2 Q9Q3F9           | 2 Q84501          | 2 Q912A7           | Q9L1F8             | 2 Q9WAX4           | 044021            | Q9L121             | 2 Q87696          | 058900            | Q9KGU0             | 0015NO             | 2 098587          | 026913             | 000819             |
| %<br>Query<br>Match Length DB | 422 2              | 422 2              | 715 2              | 432 2              | 207 2              | 901 1              | 830 1             | 902 1              | 684 2              | 836 1              | 453 5             | 246 2              | 349 I             | 743 1             | 2233 2             | 568 2              | 1176 1            | 395 5              | 449 5              |
| %<br>Query<br>Match           | 99.7               | 99.7               | 99.1               | 66.7               | 57.2               | 7.9                | 7.6               | 7.6                | 7.3                | 7.3                | 7.2               | 7.2                | 7.1               | 7.1               | 7.1                | 7.1                | 7.0               | 7.0                | 7.0                |
| Score                         | 1162               | 1162               | 1156               | 778                | 667                | 92.5               | 88.5              | 88.5               | 85.5               | 85.5               | 84                | 83.5               | 83                | 83                | 83                 | 82.5               | 82                | 81.5               | 81.5               |
| Result<br>No.                 | 1                  | ~                  | e                  | 4                  | S                  | 9                  | 7                 | 8                  | თ                  | 10                 | 11                | 12                 | 13                | 14                | 15                 | 16                 | 17                | 18                 | 19                 |

|    | Q9iza8 bovine aden | Q9fdc0 bacillus th | P72800 synechocyst | O66864 aquifex aeo | Q9aqu3 pseudomonas | O50499 streptomyce | Q9q3q0 bovine aden | Q9v057 pyrococcus | Q59078 alteromonas | O71149 bovine aden | Q9klf5 vibrio chol | Q9rb20 erwinia car | O80804 arabidopsis | Q9z155 helicobacte | Q9vku7 drosophila | Q9ulj7 drosophila |          | 050371 methyloph11 | Q9ftm2 oryza sativ | 097699 bos taurus | Q9ttk4 bos taurus | Q9sua4 arabidopsis | Q9hle8 thermoplasm | 09tit2 phacelia ra | Q9h133 homo sapien | O28945 archaeoglob |  |
|----|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|----------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| •  | 12 Q91ZA8          | 2 Q9FDC0           | 2 P72800           | 2 066864           | 2 Q9AGU3           | 2 050499           | 12 0903G0          | 1 09v057          | 2 Q59078           | 12 071149          | 2 Q9KLF5           | 2 Q9RB20           | 10 080804          | 2 Q9ZL55           | 5 Q9VKU7          | 5 0901J7          | 5 Q9VKT8 | 0                  | 10 Q9FTM2          | 6 097699          | 6 Q9TTK4 ·        | 10 Q9SUA4          | 1 Q9HLE8           | B Q9TIT2           | 4 Q9H133           | 1 028945           |  |
|    | 006                | 1128               | 214                | 409                | 447                | 469                | 902                | 644               | 290                | 910                | 195                | 473                | 482                | 499                | 648               | 650               | 387      | 412                |                    | 3796              | 3796              | 753                | 925                | 969                | 3186 '             | 202                |  |
| É, | 7:0                | 6.9                | 6.9                | 6.9                | 6.9                | 6.9                | 6.9                | 6.9               | 9.9                |                    | 8.9                | 6.8                | 6.8                | 6.8                | 8.9               | 8.9               | 6.7      | 6.7                | 6.7                | 6.7               | 6.7               | 6.7                | 6.7                | 9.9                | 9.9                | 9.9                |  |
|    | 81.5               | 81                 | 80.5               | 80.5               | 80.5               | 80.5               | 80.5               | 80                | 79.5               | 79.5               | 79                 | 79                 | 79                 | 79                 | 79                | . 79              | 78.5     | 78.5               | 78.5               | 78.5              | 78.5              | 78                 | 78                 | 77.5               | 77.5               | 77                 |  |
|    | 50                 | 21                 | 22                 | 23                 | 24                 | 25                 | 56                 | 27                | 28                 | 29                 | 30                 | 31                 | 3.2                | 33                 | 34                | 32                | 36       | 3.7                | 38                 | 39                | 40                | 41                 | 42                 | 43                 | 44                 | 45                 |  |
|    | ٠                  |                    |                    |                    | •                  |                    | •                  |                   | •                  |                    |                    |                    |                    |                    |                   |                   |          |                    |                    | •                 |                   | •                  | ٠.                 |                    | ٠,                 | ,                  |  |

## ALIGNMENTS

Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative granomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999). STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.; Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39."; Hypothetical protein; Complete proteome. SEQUENCE 422 AA; 48374 MW; 1CFE5B64B0ED3084 CRC64; Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila. NCBI\_TaxID=83558; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) CHLPN 76 KDA HOWOLOG\_2 (CT623). 422 AA Nucleic Acids Res. 28:1397-1406(2000). EMBL: A0001654; AAD18868.1; EMBL: A002165; AAF37913.1; PRT; [1] SEQUENCE FROM N.A. STRAIN-CWL029, MEDLINE-99206606; Pubmed-10192388; PRELIMINARY; SEQUENCE FROM N.A. CPN0729 OR CP0017 MIGR; CP0017; -. 9HLZ60 9н7260 RESULT Q927H6 

Gaps ö Ouery Match 99.7%; Score 1162; DB 2; Length 422; Best Local Similarity 99.5%; Pred. No. 6.7e-99; Matches 216; Conservative 0; Mismatches 1; Indels

Gaps

Q9JSB3 **09JSB3** 

RESULT 09JSB3

Length 715; Indels

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56 WQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAK------ATKTT--LNGKENLAWFI 105
 66.7%; Score 778; DB 2; Length 432;
63.8%; Pred. No. 1.5e-63;
Live 26; Mismatches 42; Indels 15; Gaps
 121 TVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGI 180
 1 MTKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFV----PSETSTTEKAATNAMKTKYCV 55
 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSA 120
 1 MTKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQMLV 60
 STRAIN=D/UW-3/CX;
BYDELTNE-29008089; Pubmed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 202 MAEKEYAWVVEAILNKLPGNFVVKTSVVDWNTLTAKTNDPADASAAQPAKPNT-KYDYLV
 sequence of an obligate intracellular pathogen of humans:
 MEDLINE=94156481; PubNed=7509320; Perez-Melgosa M., Kuo C.C., Campbell L.; Perez-Melgosa M., Kuo C.C., Campbell L.; Isolation and characterization of a gene encoding a Chlamydia pneumoniae 76-kilodalton protein containing a species-specific
 432 AA; 48365 MW; 46B3BA0A193A86BA CRC64;
 EMBL; L23921; AAA23117.1; -.
SEQUENCE 715 AA; 76626 MW; 3F01C9A59DE964C5 CRC64;
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
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Last sequence update)
Last annotation update)
 Chlamydiales; Chlamydiaceae; Chlamydia
 Score 1156; DB 2;
Pred. No. 4.9e-98;
0; Mismatches 1;
 181 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISA 216
 432
 epitope.";
Infect. Immun. 62:880-886(1994).
 Chlamydia trachomatis.";
Science 282:754-759(1998).
EMBL; AE001333; AAC68227.2;
 99.18;
 Conservative
 Query Match
Best Local Similarity 99.5
Matches 215; Conservative
 PRELIMINARY;
 01-NOV-1998 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.
 01-JUN-2001 (TrEMBLrel.
 Chlamydia trachomatis.
Bacteria; Chlamydiales
 CHLPN 76 KDA HOMOLOG.
 Best Local Similarity
Matches 148; Conserv
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 121 TVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGI 180
 TVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGI 180
 100 MIKKHYAWVVEGILNRLPRQFFVKCSVVDWNTFVPSETSTTERAATNAMKYKYCVWQWLV 265
 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSA 120
 266 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSA 325
 1 MTKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLV 60
 Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

EMBL; AP002547; BAA99936.1; - SEQUENCE 422 AA, 48373 MW; FDC2F564B2679C0E CRC64;
 MTKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLV
 ;
 Length 422;
 Indels
 CPJ0729.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Batteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
 Last sequence update)
Last annotation update)
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHLPN 76 KDA HOMOLOG_2 (CT623).
 046166 PRELIMINARY; PRT; 715 AA. 046166; 0.046166; 0.1-NOV-1996 (TrEWBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) 76 KDA PROPEILY.
 99.7%; Score 1162; DB 2; 99.5%; Pred. No. 6.7e-99;
 386 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 422
 181 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 217
 181 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 217
 AA.
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 MEDLINE=20330349; PubMed=10871362;
 Query Match
Best Local Similarity 99.55
Matches 216; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID-83558
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Indels

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Length 901;

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658 -----FYLSHTF--QRVSIQWDSSVPWPGDDRLLIPNWFEIKRDNNIDAEGYNMSQ 706
 602 IPPNTNIVVVNIPDRSWGAFRGWSFNRLKASETPMIGATKDPNFLYSGSI--PLLDGT-- 657
 94 TLNGKENLAWFIGGTLGGLRKAGDWSATVRYEYVEALSVP------EIDVSG--IGR 142
 143 GNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLS------FRAY 189
 Paramecium bursaria chlorella virus l (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
NCBL_raxID=10506;
 50 ENFTWFSEGDLVRKGNKVTMIPK ------ DWNMSIPAGTTKIIPFGGVKALPGNLKY 100
 52 KYCVWQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGG 111
 34 VPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATKT 93
 4 KHYAWVVEGILNR-----LPKQFFVKCSVVDWNTFVPSETSTT-----EKAATNAMKY 51
 MEDLINE-56187795; PubMed=8614977; Med. D.L., Van Etten J.L.; "Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map positions 88 to 182."; Virology 216:102-123(1996). Wirology 216:102-123(1996). EMBL: U42880; AAC95549.2; -.
 112 LRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPK 161
 5E74B05C8246F353 CRC64;
 PR01217; PRICHEXTENSN.
: 830 AA; 90929 MW; 12D20FFFDE008076 CRC64;
 Last sequence update)
Last annotation update)
 7.6%; Score 88.5; DB 12;
22.4%; Pred. No. 11;
tive 19; Mismatches 44;
 7.9%; Score 92.5; DB
21.3%; Pred. No. 5.2;
iive 28; Mismatches
 Created)
 InterPro; IPR002965; P_rich_extensn.
 PRT;
 PRT;
 1
901
101998 MW; :
 Q84501; Q84502;
01-NOV-1996 (TrEMBLrel: 01,
01-NOV-1999 (TrEMBLrel: 12,
01-UNN-2001 (TrEMBLrel: 17,
PBCV-1 CHITINASE.
 Local Similarity 21.3% nes 40; Conservative
 Query Match
Best Local Similarity 22.49
Matches 38; Conservative
 PRELIMINARY;
 PRELIMINARY;
 101 NQIL--PLVGK-----
 901 S
901 AA;
 SEQUENCE FROM N.A.
 763 NAYLSNPN 770
 190 GAYSKPAN 197
NON_TER
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SEQUENCÉ
 Querry Match
Best Local S:
Matches 40
 SEQUENCE
 PRINTS;
 0912A7
0912A7;
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 GGTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANS 165
 78 LYGAFLMNPLAK-----ATKTTLNGKENLAWFIGGTLGGLRKAGDWSATVRYEY 126
 127 VEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLSF 186
 Gaps
 23 VKCSVVDWNTFV----PSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLY
 bovine adenovirus 6.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Atadenovirus.
NCBI_TaxID=111167;
 SEQUENCE FROM N.A.
Myers G.S.A., Sriprakash K.S.;
Myers G.S.A., Sriprakash K.S.;
Myens G.S.A., Sriprakash K.S.;
Myenbrane-associated gene cluster of Chlamydia trachomatis.";
Submitted (JAN-199) to the EMBL/GenBank/DDBJ databases.
EMBL; U50732; AAD08717.1;
SEQUENCE 207 AA; 23254 MW; 9887DBB46DCB55C8 CRC64;
 SEQUENCE FROM N.A.
STRAIN-671130;
Lehmkuhl H.D., Hobbs L.A.;
Lehmkuhl H.D., Hobbs D.A.;
Partial sequence of the bovine adenovirus type 6 hexon gene.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF20769; AF20945.1;
HSSP; P03277; LDHX.
 20;
 57.2%; Score 667; DB 2; Length 207; 61.6%; Pred. No. 9.4e-54;
ive 24; Mismatches 37; Indels
 37; Indels
 717.1; -.
23254 MW; 9887DB846DCB55C8 CRC64;
 Last sequence update)
Last annotation update)
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
76 KDA PROTEIN HOMOLOG.
Chlamydia trachomatis.
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
 901 AA
 207
 RAYGAYSKPANDKLGSDFTFRKFDLGIISAF 217
 PRT;
 InterPro; IPR000736; Adeno_hexon. Pfam; PF01065; Adeno_hexon; 1. ProDom; PD002815; Adeno_hexon; 1.
 Query Match 57.2
Best Local Similarity 61.6
Matches 130; Conservative
 PRELIMINARY;
 PRELIMINARY;
 HEXON (FRAGMENT)
 NCBI_TaxID=813
 RESULT 5
046380
DC 046380;
DT 01-NOV-1
DT 01-MAY-1
DT 01-MAY-1
DE 76 KDA F
OS Chlamydio
OX NCBI_TAN
RN [1]
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RA MYERS G.
RA MYERS G.
RA MYERS G.
RE EMBL; UE SOUENCE
SO SEQUENCE
RA MYERS G.
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Indels

Length 830;

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902 AA

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SEQUENCE FROM N.A.
 Viruses; dsDNA vi.
NCBI_TaxID=10507;
 Chlorella virus.
 STRAIN=CVK2;
 206 F 206
 573
 <u> [14</u>
 Q9WAX4
 573
 RESULT 10
 112
 159
 Matches
 Q9WAX4
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 7;
 STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
 94 TLNGKENLAWFIGGTLGGLRKAGDWSATVRYEYVEALSVP------EIDVSG--IGR 142
 659 ------FYLTHTF--QRVSIQWDSSVPWPGDDRLLIPNWFEIKRDYSVDAEGYNMSQ 707
 143 GNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLS------FRAY 189
 34 VPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATKT 93
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Atadenovirus.
NCBI_TaxID=120509;
 STRAIN-MISK/67;
Lehmkuhl H.D., Hobbs L.A.;
Lehmkuhl H.D., Hobbs L.A.;
Lehmkuhl H.D., Hobbs L.A.;
Subartial sequence of the bovine adenovirus type 8 hexon gene.";
Subartial sequence of the EMBL/GenBank/DDBJ databases.
EMBL; AF38233; AAF63489.1;
EMBL; AF38233; AAF63489.1;
Interpro. IPRO00736; Adeno_hexon.
Pfam; PF01065; Adeno_hexon;
ProDom; PD002815; Adeno_hexon; 1.
 Length 902;
 Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
 Indels
 STRAIN-A3(2);
Brown S.P., Harris D.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
 102443 MW; 450C5E09AD3A2243 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE NEUTRAL ZINC METALLOPROTEASE.
(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel..17, Last annotation update)
 DB 12;
 684 AA
 7.6%; Score 88.5; D
20.7%; Pred. No. 12;
iive 29; Mismatches
 PRT;
 Conservative
 PRELIMINARY;
 Streptomyces coelicolor
 902
 HEXON (FRAGMENT).
bovine adenovirus 8.
 902 AA;
 Local Similarity
es 39; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 [1]
SEQUENCE FROM N.A.
 190 GAYSKPAN 197
 764 SAYIKSPN 771
 STRAIN-A3(2);
 01-OCT-2000
01-JUN-2001
 SC3D11.04C.
 NON_TER
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SEQUENCE
 Query Match
 Q9L1F8
 09L1F8
 Matches
 RESULT
Q9L1F8
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------LRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANY 158
 DPKEANSFINYKG-----FSALYMYGITDSLSFRA-----YGAYSKPANDKLGSDFT 205
 52 KYCVWQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGG 111
 --S 112
 Gaps
 55 VWQWLVGKHSQVPWINGQKKPL-YLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGG-- 111
 viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 4 KHYAWVVEGILNR-----LPKQFFVKCSVVDWNTFVPSETSTT-----EKAATNAMKY 51
 460 VHYSSGPANHFFYLLSEGSGTKTINGVTYNSPISDGLPVTGIGRAKAEKIWF-RALTTKF
 53;
 Length 836;
 7.3%; Score 85.5; DB 2; Length 684;
23.8%; Pred. No. 16;
Live 23; Mismatches 62; Indels 5
 112 LRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPK 161
 Indels
 Hiramatsu S., Yamada T.;
"Chlorella virus vChti-1 gene, complete cds.";
submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB022343; BAA78554.1;
HSSP; P07986; 1EXG.
 91356 MW; 6C283A494BA908E2 CRC64;
 594F70DDAB732BCF CRC64;
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL157916; CAB76001.1;
InterPro. IPR001370; Peptidase_M4.
InterPro: IPR000330; Zn_MTpeptdse.
Pfam. PF01447; Peptidase_M4; 1.
PROSTTE; PS00742; ZINC_PROTEASE; UNKNOWN_1.
 Last sequence update)
Last annotation update)
 7.3%; Score 85.5; DB 12;
21.8%; Pred. No. 21;
tive 20; Mismatches 44;
 ----dQ-----
 836 AA
 InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 836 AA; 91356 MW; 6C283
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
 Protease; Metalloprotease.
SEQUENCE 684 AA; 71289 MW;
 37; Conservative
 43; Conservative
 PRELIMINARY;
 101 NOIL--PLVGK----
 Query Match
Best Local Similarity
Matches 37; Conserv
 Query Match
Best Local Similarity
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physical map for
 1113 -RKAGDWSATVRYEYVEALSVPEIDVSGIGRGNILKFWFAQAIAANYDPKEANSFTNYKG 171
 Trivedi P., Horejsh D.R., Hinds S.B., Hinds P.W., Wu M.S.,
Salvato M.S., Pauza C.D.;
"Intrarectal transmission of simian immunodeficiency virus in rhesus macaques: selective amplification and host responses to transient or persistent viremia.";
J. Virol. 70:6875-6883(1996).
EMBL: U62382; AAB09526:1;
PinterPro; IPR000777; GP120.
 Gaps
 5 HYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHS
 75;
 99
 65 QVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGL------
 Length 246;
 Indels
 120 MRKA--WEAGV-------VLSGVSAGSLC--WFRGGATDSFGPE-
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
 40331 MW; 33982237F5B8A118 CRC64;
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).

EMBL, AL158061; CAB76358.1; -.
 B901487D58902E4D CRC64,
 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi, H., Hopwood D.A.; A set of ordered cosmids and a detailed genetic and
 30 HHAVDLSGAHGRRPRVLYVGTAIGDAEHFTARMTEAARVAGFDL----
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
 59;
 82;
 5;
 7.1%; Score 83; DB 12;
20.9%; Pred. No. 11;
tive 26; Mismatches 82;
 DB
 ; Score 83.5; DI
; Pred. No. 6.1;
24; Mismatches
 interpro; IPR000734; Lipase.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
 STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
 STRAIN=SIVMAC251;
MEDLINE=96386580; PubMed=8794330;
 l protein.
246 AA; 26231 MW;
 : |||:| | ||
153 ----LRPITDALDFLPYG 166
 Query Match
Best Local Similarity 20.6%;
Matches 41; Conservative 2.
 172 FSALYMYGITDSLSFRAYG 190
 ENVELOPE PROTEIN (FRAGMENT)
 46; Conservative
 PRELIMINARY;
 349 AA;
 Best Local Similarity
Matches 46; Conserv
 SEQUENCE FROM N.A.
 Envelope protein.
 349
 Hypothetical
SEQUENCE 24
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NON_TER
SEQUENCE
 Query Match
 987696
 969280
 RESULT
 087696
 REPRESENT REPRES
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 10;
 59 LVG-----KHSQVPWINGQKKPLYLYGAFLMNPLAKATKTT----LNGKENLAWFIG 106
 Gaps
 107 GTLGGLRKAGDWS-----ATVRYEYVEALSVPEIDVS------GIGRGNLLKFWFA 151
 13 ILNRLPKQFFVKCSVVDWNT---FVPSETS------TTEKAATNAMKYKYCVWQW 58
 Tardieux I., Liu X., Poupel O., Parzy D., Dehoux P., Langsley G.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJO02197, CAA05244.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
SMART; SM00320; WD40; 2.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.
PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
 175 DIGGNLLSGTCQNKQIHIDDPRKQE--ICNSFLIHDGGKSTKCIWIDGLGGEDKCILTTG
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1902;
 .99
 Plasmodium falciparum (isolate 3D7).
Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
 ; Score 84; DB 5; Length 453;
; Pred. No. 12;
31; Mismatches 77; Indels
 [2]
SEQUENCE FROM N.A.
STRAIN=A3(2);
Thomson N.R., Parkhill, J., Barrell B.G., Rajandream M.A.;
 Seeger K.J., Harris D.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
 453 AA; 51774 MW; A9C7525721EDD431 CRC64;
 152 QAIAANYDPKEANSFINYKGFSALYMYGITDSLSFRAYGAYSK 194
 293 QGSIRKVD-----EYK-----SCLPFRSFGFLPK 316
 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 26.2 KDA PROTEIN.
 Ā
 Query Match 7.2%;
Best Local Similarity 22.0%;
Matches 49; Conservative 3:
 PRELIMINARY;
 PRELIMINARY;
 Streptomyces coelicolor.
 [1]
SEQUENCE FROM N.A.
STRAIN-A3(2);
 SEQUENCE FROM N.A.
 Repeat; WD repeat
SEQUENCE 453 AA
 STRAIN-3D7;
 SC6D11.35
 CORONIN.
 044021
 RESULT 11
044021
 RESULT 12
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 Q9L121
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 388 APEAAKFTARQTKVSGASSNLIARLWSAPLHMLNATVAYRFYVQANPGYFDPFSPSIIDE 447
 69 INGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSATVRYEYVE 128
 -----FAQAIAANYDPKEANSFTN 168
 347 IFDHKEPF------SAKYTTLSGYRHIG-----GGVYVIGGFAGSLPADYKD 387
 GTRAENRTHIYWHGRDNRPIFSLNQYYNLTMNCRRPGNKTVLPVTIISGWVFHSLPINDS 240
 KHY-W--DAIRFRYCAPPGYALLRCNDTNYSGFMPNCSRVVASSCTRTWETQTPTWFGFN 180
 99 ENLAWFIGGTLGGLRKAGDW-----SATVRY-EYVEALSVPEIDVSGIGRG----- 143
 241 PNQAWCWFG------GKWKDAIKEVKQAIVKHPRYTGANNTDEINLTPPGGGDPEVTF 292
 Gaps
 9 VVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPW 68
 Pyrococcus horikoshii.
Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
 KHYAWVVEGILNRL---PKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLV
 74;
 Ouery Match 7.1%; Score 83; DB 1; Length 743; Best Local Similarity 18.5%; Pred. No. 30; Matches 42; Conservative 35; Mismatches 76; Indels
 : :: | | | :: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 169 YKGFSALYMYGITDSLSFRAYGAYSKPAN--DKLGSDFTFRKFDLGI 213
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 81.5 KDA PROTEIN PH1196.
 293 MWINCRGEFLYCKMNWFLNWVEDRNTANOKPKEHHK-RNY 331
 GKHSQ----VPWINGQKKPLY---LYGAFLMNPLAKATKTTL-
 743 AA.
 129 A----LSVPEIDVSGIGRGNLLKFW-----
 MEDLINE-98344137; Pubmed-9679194;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 058900;
 058900
 RESULT 14
058900
 RESULT 15
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2233 AA.

Created) PRT;

Q9KGU0; 01-OCT-2000 (TrEMBLrel. 15,

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PRELIMINARY;

Q9KGU0

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14;
 -QAIAANYDPKEANSFINYKGFSALY----MY 178
 589 DKTRYVTMGADKFRFGNGSGGHEKIADELDAVGFNY-----SEDNYKALRAKHPKWLIY 642
 -----SDFTFRKFULG 213
 88 AKA-----TKTTL-NGKENLA---WFIGGTLGGLRKAGDWSATVRYEYVEALSVPEI 135
 483 THNPASEQTLOIAAELGL-----LVQEEAFDTWYGG-KKP-YDYGRFFEKDATHPE 531
 Gaps
 32 TFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYLYGAFL----MNPL 87
 Sacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 78;
 STRAIN-KNR7/87;
Zaehner D., Hakenbeck R.;
"The Streptococcus pneumoniae beta-galactosidase is a surface
 ; Score 83; DB 2; Length 2233;
; Pred. No. 1.3e+02;
28; Mismatches 81; Indels
 EMBL. AF282997; AAF97242.1; ...
InterPro; IPR001649; Glyco_hydro_2.
InterPro: IPR001899; Gram_pos_anchor.
Pfam: PF00746; Gram_pos_anchor; 1.
PRINTS; PR00132; GLHYDRLASE2.
PROSITE; PR00143; GRAM_POS_ANCHORING; UNKNOWN 1.
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Run on:

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| GenCore version 4.5<br>Copyright (c) 1993 - 2000 Compugen 14d                                                                                                          | Result<br>No: Score                            | Query<br>e Match Length                                                                  | 1 DB ID                                                               |                                                                                        | 1<br>1<br>1<br>1<br>1 | Description                                                                         |            |
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| using sw model                                                                                                                                                         |                                                | 99.3<br>98.6<br>97.9                                                                     | 9 17 9                                                                | .37<br>(DA<br>(31                                                                      |                       | AX045137 Sequence<br>L23921 Chlamydia p<br>AX045131 Sequence                        |            |
| February 7, 2002, 19:30:32 ; Search time 12230.8 Seconds (without alignments) 1873.512 Million cell updates/sec                                                        | c 4 1359.4<br>5 1359.4<br>c 6 1359.4<br>7 1347 | 97.9 10421<br>97.9 12548<br>97.9 300550<br>97.0 1456                                     | 1 1 AE001654<br>3 1 AE002165<br>1 1 AP002547<br>5 6 AX045135          | 554<br>165<br>135                                                                      |                       | AE001654 Chlamydia<br>AE002165 Chlamydop<br>AP002547 Chlamydop<br>AX045135 Sequence |            |
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| IDENTITY_NUC<br>Gapop 10.0 , Gapext 1.0                                                                                                                                |                                                | w w w .<br>oʻr oʻ                                                                        | 919                                                                   | 314<br>322<br>322                                                                      |                       | AX155814 Sequence<br>U51235 Mycoplasma<br>AR008322 Sequence                         |            |
| 1472140 segs, 8248589755 residues                                                                                                                                      |                                                | w w w                                                                                    | ဖြဖ                                                                   | 306<br>771                                                                             |                       | AR027306 Sequence<br>AR035771 Sequence                                              |            |
| hits satisfying chosen parameters: 2944280                                                                                                                             |                                                | 9 99 9                                                                                   | o oo u                                                                | 316<br>316                                                                             |                       | AR078816 Sequence                                                                   |            |
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| Gen                                                                                                                                                                    |                                                | ພ ພ ພ<br>ຕໍ່ຕໍ່ພໍ                                                                        |                                                                       | 310<br>521                                                                             |                       | 233043 M.capricolu<br>AE006310 Lactococc<br>AF244521 Streptoco                      |            |
|                                                                                                                                                                        | 3.0                                            |                                                                                          | 77.                                                                   | 792<br>58                                                                              |                       | AC022792 Homo sapi<br>S76368 ORF 5' of                                              | <b>妇</b> ( |
| 7: 92_0m:<br>6: 92_0m:<br>6: 92_0m:                                                                                                                                    |                                                | ມ ເກ ແ<br>ມີເມີເ                                                                         | 14                                                                    | 7KGEN<br>4D<br>13P2 0                                                                  |                       | M86409 Herpesviru<br>X64346 Herpesviru<br>ALO49185 plasmodiu                        | ທທ         |
|                                                                                                                                                                        | 3.44                                           | , m m                                                                                    | 100                                                                   | 110<br>110<br>1261                                                                     |                       | AC104261 Homo sapi                                                                  | ت          |
| 9: gb_pr:*<br>10: gb_ro:*                                                                                                                                              | 35                                             | w w c                                                                                    | 000                                                                   | 217                                                                                    | •                     | AC074040 Mus muscu                                                                  |            |
| 11: 90_5cs:<br>12: 90_5cs:<br>13: qb_un:*                                                                                                                              |                                                | 200                                                                                      | 2 01 0                                                                | 36.2<br>)7.7<br>58.3                                                                   |                       | U23862 Human clone<br>AC073077 Homo sapi<br>AC013583 Homo sapi                      |            |
| 14: gb_vi:*<br>15: em_ba:*                                                                                                                                             |                                                | 8.8                                                                                      | <b>σ</b> κ                                                            | 362                                                                                    |                       |                                                                                     |            |
|                                                                                                                                                                        |                                                | 8 8<br>2 7                                                                               | 7 m                                                                   | 180<br>13P9                                                                            |                       | AF202180 Plasmodiu<br>AL096783 Plasmodiu                                            |            |
| 18: em_in:*<br>20: em_om:*<br>20: em_or:*                                                                                                                              |                                                | 3.1                                                                                      | -                                                                     | Y <b>Y</b>                                                                             |                       | (18                                                                                 |            |
|                                                                                                                                                                        |                                                |                                                                                          | ALI                                                                   | ALIGNMENTS                                                                             |                       |                                                                                     |            |
|                                                                                                                                                                        | RESULT 1                                       |                                                                                          |                                                                       |                                                                                        |                       |                                                                                     |            |
|                                                                                                                                                                        | AX045137<br>LOCUS                              | AX045137 2238                                                                            | 38 bp DNA                                                             |                                                                                        | PAT                   | 24 - NOV - 2000                                                                     |            |
|                                                                                                                                                                        | z,                                             | 7 £                                                                                      | from Patent WOOO                                                      | 66739.                                                                                 |                       |                                                                                     |            |
|                                                                                                                                                                        | VERSION A                                      | K045137.1 GI:1                                                                           | GI:11343736                                                           |                                                                                        |                       |                                                                                     |            |
|                                                                                                                                                                        | 0,1                                            | nlamydophila pr<br>nlamydophila pr                                                       | neumoniae.<br>neumoniae                                               | ;                                                                                      |                       |                                                                                     |            |
| 33: em_ntg_num:*<br>34: em_htg_root:*<br>35: em_htg_root:*                                                                                                             | REFERENCE 1<br>AUTHORS M<br>TITLE              | acteria; Chlamy<br>(bases 1 to i<br>irdin,A.D., Oom                                      | diales; Chl<br>2238)<br>nen,R.P., Wa<br>ntigens and                   | Chlamydiaceae; Chlamydophila<br>, Wang,J. and Dunb,P.<br>and corresponding dna fragmen | hlamy<br>n,P.<br>dna  | dophila.<br>fragments and uses                                                      |            |
| is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution. | JOURNAL F<br>FEATURES                          | thereof<br>Patent: WO 0066739-A 7 09-<br>Aventis Pasteur Limited (C<br>Location/Qualifie | WO 0066739-A 7 09-NOV-<br>Pasteur Limited (CA)<br>Location/Qualifiers | 09-NOV-2000;<br>  (CA)<br> fiers                                                       |                       |                                                                                     |            |
| SUMMARIES                                                                                                                                                              | source                                         | 122:<br>/organi<br>/db xre                                                               | 38<br>ism≖"Chlamyd<br>ef="taxon:83                                    | 12238<br>∕organism≖"Chlamydophila pneumoniae<br>/db_xref="taxon:83558" .               | niae"                 |                                                                                     |            |
|                                                                                                                                                                        |                                                |                                                                                          |                                                                       | )<br>)                                                                                 |                       |                                                                                     |            |

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Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
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Kalman, S. Mitchell, W., Marathe, R., Lammel, C., Fan, J., O
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RESULT AR144067

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Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R., Araylnd, L., Mitchell, W.P., Olinger, L., Tatusov, R.L., Zhao, Q., Koonin, E.V. and Davis, R.W.
Direct Submission
Submitted (20-MAY-1998) Program in Infectious Diseases, University of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA Location/Qualifiers
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 (bases 1 to 10954)
Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W. Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
 Genome sequence of an obligate intracellular pathogen of humans
 AE001333 10954 bp DNA BCT 30-0CT-2000 Chlamydia trachomatis section 60 of 87 of the complete genome. AE001333 AE0012733 AE001333. GI:3329068
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 1537)
Probst.P., Bhatia.A., Skeiky.Y.A., Fling.S.P. and Scholler.J.
Compounds and methods for treatment and diagnosis of chlamydial
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 1 (bases 1 to 7218)
Dorner, F., Scheiflinger, F. and Falkı
Recombinant fowlpox virus
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 Falah, M. and Gupta, R.S. Cloning of Mycoplasma capricolum: Cloning of Hsp70/DnaK gene region of Mycoplasma capricolum: phylogenetic analysis of mycoplasma based on Hsp70 sequences
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 1 (bases 1 to 2085)
Briles, D.E. and Yother, J.L.
Structural gene of pneumococcal protein
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|-----------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------------------|
| 1914                                                                                                      | 1974                                                               | 2034                                                           | 2094                                                                | 2154                                                                | 8762                                                                                                            | UY 22/4 C                                                          | RESULT 4 AP002547/c LOCUS                                         | ACCESSION<br>VERSION                                                | SOURCE<br>ORGANISM                                                  | REFERENCE<br>AUTHORS<br>TITLE                                     | JOURNAL<br>MEDLINE<br>REFERENCE                                     | AUTHORS<br>TITLE<br>JOURNAL                                         | COMMENT                                                           | FEATURES<br>Source                                                 |                                                                    | gene                                                               |                                                                     |
| ~;                                                                                                        | <del></del>                                                        | <del></del>                                                    |                                                                     |                                                                     |                                                                                                                 | ·                                                                  |                                                                   |                                                                     | <del></del>                                                         | <del></del>                                                       | <del></del>                                                         | <del></del>                                                         |                                                                   |                                                                    |                                                                    | <b>.e</b> e                                                        | <del></del>                                                         |
|                                                                                                           |                                                                    |                                                                |                                                                     |                                                                     |                                                                                                                 |                                                                    |                                                                   |                                                                     |                                                                     | ٠                                                                 |                                                                     |                                                                     |                                                                   |                                                                    |                                                                    |                                                                    |                                                                     |
| 7381<br>893<br>7441                                                                                       | 953<br>7501                                                        | 1013<br>7561                                                   | 1073                                                                | 1133<br>7681                                                        | 1193                                                                                                            | 1253                                                               | 1313                                                              | 1373                                                                | 1433                                                                | 1493<br>8041                                                      | 1553                                                                | 1613<br>8161                                                        | 1673<br>8221                                                      | 1733<br>8281                                                       | 1793<br>8341                                                       | 1853<br>8401                                                       | 1913<br>8461                                                        |
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| 322 CGC<br>834 att<br>   <br>382 ATT                                                                      | 894 ttt<br>   <br>442 TT                                           | 954 tgc                                                        | 1014 att<br>   <br>7562 ATT                                         | 1074 tae<br>   <br>7622 TAA                                         | 1134 gae<br>     <br>  7682 GAA                                                                                 | 1194 tac<br>    <br>7742 TAC                                       | 1254 cad<br>    <br>7802 CAG                                      | 314 atc<br>   <br> 862 ATC                                          | 1374 gga<br>       <br>7922 GGA                                     | 1434 cga<br>       <br>7982 CGA                                   | 1494 age<br>   <br> 8042 AGC                                        | 1554 cce<br>     <br>  8102 CCA                                     | 1614 agt<br>     <br>  8162 AG                                    | 674 age<br>     <br>  222 AGC                                      | 1734 cgc<br>     <br>  8282 CGC                                    | 1794 taa<br>   <br> 8342 TAA                                       | 1854 ctc<br>   <br> 8402 CTC                                        |
| , ,                                                                                                       | 7                                                                  | 7                                                              |                                                                     |                                                                     |                                                                                                                 |                                                                    |                                                                   | 1 7                                                                 |                                                                     |                                                                   |                                                                     |                                                                     |                                                                   | 1 8                                                                |                                                                    | 1 8                                                                |                                                                     |
| 99<br>99                                                                                                  | 9.<br>10.                                                          | Oy<br>Dp                                                       | Oy<br>Db                                                            | Oy<br>Dp                                                            | Qy<br>Pb                                                                                                        | Q<br>Q                                                             | Qy<br>Db                                                          | Oy<br>Dp                                                            | 0y<br>0d<br>0d                                                      | QY<br>Db                                                          | Qy<br>Op                                                            | Qy                                                                  | Qy                                                                | Oy<br>Op                                                           | QQ<br>QD                                                           | Qy<br>Db                                                           | QQ<br>QD                                                            |

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Shirai, M.
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Direct Submission
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Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.
Mutsunori Shirai, Yamaguchi University School of Medicine,
Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
T55-8505, Japan (E-mail:mshiraidpo.cc.yamaguchi-u.ac.jp,
T61:81-865-22-227, Fax:81-836-22-2415)
Dn Sep 15, 2000 this sequence version replaced gi:6172298
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RESULT 6
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KEYWORDS
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Bacteria; Chlamydiales; Chlamydiaceae; 1 (bases 1 to 1456)

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ORGANISM

AUTHORS TITLE

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WO 0066739-A 5 09-NOV-2000; Pasteur Limited (CA) Location/Qualifiers

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24-NOV-2000

PAT

1456 bp DNA 5 from Patent W00066739.

Chlamydophila pneumoniae

GI:11343734

AX045135.1 AX045135 Sequence E AX045135

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AX045135 LOCUS

RESULT

| l (bases 1 to 1852)  Murdin,A.D., Oomen,R.P., Wang,J. an —i(chlamydia) antigens and correspo thereof Patent: WO 0066739-A 3 09-NOV-2000; Aventis Pasteur Limited (CA) Location/Qualifiers  i. 1852 / Organism="Chlamydophila p / Ab_xref="taxon:83558"  l. 1752 / note="unnamed protein pro / Codon_start="1 / transl_table=11 / protein_id="cAC17378.1" / Ab_xref="GI:1134773" / translation="MSLADKIGIASS GAPTAYDTIFTSFELADIGALUSEQ GAPTAYDTIFTSFELADIGALUSEQ GAPTAYDTIFTSFELADIGALUSE GAPTATATKYGIAEAGKKFPDSPILGEA KQQGSSTGSINVSMILDDAENETASI ARAAGDBSAAAALDADARATISTASI ARAAGDBSAAAALDAORALEAALOR GSSYKOLYKTSKGTGSDYKTOISAGY SVPRAFTEARGPEKTDQALLENETASI ARAAGDBSAAAAALDAORALEAALOR GSSYKOLYKTSKGTGSDYKTOISAGY SVPRAFTEARGPEKTDQALLANISGN ROKLTSAVTKPPOPGSTYVOLSNDST ARABA | arity 45.4%; nnservative 0 ggcagataagctgggt [                 | Oy 1564 gcaacaataacaaagcagctgagcttcttaaagagatgcaagataacccagtagtccca 1623                  |
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 FEATURES
COMMENT
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

1 (bases 1 to 14690)
Read.T.D. Brunham.R., Shen.C., Gill,S.R., Heidelberg,J.F., White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,T., Berry,K., Bass,S., Linher,K., Welson,W., DeBoy,R., Caven,B., McClarty,G., Salzberg,S.L., Eisen,J. and Fraser,C.M. Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 Todases 1 to 14698)

Read, T.D., Brunham, R., Shen, C., Gill, S.R., Heidelberg, J.F.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T.,
White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T.,
Bowman, C., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B.,
McClarty, K., Salzberg, S.L., Eisen, J. and Fraser, C.M.
Direct Submission

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Location/Qualifiers
 Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W., Olinger,L., Grimwood,J., Davis,R.W. and Stephens,R.S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

1 (bases 1 to 10954)
Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R.,
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Genome sequence of an obligate intracellular pathogen of humans:
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Chlamydia trachomatis mviN homolog, lorf2; possible membrane-bound
protein, and 76 kDa protein homolog genes, complete cds.
 Kemp, D.J. and Sriprakash, K.S.
Expression of two novel proteins in Chlamydia trachomatis during
natural infection
 Myers,G.S.A. and Sriprakash,K.S.
Direct Submission
Submitted (05-MAR-1996) Molecular Genetics Unit, Menzies School
Headalth Research, Rocklands Drive, Darwin, NT 0810, Australia
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Ubhi,B.T.S., Rainey,D.R. and Meredith,D.M.
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1 (bases 1 to 5111)
Morsey,M.A. and Sheppard,M.G.
Frowth hormone and growth hormone releasing hormone compositions
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Morsey, M. A. and Sheppard, M.G.
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**SIDSZ/gcgdata/geneseqn/geneseqn/Nh1993.DhT:*

**SIDSZ/gcgdata/geneseqn/geneseqn/Nh1994.DhT:*

**SIDSZ/gcgdata/geneseqn/geneseqn/Nh1994.DhT:*

**SIDSZ/gcgdata/geneseqn/geneseqn/Nh1994.DhT:*

**SIDSZ/gcgdata/geneseqn/geneseqn/Nh1995.DhT:*

**SIDSZ/gcgdata/geneseqn/geneseqn
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 1861242
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 930621 seqs, 428662619 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM nucleic - nucleic search, using sw model
 IDENTITY_NUC SS.
Gapop 10.0 , Gapext 1.0
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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 Title:
Perfect score:
Sequence:
 Scoring table:
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 Database
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|        |   |        | Description        | C. pneumoniae 76 k | Nucleotide sequenc | Chlamydia pneumoni | 3'-truncated Chlam | 5'-truncated Chlam | Chlamydia pneumoni | Rhesus monkey mela | Recombinant vector | Plasmid VR-1012 DN | Plasmid GHRH1-29WT | Plasmid GHRH1-29YW |
|--------|---|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| COTTUE |   |        | ΩI                 | AAD02066           | AAX91990           | AAD02063           | AAD02065           | AAD02064           | AAA28411           | AAA27110           | AAX08423           | AAA71402           | AAC86258           | AAC86259           |
|        |   |        | 98                 | 21                 | 20                 | 21                 | 21                 | 21                 | 21                 | 21                 | 20                 | 21                 | 22                 | 22                 |
|        |   |        | Match Length DB ID | 87.4 2238 21 A     | 1230025            | 2156               | 1456               | 1852               | 1550               | 1909               | 4912               | 4912               | 5108               | 5108               |
|        | ф | Query  | Match              | 87.4               | 83.0               | 57.3               | 56.9               | 45.4               | 32.7               | 7.0                | 6.7                | 6.7                | 6.7                | 6.7                |
|        |   |        | Score              | 2225.2             | 2111.2             | 1459.4             | 1447               | 1155.4             | 832.8              | 179                | 171                | 171                | 171                | 171                |
|        |   | Result | NO.                | 7                  | °                  | m                  | 4                  | S                  | 9                  | 7                  | œ                  | თ                  | 10                 | 11                 |

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| AAC86262<br>AAC86266<br>AAC86266<br>AAC86266<br>AAX89797<br>AAX59392<br>AAX59392<br>AAX89796<br>AAX89796<br>AAX89796<br>AAX89796<br>AAX89796<br>AAX89796<br>AAX89796<br>AAX89796<br>AAX1562<br>AAX1562<br>AAX1666<br>AAX1668<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688<br>AAX1688                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ALIGNMENTS  BP.  truncation mutant  diagnosis; preven  tract disease; bro  cough; sore throat;  ment; truncation mu  lifiers  part of the sequen  e 76 kDa gene"  runcated Chlamydia  n"  part of the sequen  e 76 kDa gene"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 55111<br>55185<br>55284<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7285<br>7382<br>7407<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>7603<br>760 | NA; 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Locati ture l.655 /*tag=//note=//tag=//rote 766.2 /*tag=//note=//rag=//rote 766.2 /*tag=//note=//rag=//rote 789.42.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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 The present sequence is a DNA coding for a fusion protein comprising truncated Chlamydia pneumoniae 76 kDa protein and vector-encoded residues. C. pneumoniae 76 kDa protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory diseases such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
 234
 Gaps
 9
 atgacaaaaaacattatgcttgggttgtagaagggattctcaatcgtttgcctaaacag
 ggaaagcatagtcaggttccttggatcaatggacagaaaaagcctctatatgta
 ctagcttggtttattggaggaactttagggggactcagaaaagctggagactggtctgcc
 1 atgacaaaaaaacattatgcttgggttgtagaagggattctcaatcgtttgcctaaacag
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 getttettaatgaaceetttageaaaggetaegaagaetaegttaaatggaaaagaaaae
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 21; Length
 8; Indels
 s acids encoding a 76 kDa protein from Chlamydia for vaccinating against Chlamydia infections -
 0 other;
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 Score 2225.2;
Pred. No. 0;
0; Mismatches
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 Dunn
 BP; 689 A; 459 C; 497
 32; Fig 3; 112pp; English
 Wang J,
 Query Match 87.4%;
Best Local Similarity 99.6%;
Matches 2230; Conservative
 99US-0132270.
99US-0141276.
 2000WO-CA00511
 (AVET) AVENTIS PASTEUR LTD
 caused by C. pneumoniae
 Oomen RP,
 WPI; 2000-687542/67.
P-PSDB; AAY71957.
 Sequence 2238
 03-MAY-2000;
 03-MAY-1999;
30-JUN-1999;
 09-NOV-2000
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 tcactagctgacatacaggctgctttggtgagcctccaggatgctgtcactaatataaag
 tttttataataaaactaaaagatttttattattttttgagtttttatggttaatcctatt
 ttggaggcgagtgcagcaaataagagtgcggaagctcaaaagaatagcaggtgcggaagct
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WPI; 1999-357842/30

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 1974
 2154
 Nucleotide sequence of the complete genome of Chlamydia pneumoniae
 caacaaggaagtagtagtagtagtattcgtgtttccatgctgttagatgatgctgaaaat
 tctccaattcttcaagaagcggaacaaatggtaatacaggctgagaaagatcttaaaaaat
 caacaaggaagtagtattggtagtattcgtgtttccatgctgttagatgctgaaaat
 aatcctgattctcaagctgcccaacaggagctcgcagcacaagctagagcagcgaaagcc
 gottggagatgacagtgotgctgcagogctggcagatgctcagaaagctttagaagcggct
 ctaggtaaagctgggcaacaacagggcatactcaatgctttgggacagatcgcttctgct
 media; erythema nodosum; pharyngitis;
ope; ss.
 heart disease;
 Respiratory disease; pneumonia; bronchitis;
 ВР
 DNA; 1230025
 epitope;
 98US-0107078
97FR-0014673
 98WO-IB01890
 otitis
 (first entry)
 sinusitis; purulent ot
vaccine; neutralising
 Chlamydia pneumoniae
 1621
 1855
 1915
 1741
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 1801
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 The present sequence represents the complete genome of Chlamydia pheumoniae, and encodes proteins AAY3584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchits and is thought to be a contributing factor in heart disease, sarcoidosis, sinustis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
 829245
 829185
 829125
 829062
 828885
 Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;
 353
 413
 473
 593
 653
 713
 773
 293
 533
 Length 1230025;
 828824 CACAGATTCTCTATCATTCAGAGCTTATGGGGCTTACTCCCAAACCGAAACGATAAAACT
 tacagaaaaagctgctacaaacgctatgaatacaaatactgtgtttggcagtggctcgt
 CGGAAAGCATAGTCAGGTTCCTTGGATCAATGGACAGAAAAAGCCTCTATATCTTTATGG
 cacagtacgttatgagtatgtcgaagccttgtcagttccagaaatagatgtttcagggat
 attittaataaaatcittaaaaaacaggcicgcattaattaitagigagagcittittita
 829244 TACAGAAAAAGCTGCTACAAACGCTATGAAATACAAATACTGTGTTTGGCAGTGGCTCGT
 cctagcttggtttattggaggaactttagggggactcagaaaagctggagactggtctgc
 cacagattototattoattoagagottatggggottactocaaaccagoaaacgataaact
 cggcagtgattttactttccgaaagtttgatctaggtataatttcagcgttttaagtcaa
 Indels
 DB 20;
 .;
8
 Score 2111.2;
Pred. No. 0;
 0; Mismatches
 sequence of Chlamydia pneumoniae
 Page 291-611; 1912pp; English
 83.0%;
99.5%;
 Conservative
 Query Match
Best Local Similarity
Matches 2138; Conserv
 Claim 1;
 Genome
 354
 414
 234
 829304
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|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy         894 ttttttataataaactaaaagatttttattatttttttggtttttatggttaatcctat         953           Db         828644 TTTTTATAAAAACTAAAAGATTTTTATTTTTGAGTTTTTATGGTTAATCCTAT         828585           Qy         954 tggtccaggtcctatagacgaacagaacgcacacctcccgcagatctttctgctcaagg         1013           Db         828584 TGGTCCAGGTCCTATAGACGAACCCCCCCCCCCCAGACTTCTCTCCTCAAGG         828525           Qy         1014 attggaggcgagtgcagcaaataagagtgcggaagctcaaagaatagcaggtgcggaagc         1073           Qy         1014 attggaggcgagtgcagcaaataagagtgcggaagctcaaagaatagcaggtgcggaagc         1073           PB         828524 ATTGGAGGCAGCAGCACACCCCCCCCCAAGCTCTCCCCCCAAGCTCCGCAAGC         828465           Qy         1074 taagcctaaagaacttaagactggtattgfcttggagcatcttgcgttctgcagt         1133           Db         828464 TAAGCCTAAAGAATTAAAGACCGAAGCTGAGGCAAGGCA | Oy 1254 cacgtctgatgattataagactcaagcgcaaacagcttacgatactatctttacctcaac 1313                                                                                | DB 828044   AGCGATTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | Oy 1734 cgctagtggagctgtagaaaatgctaaatctaataacagtataagcaacatagattcagc 1793                                                                                                                       |

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evention; treatment;
bronchitis; sinusitis;
at; hoarseness; fever;
 m Chlamydia pneumoniae, fections -
 reatment
a, upper respiratory
cute respiratory
ness, fever; and
 niae 76KDa protein"
 lamydia pneumoniae
 aagttctatgg 2319
|||||||||||||
|AGTTCTATAG 827217
 tein encoding DNA.
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WO200066739-A2
 3'-truncated
 03-MAY-2000;
 03-MAY-1999;
30-JUN-1999;
 26-MAR-2001
 09-NOV-2000
 Chlamydia
 Synthetic
 AAD02065
 AAD02065;
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 1860
 1021
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 tggagctgtagaaaatgctaaatctaataacagtataagcaacatagattcagctaaagc 1799
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 541 agoggotactgatgaggaaaccgcaatcgctgcggagtgggaaactaagaatgccgatgc
 1440 aattaaagttggcgcaaattacagaattagcgaaatatgcttcggataaccaagcgat
 601 agttaaagttggcgcgcaaattacagaattagcgaaatatgcttcggataaccaagcgat
 tettgactetttaggtaaactgactteettegacetettacagactgetetteteeaate
 tgtagcaaacaataacaaagcagctgagcttcttaaagagatgcaagataacccagtagt
 900 ataataaaaactaaaagatttttattattttttgagtttttatggttaatcctattggtcc
 tctcatgagtctggcagataagctgggtattgcttctagtaacagctcgtcttctactag
 Length 2156;
 C. pneumoniae sequence
humans against diseases
 1;
 Indels
 672 A; 461 C; 471 G; 552 T; 0 other;
 DB 21;
 ;
 57.3%; Score 1459.4;
99.5%; Pred. No. 0;
 0; Mismatches
abnormal chest sounds on auscultation). is also used as vaccines for immunising
 Conservative
 C. pneumoniae.
 Best Local Similarity
Matches 1474; Conser
 BP;
 Sequence 2156
 caused by
 Query Match
 1020
 241
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 1140
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 sinusitis;
tygagotytagaaaatyotaaatotaataacagtataagocaacatagattcagotaaago
 agcaatcgctactgctaagacacaaatagctgaagctcagaaaaagttccccgactctcc
 acctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaaca
 1081 acctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaaca
 tgattctcaagctgcccaacaggagctcgcagcacaagctagagcagcgaaagccgctgg
 agatgacagtgctgctgcagcgctggcagatgctcagaaagctttagaagcggctctagg
 agatgacagtgctgcagcgctggcagatgctcagaaagctttagaagcggctctagg
 76 kDa protein; bactericidal; diagnosis; prevention; premomonia; sinusitis premomonia; upper respiratory tract disease; bronchitis; sinusitis acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; truncation mutant; ds.
 stop
 /product= "3'-truncated Chlamydia pneumoniae 76KDa protein" /note= "The coding region does not include st
 Chlamydia pneumoniae 76 kDa protein encoding
 Location/Qualifiers
101..1456
/*tag= a
 BP
 DNA; 1456
 99US-0132270.
 2000WO-CA00511
 /partial
 pneumoniae.
 standard;
```

us-09-391-606-1.rng

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AAD02064
 AAD02064
 1141
 1261
 2280
 1980
 2100
 1321
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 Gaps
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 agotgacatacaggotgotttggtgagcotocaggatgotgtcactaatataaaggatac
 agctgacatacaggctgctttggtgagcctccaggatgctgtcactaatataaaggatac
 agcggctactgatgaggaaaccgcaatcgctgcggagtgggaaactaagaatgccgatgc
 aattaaagttggcgcgcaaattacagaattagcgaaatatgcttcggataaccaagcgat
 ataataaaaactaaaaagatttttattattatttttgagtttttatggttaatcctattggtcc
 acids encoding a 76 kDa protein from Chlamydia pneumoniae, for vaccinating against Chlamydia infections
 protein is used in the diagnosis, prevention and treatment of C. pneumoniae diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory diseases such as cough, sore throat, harseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
 0;
 Length 1456;
 Indels
 3'-truncated
 Seguence 1456 BP; 452 A; 308 C; 331 G; 365 T; 0 other;
 The present sequence is a DNA coding for 3'-truncat
Chlamydia pneumoniae 76 kDa protein. C. pneumoniae
 21;
 5,
 DB
 0; Mismatches
 Score 1447;
Pred. No. 0;
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Б
 2c; Page 102-104; 112pp; English
 Dunn
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 56.9%;
 Wang
 Best Local Similarity 99.7
Matches 1450; Conservative
 caused by C. pneumoniae.
 (AVET) AVENTIS PASTEUR
 Oomen RP,
 WPI; 2000-687542/67.
P-PSDB; AAY71956.
 Murdin AD,
 Query Match
Best Local S
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 tottgactetttaggtaaactgactteettegacetettacagactgetettetecaate 1559
 tgattctcaagctgcccaacaggagctcgcagcacaagctagagcagcgaaagccgctgg
 tgattctcaagctgcccaacaggagctcgcagcacaagctagagcgaaagccqctgg
 fever;
agttaaagttggcgccaaattacagaattagcgaaatatgcttcggataaccaagcgat
 76 kDa protein; bactericidal; diagnosis; prevention; pneumonia; upper respiratory tract disease; bronchitis; sin acute respiratory disease; cough; sore throat; hoarseness; vaccine; immunisation; treatment; truncation mutant; ds.
 5'-truncated Chlamydia pneumoniae 76 kDa protein encoding
 BP
 standard; DNA; 1852
 tgtgagcgcaggagt 2294
 1441 tgtgagcgcaggagt 1455
 26-MAR-2001
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us-09-391-606-1.rhg

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totcaagctgcccaacaggagctcgcagcacaagctagagcagcgaaagccgctggagat 1020
 gcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaagga 1983
 tocattttgatgtctgggtttcgtcagatgattcacatgttcaatacggaaaatcctgat
 atcgctactgctaagacacaaatagctgaagctcagaaaaagttccccgactctccaatt
 cttcaagaagcggaacaaatggtaatacaggctgagaaagatcttaaaaatatcaaacct
 gacagtgctgctgcagcgctggcagatgctcagaaagctttagaagcggctctaggtaaa
 601 gctgtagaaaatgctaaatctaataacagtataagcaacatagattcagctaaagcagca
 agtagtattggtagtattcgtgttttccatgctgttagatgatgctgaaaatgagaccgct
 getgggcaacaacagggcatactcaatgetttgggacagatcgettetgetgetgttgtg
 tctcaagctgcccaacaggagctcgcagcacaagctagagcagcgaaagccgctggagat
 gacagigetgetgeagegetggcagaigeteegaaaageiitagaaagegetetaggiaaa
 gcaaacaataacaaagcagctgagcttcttaaagagatgcaagataacccagtagtccca
 2284 agogcaggag-tecteegetgeageaagttetatgg
 Chlamydia pneumoniae lorf2 coding sequence.
 Lorf2; vaccine; antibacterial; antigen;
 Location/Qualifiers
 BP
 DNA; 1550
 Chlamydia pneumoniae
 AAA28411 standard;
 29-AUG-2000
 AAA28411;
 1504
 1624
 1684
 1744
 1804
 1864
 1924
 781
 1984
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 1021
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 AAA28411
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 gattataagactcaagcgcaaacagcttacgatactatctttacctcaacatcactagct 1323
 gacatacaggctgctttggtgagcctccaggatgctgtcactaatataaaggatacagcg 1383
 gctactgatgaggaaaccgcaatcgctgcggagtgggaaactaagaatgccgatgcaatt 1443
 aaagttggcgcgcaaattacagaattagcgaaatatgcttcggataaccaagcgattctt 1503
 180
 240
 360
 Gaps
 1 atgagtctggcagataagctgggtattgcttctagtaacagctcgtcttctactagcaga 60
 pneumoniae,
 diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
 DB 21; Length 1852;
 1;
 pneumoniae
 The present sequence is a DNA coding for 5'-truncated Chlamydia pneumoniae 76 kDa protein. C. pneumoniae 76 kDa protein is used in the
 Score 1155.4; DB 21; Lengt
Pred. No. 1.2e-262;
0; Mismatches 6; Indels
 /*tag= a product= "5'-truncated Chlamydia pneumo 76KDa protein" /transl_except= (pos:1489..1491, aa:11e)
V.
 Chlamydia
 Sequence 1852 BP; 578 A; 409 C; 407 G; 458 T; 0 other;
 Nucleic acids encoding a 76 kDa protein from Chlamyć
useful for vaccinating against Chlamydia infections
 Dunn P;
 Claim 2b; Page 97-99; 112pp; English.
 Location/Qualifiers
 Wang J,
 Query Match 45.4%;
Best Local Similarity 99.4%;
Matches 1170; Conservative
 2000WO-CA00511
 99US-0132270.
 (AVET) AVENTIS PASTEUR LTD
 caused by C. pneumoniae
 1..1752
 Murdin AD, Oomen RP,
 Chlamydia pneumoniae.
Synthetic.
 WPI; 2000-687542/67
P-PSDB; AAY71955.
 WO200066739-A2
 03-MAY-2000;
 03-MAY-1999;
30-JUN-1999;
 09-NOV-2000
 1144
 181
 241
 1264
 1324
 1384
 1444
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WO200024901-A1

28-OCT-1998; 20-SEP-1999; 26-OCT-1999;

28-OCT-1999; 04-MAY-2000

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1075 cacagtacgitatgagiaigicgaagcetigicggitecagaaatagaigiticagggai 1134
 1135 tggccgtggtaatttattaaagtttttggttcgcccaagcaattgctgctaactatgatcc 1194
 1255 cacagattctctatcattcagagcttatggggcttactccaaaccagcaaacgataaact 1314
 New DNA encoding Rhesus monkey melanocortin 3 receptor protein, recombinant vectors and host cells, useful in methods for identifying
 ttttttataataaaactaaaagatttttattatttttttgagtttttatggttaatcotat 953
 tggtccaggtcctatagacgaaacagaacgcacacctcccgcagatctttctgctc 1009
 cacagattctctatcattcagagcttatggggcttactccaaaccagcaaacgataaact
 tggccgtggtaatttattaaagttttggttcgcccaagcaattgctgctaactatgatcc
 Rhesus monkey; melanocortin-3 receptor protein; G-protein coupled receptor; GPCR; obesity; ss.
 Rhesus monkey melanocortin-3-receptor cDNA
 /*tag= a
/product= MC-3R protein
 Huang RC;
 Location/Qualifiers
148..1119
 selective agonists and antagonists
 AAA27110 standard; cDNA; 1909 BP.
 Van Der Ploeg LHT,
 99WO-US25747
 98US-0107725
 (first entry)
 (MERI) MERCK & CO INC.
 2000-387404/33.
 P-PSDB; AAY94427
 WO200027862-A1.
 Macaca mulatta
 05-NOV-1999;
 09-NOV-1998;
 04-AUG-2000
 18-MAY-2000
 Fong TM,
 AAA27110;
 894
 594
 AAA27110
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 This sequence encodes lorf2 protein of a strain of chlamydia pneumoniae. Comparison of this sequence as to the recently published genome sequence of C. pneumoniae reveals that the sequence actually contains at least two open reading frames, a first one in the 5' portion and a second one in the 3' portion of the sequence. Despite the presence of the stop codon at the end of this sequence. C. pneumoniae does make a 76 kba product. It appears possible that C. pneumoniae is able to read through this stop codon and produce a full-length product terminated by the stop codon at the end of the second open reading frame. There is at least one in-frame ATG upstream of the start codon. This suggests that the first open reading frame may form part of one or more larger open reading frames. The lorf2 protein or DNA can be used as a vaccine for humans to treat or prevent disease caused by chlamydia infection. The sequences or an antibody to lorf2 can be used to diagnose a chlamydial infection.
 cctagcttggtttattggaggaactttagggggactcagaaaagctggagactggtctgc 533
 agctttcttaatgaaccctttagcaaaggctacgaagactacgttaaatggaaaagaaaa 473
 tacagaaaaagctgctacaaacgctatgaaatacaaatactgtgtttggcagtggctcgt 894
 .tacagaaaaagctgctacaaacgctatgaaatacaaatactgtgtttggcagtggctcgt
 Isolated polynucleotide encoding a Chlamydia polypeptide useful to treat, diagnose and prevent disease caused by Chlamydia infection
 32.7%; Score 832.8; DB 21; Length 1550; 99.8%; Pred. No. 1.2e-186;
 2; Indels
 Sequence 1550 BP; 472 A; 268 C; 317 G; 493 T; 0 other;
 0; Mismatches
 Claim 1; Fig 1A-C; 88pp; English
 99WO-GB03565
 98US-0106037
 99US-0154658
99US-0427501
 (CONN-) CONNAUGHT LAB LTD.
 101..1369
 Best Local Similarity 99.8
Matches 834; Conservative
 /*tag=
 Oomen RP,
 WPI; 2000-350742/30.
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P-PSDB; AAY92716

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MC-3R;

A random primed probe from human melanocortin-3-receptor (MC-3R) was

Claim 1; Fig 1; 54pp; English.

cacagtacgttatgagtatgtcgaagccttgtcagttccagaaatagatgtttcagggat 593

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Synthetic.
 Klein MH,
 AAA71402;
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 gaacaaaaactcatctcagaagaagaatctgaatagcgccgtcgaccatcatcatcat 2406
used to screen a rhesus monkey genomic DNA library. One positive lambda phage clone was identified. From this the rhesus monkey MC-3R sequence was identified. Melanocortin receptors belong to the rhodopsin sub-family of G-protein coupled receptors (GPCR). The MC-3R protein and nucleotide sequence are useful for preparation of recombinant host cells and antibodies. This is useful for
 Gaps
 Immunogenic composition for generating antibodies against respiratory syncytial virus - comprises non-replicating vector containing the protein G sequence, useful in protective vaccines and to raise antibodies for diagnosis
 identifying ligand binding, activators and modulators, agonists and antagonists of MC-3R. Antagonists of MC-3R may have use as novel anti-obesity agents. The present sequence is rhesus monkey melanocortin-3-receptor cDNA.
 G protein; respiratory syncytial virus; RSV; recombinant vector;
vaccine; immune response; immunogenicity; tPA; antibody;
tissue plasminogen activator; ss.
 1;
 The respiratory syncytial virus (RSV) G protein can be used in
 7.0%; Score 179; DB 21; Length 1909; 99.5%; Pred. No. 1.6e-32; 1ve 0; Mismatches 0; Indels 1
 Sequence 1909 BP; 388 A; 581 C; 456 G; 484 T; '0 other;
 Recombinant vector VR-1012 comprising RSV G gene.
 1; Figure 6; 67pp; English.
 AAX08423 standard; cDNA; 4912 BP.
 Sambhara S;
 98WO-CA00697.
 97US-0896442.
 (first entry)
 (CONN-) CONNAUGHT LAB LTD.
 Local Similarity 99.5
mes 190; Conservative
 2527 gccactcccac 2537
 1899 gccactcccac 1909
 WPI; 1999-132254/11
 Klein MH, Li X,
 WO9904010-A1
 16-JUL-1998;
 18-JUL-1997;
 28-JUN-1999
 28-JAN-1999
 Synthetic
 AAX08423;
 Query Match
 Best Loca
Matches
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vectors by inserting the G protein gene into a non-replicating vector. The G protein is placed under the control of alternative vector. The G protein is placed under the control of alternative signal and expression sequences, for example the chimeric G protein produced may also comprise the signal peptide of tissue plasminogen activator (tPA). The recombinant vector may also comprise sequences immunoprotective ability. The resulting immunogenic composition will generate antibodies directed against the RBV G protein when common to a host organism. The composition is useful as a vaccine to immunise against RBV-associated disease, particularly resulting in a balanced ThI/TH2 immune response and for raising Ab, by usual immunisation and cell fusion methods. VR-1012 is a recombinant vector comprising the immediate-early cytomegalovirus and cell by promoter and Intron A sequences of human cytomegalovirus and the bovine growth hormone poly A site. The VR-1012 vector was used as a basis for the creating immunogenic expressing the RSV G protein. Two resulting vectors designated pxL5 have been deposited with the American Type Culture Collection (ATCC 209143 and ATCC 209144 respectively).
 Immunizing a host against diseases caused by respiratory syncytial virus (RSV) infection comprises administering a non-replicating vector \,
 1802 gégecaccagacataatagetgacagactaacagactgttcetttccatgggtetttet 1861
 1742 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcg 1801
 61 gegecaccagacataatagetgacagactaacagaetgtteettteeatgggtetttee 120
 1 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc
 F protein; immunization; vaccine; infection; seronegative; anti-F antibody; viral antigen; cytotoxic T-cell induction; ds.
 ö
 Length 4912;
 121 gcagtcaccgtcgtcgacacgtgtgatcagatatcgcggccgctctagacc 171
 Sequence 4912 BP; 1241 A; 1235 C; 1188 G; 1248 T; 0 other;
 Indels
 Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.8e-30;
Matches 171; Conservative 0; Mismatches 0;
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 ī
 Ewasyshyn ME,
 AAA71402 standard; DNA; 4912 BP
 96US-0659939.
97US-0896500.
 95US-0476397
 99US-0262927
 01-DEC-2000 (first entry)
 CONN-) CONNAUGHT LAB LTD.
 Sambhara S,
 WPI; 2000-464371/40
 Plasmid VR-1012 DNA
 07-JUN-1995;
 05-MAR-1999;
 07-JUN-1996;
18-JUL-1997;
 US6083925-A.
 04-JUL-2000
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12-APR-2000; 2000EP-0302790.

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This invention describes a novel method for immunizing a host against diseases caused by infection with RSV which comprises administering a plasmid vector comprising a nucleotide sequence encoding an RSV F protein generates antibodies and/or cytotoxic cray and a promoter sequence operatively coupled to the nucleotide sequence. The RSV F protein generates antibodies and/or cytotoxic cray in that specifically react with the RSV F protein. The method is useful for administering RSV vaccines to seronegative infants. The method is useful for administering RSV vaccines to seronegative infants. The munogens in diagnostic applications. The RSV F genes and vectors are also useful as immunogens for the generation of anti-F antibodies for use in immunogens (e.g. enzyme linked immunosorbent assay (ELISA), cradioimmunosasy (RLA) or other non-enzyme linked antibody be proven to be poorly immunogenic with regard to the induction of neutralizing cassays). Prior methods of administering RSV vaccines have proven to be poorly immunogenic with regard to the induction of neutralizing cause disease enhancement or immunopotentiation, and have the risk of residual virulence and genetic instability. In the present method, the continody to the virus itself, without loss of potency due to neutralization of virus by the antibodies. The antibody to the virus itself, without loss of potency due to exhibits a native conformation. Therefore, it induces an antibody response similar to that induced by the antigen present in the wild-type virus infection. The expression of proteins from injected plasmid DNA can virus infected by the antigen present in the wild-type wild and the serior of virus is administration of expression of proteins from injected planting virtual entities is a partial and present in the expression of virus infection. The expression of proteins from injected planting virtual entities is a partial and present in the present in the virus infection. The expression of proteins from injected planting virtual and present in the pre
 virus infected cells. This is advantageous since it prolongs cytotoxic T-cell induction and enhances antibody responses. The in vivo expression of antigen may also provide protection without the need for an extrinsic adjuvant. This sequence the encoding DNA sequence of the plasmid VR-1012 which is used in the method of the invention.
nucleotide sequence coding for RSV F protein and a promoter of
 Example 7; Fig 11; 61pp; English
 the sequence
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0;
 Gaps
 0;
Length 4912;
 Indels
 ..
6.7%; Score 171; DB 21;
100.0%; Pred. No. 1.8e-30;
tive 0; Mismatches 0;
 Conservative
 Similarity
 Query Match
Best Local Simil
Matches 171;
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Sequence 4912 BP; 1241 A; 1236 C; 1188 G; 1247 T; 0 other;

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gegecaccagacataatagetgacagactaacagactgtteettteeatgggtetttet 120
1 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgccgcgc 60
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GHRH; growth hormone-releasing hormone; enzyme degradation; ds
AAC86258 standard; DNA; 5108 BP.
 (first entry)
 Plasmid GHRH1-29WTCMV
 28-FEB-2001
 AAC86258;
 RESULT 10
 1862
 AAC86258
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EP1052286-A2

Synthetic.

15-NOV-2000.

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1 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc 60
 New polypeptide variants of growth hormone releasing hormone with enhanced resistance to enzymatic degradation, useful for treating growth hormone deficiency related disorders or to improve growth and
 The present invention relates to growth hormone-releasing hormone (GHRH) variants having enhanced resistance to enzymatic degradation. The variant GHRH polypeptides can be administered to animals to treat growth hormone deficiency related disorders, or to improve growth and/or performance. The variants can be included in pharmaceutical compositions to promote expression and elevation of growth hormone. The variants can be produced recombinantly at much higher levels than prior art variants modified using traditional chemical methods: They have enhanced resistance to enzymatic degradation, therefore have increased length of activity.
 .;
 GHRH; growth hormone-releasing hormone; enzyme degradation; ds.
 Length 5108;
 Sequence 5108 BP; 1279 A; 1312 C; 1231 G; 1286 T; 0 other;
 Indels
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 Score 171; DB 22;
Pred. No. 1.8e-30;
 6.7%; Scur.
100.0%; Pred. No. 1.
... 0; Mismatches
 Examples; Page 39-41; 67pp; English.
 AAC86259 standard; DNA; 5108 BP.
 99US-0128830.
 12-APR-2000; 2000EP-0302790.
 99US-0128830
 (first entry)
 Query Match 6.77
Best Local Similarity 100.
Matches 171; Conservative
 Sheppard MG;
 Sheppard MG;
 (PFIZ) PFIZER PROD INC.
 Plasmid GHRH1-29YWTCMV.
 (PFIZ) PFIZER PROD
 WPI; 2001-026585/04
 12-APR-1999;
 EP1052286-A2.
 12-APR-1999;
 15-NOV-2000.
 28-FEB-2001
 performance
 Morsey MA,
 Synthetic.
 Morsey MA,
 AAC86259;
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 gegecaccagacataatagetgacagactaacagactgtteettteeatgggtetttet 120
 New polypeptide variants of growth hormone releasing hormone with enhanced resistance to enzymatic degradation, useful for treating growth hormone deficiency related disorders or to improve growth and performance -
 polypeptide variants of growth hormone releasing hormone with unced resistance to enzymatic degradation, useful for treating rth hormone deficiency related disorders or to improve growth and
 Gaps
 The present invention relates to growth hormone-releasing hormone (GHRH) variants having enhanced resistance to enzymatic degradation. The variant GHRH polypeptides can be administered to animals to treat growth hormone deficiency related disorders, or to improve growth and/or performance. The variants can be included in pharmaceutical compositions to promote expression and elevation of growth hormone. The variants can be produced recombinantly at much higher levels than prior art variants modified using traditional
 ö
 GHRH; growth hormone-releasing hormone; enzyme degradation; ds
 4843 gcagtcaccgtcgtcgacacgtgtgatcagatatcgcggccgctctagacc 4893
 Length 5108;
 chemical methods. They have enhanced resistance to enzymatic degradation, therefore have increased length of activity.
 Sequence 5108 BP; 1279 A; 1313 C; 1230 G; 1286 T; 0 other;
 Indels
 121 gcagtcaccgtcgtcgacacgtgtgatcagatatcgcggccgtctagacc
 6.7%; Score 171; DB 22;
100.0%; Pred. No. 1.8e-30;
iive 0; Mismatches 0;
 Examples; Page 41-43; 67pp; English.
 promoter ehancer elements.
 AAC86262 standard; DNA; 5111 BP
 99US-0128830.
 12-APR-2000; 2000EP-0302790
 (first entry)
 Query Match 6.7
Best Local Similarity 100.
Matches 171; Conservative
 (PFIZ) PFIZER PROD INC.
 Morsey MA, Sheppard MG;
 WPI; 2001-026585/04
 WPI; 2001-026585/04
 28-FEB-2001
 EP1052286-A2
 12-APR-1999;
 growth hormo
 15-NOV-2000,
 Synthetic.
 AAC86262;
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 RESULT 1
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4723 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc 4782
 gegeceaceagacataatagetgacagactaacagactgtteettteeatgggtetttet 120
 Gaps
 New polypeptide variants of growth hormone releasing hormone with enhanced resistance to enzymatic degradation, useful for treating growth hormone deficiency related disorders or to improve growth and
 1 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc 60
 The present invention relates to growth hormone-releasing hormone (GHRH) variants having enhanced resistance to enzymatic degradation. The variant GHRH polypeptides can be administered to animals to treat growth hormone deficiency related disorders, or to improve
 GHRH) variants having enhanced resistance to enzymatic degradation. The variant GHRH polypeptides can be administered to animals to treat growth hormone deficiency related disorders, or to improve prowth and/or performance. The variants can be included in pharmaceutical compositions to promote expression and elevation of growth hormone. The variants can be produced recombinantly at much higher levels than prior art variants modified using traditional chemical methods. They have enhanced resistance to enzymatic
 to growth hormone-releasing hormone
 ds.
 ;
0
 Length 5111;
 GHRH; growth hormone-releasing hormone; enzyme degradation;
 Sequence 5111 BP; 1280 A; 1314 C; 1230 G; 1287 T; 0 other;
 Indels
 degradation, therefore have increased length of activity
 6.7%; Score 171; DB 22;
100.0%; Pred. No. 1.8e-30;
tive 0; Mismatches 0;
Examples; Page 47-49; 67pp; English.
 Examples; Page 32-34; 67pp; English.
 ВР
 The present invention relates
 AAC86254 standard; DNA; 5185
 12-APR-2000; 2000EP-0302790.
 99US-0128830
 Query Match
Best Local Similarity 100.(
Matches 171; Conservative
 Sheppard MG;
 (PFIZ) PFIZER PROD INC
 WPI; 2001-026585/04
 pGHRH-4 construct.
 12-APR-1999;
 EP1052286-A2.
 28-FEB-2001
 15-NOV-2000
 performance
 Morsey MA,
 Synthetic
 AAC86254;
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Length 5188; Indels DB 22; 1.8e-30; ö Matches 171; Conservative Query Match Best Local Similarity

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Gaps

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1 ttgcggtgctgttaacggtggagggaggtgtagtctgagcagtactcgttgctgccgcgc

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Query Match Best Local S

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121 gcagtcaccgtcgtcgacacgtgtgatcagatatcgcggccgctctagacc 171 Qγ

4843 gcagtcaccgtcgtcgacacgtgtgatcagatatcgcggccgctctagacc 4893

GHRH; growth hormone-releasing hormone; enzyme degradation; ds.

12-APR-2000; 2000EP-0302790.

GHRH; growth hormone-releasing hormone; enzyme degradation; ds.

28-FEB-2001

AAC86266;

RESULT 14 AAC86266 ID AAC8 12-APR-2000; 2000EP-0302790

EP1052286-A2

Synthetic.

15-NOV-2000.

99US-0128830

12-APR-1999;

(PFIZ ) PFIZER PROD INC.

Sheppard MG;

Morsey MA,

WPI; 2001-026585/04.

99US-0128830. 12-APR-1999;

(PFIZ ) PFIZER PROD INC

Sheppard MG; Morsey MA,

WPI; 2001-026585/04.

New polypeptide variants of growth hormone releasing hormone with enhanced resistance to enzymatic degradation, useful for treating growth hormone deficiency related disorders or to improve growth and performance

Examples; Page 56-58; 67pp; English.

New polypeptide variants of growth hormone releasing hormone with enhanced resistance to enzymatic degradation, useful for treating growth hormone deficiency related disorders or to improve growth and

Examples; Page 54-56; 67pp; English.

performance

The present invention relates to growth hormone-releasing hormone (GHRH) variants having enhanced resistance to enzymatic degradation. The variant GHRH polypeptides can be administered to animals to treat growth hormone deficiency related disorders, or to improve growth and/or performance. The variants can be included in pharmaceutical compositions to promote expression and elevation of growth hormone. The variants can be produced recombinantly at much higher levels than prior art variants modified using traditional chemical methods. They have enhanced resistance to enzymatic degradation, therefore have increased length of activity.

The present invention relates to growth hormone-releasing hormone (GHRH) variants having enhanced resistance to enzymatic degradation. The variant GHRH polypeptides can be administered to animals to treat growth hormone deficiency related disorders, or to improve growth and/or performance. The variants can be included in pharmaceutical compositions to promote expression and elevation of growth hormone. The variants can be produced recombinantly at much higher levels than prior art variants modified using traditional chemical methods. They have enhanced resistance to enzymatic degradation, therefore have increased length of activity.

Sequence 5254 BP; 1318 A; 1334 C; 1285 G; 1317 T; 0 other

; Length 5254; Indels 6.7%; Score 171; DB 22; 100.0%; Pred. No. 1.8e-30; ive 0; Mismatches 0; Query Match 6.7 Best Local Similarity 100. Matches 171; Conservative

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Gaps

4723 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcg 4782 AAC86267 standard; DNA; 5254 BP Plasmid pGHRH1-44WTGHpep 28-FEB-2001 EP1052286-A2 15-NOV-2000. Synthetic. AAC86267; 15 AAC86267 RESULT a qq ; 0 4842 61 gegecaccagacataatagétgacagactaacagactgttectttecatgggtetttet 120 Gaps growth and/or performance. The variants can be included in pharmaceutical compositions to promote expression and elevation of growth hormone. The variants can be produced recombinantly at much higher levels than prior art variants modified using traditional chemical methods. They have enhanced resistance to enzymatic degradation, therefore have increased length of activity. 4783 gegecaceagacataatagetgacagactaacagactgtteettteeatgggtettttet ;0 Length 5185; 121 gcagtcaccgtcgtcgacacgtgtgatcagatatcgcggccgctctagacc 171 Sequence 5185 BP; 1302 A; 1326 C; 1260 G; 1297 T; 0 other Indels ; Score 171; DB 22; Pred. No. 1.8e-30; 6.7%; Scor. 100.0%; Pred. No. 1... ... 0; Mismatches AAC86266 standard; DNA; 5188 BP. (first entry) Matches 171; Conservative Plasmid GHRH1-44YWTCMV Local Similarity

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| . ***                                  | a erang na kabangangan na manan na manang gaban ang manahari sa panahar manan sa sa kalang a manahari sa kalan                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |   |
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Sequence 5, A Sequence 19, Sequence 33, A Sequence 3, A Sequence 1, A Sequence 1, A Appli Appli Appli Appli Appli Appli

Sequence 1, Al Sequence 1, Al Sequence 3, Al Sequence 1, Al Sequence 5, Al Sequence 5, Al Sequence 15, Al

Sequence 17, Sequence 19, Sequence 1, 1

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APPLICANT: Hobart, Peter
APPLICANT: Parker, Suzanne
APPLICANT: Marqalith, Michal
APPLICANT: Khatibi, Shirin
APPLICANT: RNATIbi, Shirin
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
 US-08-627-151A-5
US-08-801-092-5
US-08-801-092-39
US-08-343-401A-3
US-08-990-442-1
US-08-64-313-1
US-08-64-313-1
US-08-64-6669-1
US-08-67-38-6-3
 US-08-893-327-15
 US-08-893-327-19
US-08-470-299-1
 US-08-893-327-17
 US-08-646-538-5
 US-09-503-222-5
 us-08-235-277-1
 ALIGNMENTS
 CLASSIFICATION 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Ways Venisko, Namcy
RECISTRATION NUMBER: 36,298
RECISTRATION NUMBER: VICAL.043A
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFROME: 619-235-8550
TELEFRAX: 619-235-8550
 COMUTER READABLE FORM:

| MEDIUM TYPE: Diskette
| COMPUTER: IBM Compatible
| OPERATING SYSTEM: DOS
| SOFTWARE: FastSEQ Version 1.5
| CURRENT APPLICATION DATA:
| APPLICATION NUMBER: US/08/345,913
| FILING DATE:
 Sequence 1, Application US/08345913
Patent No. 5641665
GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
LENGTH: 4928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
m7000000000000000
 USA
 ANTI-SENSE: NO
 FRAGMENT TYPE:
ORIGINAL SOURCE:
 92660
 CA
 COUNTRY:
 US-08:-345-913-1
 STATE:
 FEATURE
 (without alignments)
2367.188 Million cell updates/sec
 7, Appli
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 3, App
Sequence 4, App
Sequence 1, App
Sequence 57, App
Sequence 57, App
Sequence 57, App
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2545
1 ttgcggtgctgttaacggtg......tgccactcccactgtcctt 2545
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 170,
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 Description
 Sequence 1
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 Sequence 2
Sequence 4
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 Sequence 1
Sequence 1
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Sequence 7
Sequence 6
Sequence 7
 Sequence 1
 Seguence
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... /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
... /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
... /cgn2_6/ptodata/2/ina/Ba_COMB.seq:*
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... /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
... /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 US-08-659-473-8
US-08-0713-8
US-08-131-146-13
US-08-132-808-13
US-08-101-647-2
US-08-910-647-4
US-08-910-647-1
US-08-663-998-3
US-08-663-998-3
US-08-663-998-1
US-08-663-998-1
US-08-663-998-1
US-08-663-998-1
US-08-663-998-1
US-08-653-998-1
US-08-653-998-1
US-08-683-998-1
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US-08-999-575-156
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US-08-899-575-156
 US-09-158-863C-64
US-08-450-945-70
 Potal number of hits satisfying chosen parameters:
 351203 segs, 113238999 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 nucleic search, using sw model
 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 DB
 3125
4328
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4328
5107
9600
5676
5582
2057
2057
13254
 Query
Match Length
 13254
 13254
13254
13254
 142
139.8
139.8
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138.2
138.2
138.2
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138.2
138.2
137.8
137.8
137.8
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137.8
 Title:
Perfect score:
 Score
 Scoring table:
 OM nucleic
 Seguence:
 Searched:
 Database
 Run on:
 Result
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 1500 gitgetgitaaeggitgaagggeagtgitagietgageagtaetegtigetgeegegegege 1559
 65 caccagacataatagctgacagactaacagactgttcctttccatgggtctttctgcag 124
 Gaps
 0;
 Length 4928;
 Length 4928;
 Sequence 1, Application US/08818562
; Betent No. 6147055
; GENERAL INFORMATION:
 APPLICANT: Hobart, Peter M.
 APPLICANT: Margalith, Michal
 APPLICANT: Parker, Suezanne E.
 APPLICANT: Rattbi, Shirin
 TILE OF INVENTION: Plasmids Suitable for IL-2 Expression
 TILE OF INVENTION: Plasmids Suitable for IL-2 Expression
 TILE REFERENCE: 1530.0080001
 CURRENT APPLICATION NUMBER: US/08/818,562
 CURRENT FILING DATE: 1997-03-14
 BARLIER FILING DATE: 1994-11-28
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NOS: 3
 SEQ ID NOS: 3
 SEQ ID NOS: 3
 SEQ ID NOS: 3
 Indels
 Indels
 1620 TCACCGTCGTCGACACGTGTGATCTAGCCTCAACCT 1661
 125 tcaccgtcgtcgacacgtgtgatcagatatcgcggccgctct 166
 Score 149.2; DB 3;
Pred. No. 1.7e-30;
0; Mismatches 8;
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60
 Score 149.2; DB 1;
Pred. No. 1.7e-30;
 0; Mismatches
 Sequence 8, Application US/08659473
Patent No. 6210876
GENERAL INFORMATION:
APPLICANT: M. B. Cerney
 Query Match 5.9%;
Best Local Similarity 95.1%;
Matches 154; Conservative (
 Coding Sequence
1689...2159
 Query Match
Best Local Similarity 95.1%;
Matches 154; Conservative
 ; NAME/KEY: CDS
; LOCATION: (1689)..(2159)
US-08-818-562-1
 TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: Coding LOCATION: 1689... OTHER INFORMATION:
 LENGTH: 4928
 US-08-659-473-8
 RESULT 2
US-08-818-562-1
 US-08-345-913-1
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1305 tacctcaacatcactagctgacatacaggctgctttggtgagcctccaggatgctgtcac 1364
 APPLICANT: Hasel, Karl W.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: HIV-1 VACCINES, ANTIBODY COMPOSITIONS RELATED
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
OURBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
 Ċ.
 Length 150;
 Indels
 NUCLEIC ACID SEQUENCES FOR DETECTING
 DB 4;
 Score 146.8; DB 4;
Pred. No. 1.2e-30;
0; Mismatches 2;
 ; MOLECULE TYPE: genomic DNA (C. pneumoniae) US-08-659-473-8
 1425 taagaatgccgatgcaattaaagttggcgc 1454
 121 TAAGAATGCCGATGCAGTTAAAGTTGGCGC 150
 SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,473
FILING DATE:
TITLE OF INVENTION: NUCLEIC ACID & NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: ADDOLT LABORATORIES STREET: 100 Abbott Park Road CITY: Abbott Park STATE: 11linois COUNTRY: USA
 Sequence 13, Application US/08037816A, Patent No. 5869624 GENERAL INFORMATION:
 ADDRESSEE: Cooper & Dunham STRRET: 30 Rockefeller Plaza CITY: New York STATE: New York
 ATTORNEY/AGENY INFORMATION:
NAME: Paul D. Yasger
REGISTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: 708/937-2341
 Ouery Match 5.8%;
Best Local Similarity 98.7%;
Matches 148; Conservative
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System
 LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 TELEFAX: 708/938-2623
TELEX:
 ZIP: 60064-3500
COMPUTER READABLE FORM:
 linear
 USA
 STRANDEDNESS:
 US-08-037-816A-13
 TELEPHONE:
 COUNTRY:
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Sequence 1, Application US/09132808
Patent No. [6197332
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ronald Zuckermann et al.
TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related TITLE OF INVENTION: Compositions and Methods Thereof NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
 ö
 Length 3125;
 Indels
 1534 GCAGTCACCGTCCTTGACACGATGCAATGAAGAGAGGGCTCT 1579
 121 gcagtcaccgtcgtcgacacgtgtgatcagatatcgcggccgctct 166
 SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US/09/132,808
 Score 142; DB 2; L
Pred. No. 1.2e-28;
0; Mismatches 15;
 APPLICATION NUMBER: US/08/037,816
FILING DATE: 26-MAR-1993
ATTONEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41190/JPW/AJM
TELEPHONE: (212) 977-9550
TELEPAX: (212) 664-0525
TELEPAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 13:
(SEQUENCE CHARACTERISTICS:
LENGTH: 3125 base pairs
 REFERENCE/DOCKET NUMBER: 1387.002
TELECOMNUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 Chiron Corporation
 38,459
 4560 Horton Street
 MOLECULE TYPE: DNA (genomic)
 Query Match 5.6%;
Best Local Similarity 91.0%;
Matches 151; Conservative
 ATTORNEY / AGENT INFORMATION:
 Floppy disk
 NAME: Fujita, Sharon M
REGISTRATION NUMBER: 38
 TYPE: nucleic acid
STRANDEDNESS: single
 NAME/KEY: CDS
LOCATION: 1555..3115
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 CITY: Emeryville
STATE: California
 OTHER INFORMATION:
US-08:530-146-13
 linear
 COUNTRY: U.S.A. ZIP: 94608-2916
 CLASSIFICATION:
 ADDRESSEE:
 JS-09-132-809-1
 STREET:
 ö
 61 gcgccaccagacataatagctgacagactaacagactgttcctttccatgggtcttttct 120
 APPLICANT: Hasel, Karl W.
APPLICANT: Hasel, Karl W.
APPLICANT: Hasel, Paul J.
TITLE OF INVENTION: HIV-1 VACCINES, ANTIBODY COMPOSITIONS RELATED
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
 ö
 Length 3125;
 15; Indels
 Score 142; DB 2;
Pred. No. 1.2e-28;
0; Mismatches 15;
 APPLICATION NUMBER: US/08/037,816A
FILING DATE: 26-WAR-1993
CLASSIFICATION: 435
ATLORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41190/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 664-0525
TELEFAX: (212) 664-0525
TELEFAX: (212) 664-0525
TELEFAX: 422523 COOPUI
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3125 base pairs
TYPE: nucleic acid
STANDEDNESS: single
 APPLICATION NUMBER: US/08/530,146
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.24
CURRENT APPLICATION DATA:
 Sequence 13, Application US/08530146
Patent No. 5886163
GENERAL INFORMATION:
 E: Cooper & Dunham
30 Rockefeller Plaza
 MOLECULE TYPE: DNA (genomic)
 Query Match 5.6%;
Best Local Similarity 91.0%;
Matches 151; Conservative
 Floppy disk
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 NAME/KEY: CDS
LOCATION: 1555..3115
OTHER INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 linear
 New York
 New York
 FILING DATE:
CLASSIFICATION:
 USA
 COUNTRY: U
 ADDRESSEE:
 US-08-037-816A-13
 RESULT 5
US-08-530-146-13
 STREET:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 FILING DATE:
CLASSIFICATION: 514
 CITY: Emeryville STATE: California COUNTRY: U.S.A. ZIP: 94608-2916
 OPERATING SYSTEM:
 linear
 GENERAL INFORMATION:
 STRANDEDNESS:
 TOPOLOGY:
 SOFTWARE:
 CENGTH:
 US-08-910-647-4
 121
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 1511 TTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGC 1570
 gegecaccagacataatagetgacagactaacagactgtteettteeatgggtettttet 120
 Gaps
 1 ttgcggtgctgttaacggtggaggcagtgtagtctgagcagtactcgttgctgccgcgc 60
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 ó
 Length 4328;
 Length 4328;
 Indels
 Indels
 Score 139.8; DB 4;
Pred. No. 5.6e-28;
0; Mismatches 7;
 GENERAL INFORMATION:
APPLICAMT: Zuckermann et al.
APPLICAMT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
 OFFINARE: PATENTIN SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT PAPLICATION DATA:
 Query Match 5.5%; Score 139.8; DB 4; Best Local Similarity 95.4%; Pred. No. 5.6e-28; Matches 144; Conservative 0; Mismatches 7;
 1631 GCAGTCACCGTCGTCGACCTAAGAATTCAGA 1661
 121 gcagtcaccgtcgtcgacacgtgtgatcaga 151
 REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
 APPLICATION NUMBER: US/08/910,647 FILING DATE:
 US-08-910-647-2; Sequence 2, Application US/08910647; Patent No. 6251433
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
 ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER:: 38,459
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4328 base pairs
TYPE: nucleic acid
STRANDEDIOSS: single
TOPOLOGO
 MOLECULE TYPE: DNA (genomic)
 Query Match
Best Local Similarity 95.4%;
Matches 144; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-132-808-1
 TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
 LENGTH: 4328 base pairs
 nucleic acid
EDNESS: single
 CLASSIFICATION: 514
 CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
 linear
 N: U.S.A. 94608-2916
 STRANDEDNESS:
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gegecaccagacataatagetgacagactaacagaetgtteettteeatgggtettttet 120
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 Query Match 5.5%; Score 139.8; DB 4; Best Local Similarity 95.4%; Pred. No. 6e-28; Matches 144; Conservative 0; Mismatches 7;
 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
 APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Polynucleotide Delivery
 1634 GCAGTCACCGTCGTCGACCTAAGAATTCAGA 1664
 gcagtcaccgtcgtcgacacgtgtgatcaga 151
 121 gcagtcaccgtcgtcgacacgtgtgatcaga 151
 1218.002
 US/08/910,647
 Sequence 4, Application US/08910647
Patent No. 6251433
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 NAME: Fujita, Sharon M. REGISTRATION NUMBER: 38,459
 REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
 ; MOLECULE TYPE: DNA (genomic) US-08-910-647-4
 ADDRESSEE: Chiron Corporat
STREET: 4560 Horton Street
 TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
 4818 base pairs
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 nucleic acid
EDNESS: single
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6676 GCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTTT 6735
 61 geyccaccagacataatagetgacagactaacagactgtteettteeatgggtetttee 120
 1 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc 60
 ö
 DB 4; Length 9600;
 Indels
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ADMINISTERING BORRELIA DNA NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 Query Match 5.5%; Score 139.8; DB 4
Best Local Similarity 95.4%; Pred. No. 8.6e-28;
Matches 144; Conservative 0; Mismatches 7
 SEE: Curtis, Morris & Safford, P.C.: 530 Fifth Avenue
New York
 6736 GCAGTCACCGTCGTCGACCTAAGAATTCAGA 6766
 121 gcagtcaccgtcgtcgacacgtgtgatcaga 151
 REFERENCE/DOCKET NUMBER: 1218.002
TELECOMONUTACATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARATERISTICS:
LENGTH: 9600 base pairs
 APPLICATION NUMBER: US/08/663,998
 US/08/910,647
 COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy disk | COMPUTER: IBM PC compatible | OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 3, Application US/08663998
Patent No. 5846946
GENERAL INFORMATION:
 APPLICANT: HUEBNER, Robert C.
APPLICANT: NORMAN, Jon A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.
 NAME: Fujita, Sharon M. REGISTRATION NUMBER: 38,459
 MOLECULE TYPE: DNA (genomic)
 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
 APPLICATION NUMBER:
 nucleic acid
 linear
 CLASSIFICATION:
 STRANDEDNESS:
 MEDIUM TYPE:
 FILING DATE:
 10036
 ADDRESSEE:
 STATE: N
COUNTRY:
 JS-08-663-998-3
 STREET:
 US-08-910-647-1
 CITY:
 RESULT
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 1514 TTGCGGTGCTGTTAACGGTGGAGGCCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGGC 1573
 1 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc 60
 5.5%; Score 139.8; DB 4; Length 5107; 95.4%; Pred. No. 6.1e-28; 1ve 0; Mismatches 7; Indels 0;
 .8;
6.1e-28;
7;
 RESULT 10
US-08-910-647-1
; Sequence 1, Application US/08910647
; Patent No. 6251433
; GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Polynucleotide Delivery
 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/910,647
Sequence 3, Application US/08910647
Patent No. 6551433
GENERAL INFORMATION:
APPLICANT: ZUCKERmann et al.
TITLE OF INVENTION: Compositions and Methods for
 1634 GCAGTCACCGTCGACCTAAGAATTCAGA 1664
 121 gcagtcaccgtcgacacgtgtgatcaga 151
 ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
 ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
 E: Chiron Corporation 4560 Horton Street
 4560 Horton Street
 MOLECULE TYPE: DNA (genomic)
 TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 LENGTH: 5107 base pairs
TYPE: nucleic acid
 Query Match 5.5
Best Local Similarity 95.4
Matches 144; Conservative
 single.
 NUMBER OF SEQUENCES: 4
 Abu...
STREET: 450v ...
CITY: Emeryville
 CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
 linear
 CLASSIFICATION:
 STRANDEDNESS:
 FILING DATE
 ADDRESSEE:
 US-08-910-647-3
 STREET:
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 1 ttgcggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc 60
 Length 5900;
 Length 5682;
 Indels
 APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: BARBOUR, Alan G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ADMINISTERING BORRELIA DNA NUMBER OP SEQUENCES: 4
CORRESPONDEDE ADDRESS: ADDRESSE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
 Score 138.2; DB 2;
Pred. No. 1.8e-27;
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 DB 2;
 Score 138.2; DB 2 Pred. No. 1.8e-27;
 0; Mismatches
 ATTORNEY AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERNCE/DOCKET NUMBER: 454312-2440
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 1:
 APPLICATION NUMBER: US/08/663,998
FILING DATE: 06-JUN-1996
CLASSIFICATION: 424
 1669 GCAGTCACCGTCGTCGACCAGAG 1691
 121 gcagtcaccgtcgtcgacacgtg 143
 US-08-663-998-1; Sequence 1, Application US/08663998; Patent No. 5846946
 GENERAL INFORMATION:
APPLICANT: HUEBNER, ROBER C.
APPLICANT: NORMAN, Jon A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUK, Alan G.
APPLICANT: LUKE, Catherine J.
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 5.4%;
 DNA (genomic)
 5.4%;
LENGTH: 5682 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 SEQUENCE CHARACTERISTICS:
 Matches 140; Conservative
 TYPE: nucleic acid
STRANDEDNESS: single
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 linear
 Query Match
Best Local Similarity
 linear
 Query Match
Best Local Similarity
 FILING DATE: 00 CLASSIFICATION:
 New York
 MOLECULE TYPE:
 ; MOLECULE TYPE:
US-08-663-998-4
 10036
 TOPOLOGY:
 COUNTRY:
 LENGTH:
 US-08-663-998-1
 STATE:
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0
 1609 GCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCT 1668
 61 gegecaccagacataatagetgacagactaacagactgtteettteeatgggtettttet 120
 Gaps
 1 ttgoggtgctgttaacggtggagggcagtgtagtctgagcagtactcgttgctgccgcgc 60
 DB 2; Length 5676;
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 APPLICANT: LUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: ADMINISTERING BORRELIA DNA
 5.4%; Score 138.2; DB 2;
nllarity 97.9%; Pred. No. 1.8e-27;
Conservative 0; Mismatches 3;
 E: Curtis, Morris & Safford, P.C.
530 Fifth Avenue
 ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REGISTRATION NUMBER: 35,147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
 454312-2440
 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/663,998
FILING DATE: 06-JUN-1996
CLASSIFICATION: 424
 1669 GCAGTCACCGTCGTCGACCAGAG 1691
 Sequence 4, Application US/08663998
Patent No. 5846946
GENEZL INFORMATION:
APPLICANT: HUEBNER, Robert C.
 121 gcagtcaccgtcgtcgacacgtg 143
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFRENCE/DOCKET NUMBER: 4543:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 3:
 APPLICANT: NORMAN, JON A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE, Catherine J.
 , MOLECULE TYPE: DNA (genomic) US-08-663-998-3
 06-JUN-1996
 SEQUENCE CHARACTERISTICS:
LENGTH: 5676 base pairs
 nucleic acid
EDNESS: single
 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 linear
 Query Match
Best Local Similarity
Matches 140; Conserv
 New York
 USA
 STRANDEDNESS:
 10036
 ADDRESSEE:
 COUNTRY:
 US-08-663-998-4
 STREET:
 STATE:
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õ qq 1672 GCAGTCACCGTCGTCGACCAGAG 1694

121 gcagtcaccgtcgtcgacacgtg 143

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Gaps

3; Indels

Mismatches

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Matches 140; Conservative

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1632 TTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGC 1573
 61 gegeceaccagacataatagetgacagactaacagaetgtteetttecatgggtetttet 120
 1 ttgcggtgctgttaacggtggaggcagtgtagtctgagcagtactcgttgctgccgcgc
 ö
 region of AD169 strain HCMV (antisense) containing antisense transcript ORFs
 Length 2057;
 Indels
 AND PROMOTERS
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 Score 138; DB 1; L. Pred. No. 1.2e-27; 0; Mismatches 5;
 3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
 Search completed: February 7, 2002, 15:53:24 Job time: 318 sec
 APPLICANT: Kondo, Kazuhiro
APPLICANT: Mocarski, Edward S. Jr.
11TLE OF INVENTION: LATENT TRANSCRIPTS
11TLE OF INVENTION: OF CYTOMEGALOVIRUS
 NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERNCE/DOCKET NUMBER: 8600-0157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
 APPLICATION NUMBER: US/08/450,945 FILING DATE: 23-MAY-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
 121 gcagtcaccgtcgtcgacacgtgtga 146
 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 57, Application US/08450945
Patent No. 5783383
GENERAL INFORMATION:
 CDNA to mRNA
 Query Match
Best Local Similarity 96.6%;
Matches 141; Conservative
 Floppy disk
 2057 base pairs
 double
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger
 COMPUTER READABLE FORM:
 ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-450-945-57
 nucleic acid
 NUMBER OF SEQUENCES:
 unknown
 STREET: 350 CITY: Palo Alto
 USA
 ÖRIGINAL SOURCE
 MOLECULE TYPE:
 STRANDEDNESS
 MEDIUM TYPE:
 JS-08 450-945-57/C
 94306
 COUNTRY:
 qq
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 δλ
 ö
1613 GCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTTT 1672
 61 gegecaccagacataatagetgacagactaacagactgtteettteeatgggtetttet 120
 Length 5952;
 Indels
 ...crilCant: LUKE, Catherine J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ADMINISTERING BORRELIA DNA NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Curtis, Morris & Safford, P.C. STREET: 830 Fifth Avenue CITY: New York STATE: NY
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,998
FILING DATE: O6-JUN-1996
 DB 2;
 Pred. No. 1.8e-27;
0; Mismatches 3;
 5.4%; Score 138.2;
illarity 97.9%; Pred. No. 1.8
Conservative 0; Mismatches
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2440
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 1673 GCAGTCACCGTCGTCGACCAGAG 1695
 Sequence 2, Application US/08663998
; Patent No. 5846946
GENERAL INFORMATION:
APPLICANT: HUEBNER RObert C.
 121 gcagtcaccgtcgtcgacacgtg 143
 APPLICANT: NORMAN, JON A.
APPLICANT: LIANG, Xiaowu
APPLICANT: CARNER, Kristin R.
APPLICANT: BARBOUR, Alan G.
APPLICANT: LUKE COSTE
 DNA (genomic)
 Floppy disk
 LENGTH: 5952 base pairs
 single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 nucleic acid
 Query Match
Best Local Similarity
Matches 140; Conserva
 linear
 STRANDEDNESS:
 ; MOLECULE TYPE:
US-08-663-998-2
 10036
 TOPOLOGY:
 RESULT 14
US-08-663-998-2
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Gaps

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Drosophil BMBAC01K0

Drosophil

Drosophil Tetraodon

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Drosophil Drosoph11 Drosophil Drosoph11 Drosoph11

ENTKS53TF

Tetraodon

Drosophil Drosophil Drosophil Drosophil

Scoring table:

Searched:

Sequence:

Database :

Result

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Run MO

Drosophil Drosophil

Drosophil Drosophil Tetraodon

nbeb0074A letraodon

retraodon Drosophil

us-09-391 4606-1.rst

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
 1 (bases 1 to 149)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 AL077798
AL078819
AL106619
AL267272
AL106180
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BH001815
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113173 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.
AW669676
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 AZ670257
CNS003B0
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 BH001815
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 CNS016DT
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 FORWARD: AGGAAACAGCTATGACCAT
 and -minmatch 12 options.
PCR PRimers
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668
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1131
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905
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 BACKWARD: G
Plate: 107
 Bos taurus
21180013
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 EST
 99999999
 48
 RESULT 1
AW669676
LOCUS
DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 JOURNAL
 REFERENCE
AUTHORS
 TITLE
 COMMENT
 Search time 7419.31 Seconds (without alignments) 3686.058 Million cell updates/sec
 AW669676 113173 MA
AW689522 112928 MA
AW785233 116166 MA
AW785901 117399 MA
AW689518 112921 MA
BKG74689 222166 MA
AW669633 113104 MA
BG355021 100689 MA
AL066953 Drosophil
AL066953 Drosophil
AL066953 Drosophil
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 ttgcggtgctgttaacggtg.......1gccactcccactgtccttt 2545
 Description
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 11351937 seqs, 5372889281 residues
 Total number of hits satisfying chosen parameters:
 •-
 SUMMARIES
 7, 2002, 15:48:06
 AW669518
BF074689
AW669634
AW669633
BG365021
CNS007BE
CNS0039G
 summaries
 AW669522
AW785253
AW785901
 - nucleic search, using sw model
 AW669676
 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 sv
 G
 em_gss_other:*
 gb_gss:*
em_gss_fun:*
em_gss_hum:*
 em_gss_pln:*
em_gss_pro:*
em_gss_rod:*
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Maximum DB seq length: 200000000
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 US-09-391-606-1
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em_esthum:*
 gb_est1:*
gb_est2:*
 em_estin:*
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em_estpl:*
em_estba:*
em_estro:*
em_estro:*
 gb_htc:*
 Length
 1001
1101
996
 February
 EST:*
 Query
 Score
 87
87
87
87
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87
84.4
84.4
61.2
60
 Title:
Perfect score:
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Length 162;

hypothalamus, and pituitary." 51 c 42 q 41 t

```
1 Similarity 100.
87; Conservative
fat,
 PCR PRimers
 AW785253.1
 Sus scrofa
 ๙
 28
 EST.
 Query Match
Best Local 9
 BASE COUNT
ORIGIN
 ORGANISM
 BASE COUNT
ORIGIN
 DEFINITION
 AUTHORS
 JOURNAL
 Matches
 ACCESSION
 REFERENCE
 RESULT
AW785253
 KEYWORDS
 FEATURES
 TITLE
 VERSION
 COMMENT
 SOURCE
 Ω
 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
V0.980904.e. Vector identified by cross_match with the .minscore 18
and -minmatch 12 options.
PCR PRimers
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.

1 (bases 1 to 162)

Sanith, T. P. L., Grosse, W. M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W. W., Rohrer, G.A., Chitko-McKown, C.G., Keele, J.W.
 ;
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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/lab_host="bH10B"
/note="Vector: pGW SPORT6; Site_1: XDaI; Site_2: XhOI;
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Library made from pooled tissue from lymph node, ovary,
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/note="vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI;
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fat, hypothalamus, and pituitary."
 Gaps
 25-APR-2001
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 AW669522 162 bp mRNA EST 2
112928 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW669522
 Contact: Smith TPL USDA, ARS, US Meat Animal Research Center USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 48390
 /organism="Bos taurus"
/db_xref="taxon:9913"
 /clone_lib="MARC 1BOV"
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
 Plate: 106 row: K column: 23
Seq primer: ATTTAGGTGACACTATAG.
 Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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 96 TGGAAGGTGCCACTCCCACTGTCTTT 122
 FORWARD: AGGAAACAGCTATGACCAT
 BACKWARD: GITTTCCCAGICACGACG
 Location/Qualifiers
 AW669522.1 GI:7526036
 87; Conservative
 ๙
 21180013
 24
 DEFINITION
ACCESSION
VERSION
 ORGANISM
 BASE COUNT
ORIGIN
 REFERENCE
 AUTHORS
 JOURNAL
 MEDLINE
 KEYWORDS
SOURCE
 AW669522
 FEATURES
 FEATURES
 TITLE
 COMMENT
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Single pass sequencing. Bases called and alt_trimmed with phred vo.980904.e. Vector identified by cross_match with the minscore 18 and -minmatch 12 options.
 ó
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 Casas, E.,
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Abases 1 to 162)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.P. Design and use of two pooled tissue normalized cDNA libraries for Err discovery in swine
Unpublished (2000)
Contact: Smith TPL
 /note="Vector: pCMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embross."
 0; Gaps
 Gaps
 09-JUL-2000
 ö
 Length 162;
 AW785253 162 bp mRNA EST 0:
116166 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW785253
 Indels
 0; Indels
 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
 ö
 Query Match
3.4%; Score 87; DB 10; Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 87; Conservative 0; Mismatches 0;
Score 87; DB 10; 1; Pred. No. 1.3e-07; 0; Mismatches 0;
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 /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
 FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 34 row. K column: 23
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
 2519 tggaaggtgccactcccactgtccttt 2545
 /tissue_type="pooled"
/lab_host="DH10B"
 42 g
 and 30 embryos.
 3.4%; £
100.0%;
 GI:7842029
 1. .162
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```
Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
 BF074689.1
 taurus
 Keele, J.W.
 21180013
 26
 Bos
 EST
 KEYWORDS
SOURCE
ORGANISM
 source
 BASE COUNT
ORIGIN
 ø
 DEFINITION
 ACCESSION
VERSION
 REFERENCE
 AUTHORS
 MEDLINE
 REFERENCE
 AUTHORS
 JOURNAL
 RESULT
BF074689
 FEATURES
 TITLE
 COMMENT
 TITLE
 LOCUS
 Single pass sequencing. Bases called and alt_trimmed with phred v0.880904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 .
0
 Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
 cow.
Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
 /note="Vector: __CMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
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 Gaps
 09-JUL-2000
 25-APR-2001
 ;
0
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammanla; Eutheria; Cetartiodactyla; Suina; Suidae; Mammanla; Eutheria; Cetartiodactyla; Suina; Suidae; Fahrenkrug; S.C., Freking; B.A., Rohrer, G.A., Smith, T.
 Length 162;
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117399 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW785901
 AW669518 243 bp mRNA EST 2
112921 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW669518.1 GI:7526032
 Indels
 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4390
Fax: 402 762 4390
 DB 10; L
1.3e-07;
 ö
 3.4%; bcc.
100.0%; Pred. No. ...
... 0; Mismatches
 41
 Email: smith@email.marc.usda.gov
 /organism="Sus scrofa"
/db_xref="taxon:9823"
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Seq primer: ATTTAGGTGACACTATAG.
 /clone_lib="MARC lPIG"
 2519 tggaaggtgccactcccactgtccttt 2545
 /tissue_type="pooled"
/lab_host="DH10B"
109 TGGAAGGTGCCACTCCCACTGTCCTTT 135
 109 TGGAAGGTGCCACTCCCACTGTCTTT 135
 FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
 Location/Qualifiers
 42 g
 and 30 embryos.
 AW785901.1 GI:7842677
 87; Conservative
 Best Local Similarity
 scrofa
 28
 Query Match
 LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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ORIGIN
 DEFINITION
 ACCESSION
VERSION
KEYWORDS
SOURCE
 ORGANISM
 ORGANISM
 REFERENCE
AUTHORS
 Matches
 RESULT
AW785901
LOCUS
 JOURNAL
 AW669518
 FEATURES
 TITLE
 COMMENT
 RESULT
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```
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
Do Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Fax: 402 762 4360
Fax: 402 762 4360
Fax: Vector usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
PCR PRimers
 ö
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoidea; Bovoinea; Bos.

1 (bases 1 to 503)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Gases, F., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.E., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 l (bases 1 to 243)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
,G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 /note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary." 67 c 59 g 61 t
 bovine cDNA
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 Gaps
 25-APR-2001
 .
,
 Sequence evaluation of four pooled-tissue normalized L
libraries and construction of a gene index for cattle
 libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 Length 243;
 BF074689 503 bp mRNA EST 2:
222166 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BF074689
 Indels
 ö
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Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 87; Conservative 0; Mismatches 0;
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/organism="Bos taurus"
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/tissue_type="pooled"
/lab_host="DH10B"
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 FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
 GI:10868200
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-minscore 18

21180013

JOURNAL MEDLINE

COMMENT

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Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 374)
Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
G.Gasa, E., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904 e. Vector identified by cross_match with the -minscore 18
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/tissue_type="pooled"
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/note="Vector: pCNV SPORT6; Site_1: Xbal; Site_2: Xhol;
Library made from pooled tissue from lymph node, ovary,
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 v0.980904.e. Vector identified by cross_match with the and "minmatch 12 options.
PCR PRIMETS
FORWARD: AGGAAACAGCTATGACCAT
 Length 328;
 Sequence evaluation of four pooled-tissue normalized L
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
 AW669633 374 bp mRNA EST 2
113104 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
 Indels
 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TET: 402 762 48390
Fax: 402 762 4390
 Score 85.4; DB 10;
Pred. No. 2.4e-07;
0; Mismatches 1;
 Email: smith@email.marc.usda.gov
 /organism="Bos taurus"
/db_xref="taxon:9913"
 Plate: 107 row: I column: 14
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Location/Qualifiers
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 BACKWARD: GTTTTCCCAGTCACGACG
 Location/Qualifiers
 and -minmatch 12 options.
 GI:7526147
 Ouery Match 3.4%;
Best Local Similarity 98.9%;
Matches 86; Conservative (
 Contact: Smith TPL
 AW669633.1
 PCR PRimers
 Keele, J.W.
 AW669633
 71
 AW669633
 21180013
 EST
 source
 BASE COUNT
ORIGIN
 RESULT 8
AW669633/c
 source
 LOCUS
 SOURCE ORGANISM
 JOURNAL
MEDLINE
COMMENT
 ACCESSION
 REFERENCE
 AUTHORS
 FEATURES
 KEYWORDS
 FEATURES
 VERSION
 TITLE
 g
 Single pass sequenting. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 ;
 Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovoinae; Bosonae; Bos
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 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
 Gaps
 25-APR-2001
 ·,
 Score 87; DB 11; Length 503;
 AW669634 328 bp mRNA EST 2
113105 MARC 1BOY Bos taurus CDNA 5', mRNA sequence.
AW669634
 0; Indels
 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4369
 Pred. No. 1.1e-07;
 100.0%; Pred. No. -
Genome Res. 11 (4), 626-630 (2001)
 adrenal, and endometrium 146 c 130 g 109
 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
 Tel: 402 762 436
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
 PCR PRIMERS
FORWARD: AGGAAACAGTATGACCAT
BACKWARD: GTTTTCCAGTCAGGACG
Plate: 82 row: E column: 4
Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 AW669634.1 GI:7526148
```

3.48;

.503

Source

FEATURES

Query Match
Best Local Similarity 100.
Matches 87; Conservative

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122

BASE COUNT ORIGIN

25-AFR-2001

bovine cDNA

/organism="Bos taurus"

Contact: Smith TPL

21180013

MEDLINE COMMENT

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JOURNAL

TITLE

Bos taurus

ORGANISM

REFERENCE

AUTHORS

EST **3**000

KEYWORDS SOURCE

LOCUS DEFINITION ACCESSION VERSION

AW669634/C

RESULT

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Gaps

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Query Match 2.8%
Best Local Similarity 100.0
Matches 71; Conservative
 Direct Submission
 2535 cactgtccttt 2545
 71
 Best Local Similarity Matches 87; Conserv
 AL066953.1
 61 CACTGTCCTTT
 fruit fly
 Genoscope
 CNS007BE
 GSS
 Query Match
 source
 DEFINITION
 ORGANISM
 10
 CNS007BE/c
 BASE COUNT
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VERSION
 AUTHORS
TITLE
 JOURNAL
 KEYWORDS
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 Fax: 402 762 4390
Email: smith/email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
 ö
 1 (bases 1 to 98)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett
,G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
Keele, J.W.
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Library made from pooled tissue from lymph node, ovary,
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Library made from pooled tissue from lymph node, ovary,
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 25-APR-2001
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0; Mismatches 1; Indels 0
 BG365021 98 bp mRNA EST 2
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 USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
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 2519 tggaaggtgccactcccactgtcctt 2544
 Location/Qualifiers
 FORWARD: AGGAAACAGCTATGACCAT
 24
 49 TGGAAGGTGCCACTCCCACTGTCATT
 and -minmatch 12 options.
 BG365021.1 GI:13254118
 Bovidae; Bovinae; Bos.
 3.3%;
98.8%;
 Best Local Similarity 98.88
Matches 85; Conservative
 Contact: Smith TPL
 Bos taurus
 18 a
 21180013
 BG365021
 84
 COW.
 EST
 Query Match
 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 BASE COUNT
ORIGIN
 LOCUS
DEFINITION
 BASE COUNT
 REFERENCE
AUTHORS
 MEDLINE
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BG365021
 JOURNAL
 FEATURES
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"Web: www.genoscope.cns.fr

"Web: www.genoscope.cns.fr

Determination of this BAC-end sequence was carried out as part of

Determination of this BAC-end sequence was carried out as part of

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see http://www.fruitfly.org The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

WY. The library is named RPCI-98 and was constructed by partial

ECORI diseation of Drosophila DNA provided by the BDGP from the

isogenic strain v2; cn bw sp, the same strain used for the BDGP's

pl and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

cound at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 ö
 submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR15H24 of RPCI-98 library from Drosophila melanogaster (fruit
 659 aggetaatagttttacaaattataaaggatttteegetetatatatgtatggeateacag 718
 599 giggtaatttattaaagttttggttcgcccaagcaattgctgctaactatgatcctaaag 658
 331 GGWWTKGGGTKGGRWKGAACCGRARGAWTTCCCYCCWWWRCCWWKGKCTKGGRRCCS 272
 719 attetetateatteagagettatggggettaetecaaaceageaaegataaaeteggea 778
 2475 ccagccatctgttgtttgccctccccgtgcttccttgaccttgaaggtgccattc 255
 Gaps
 03-JUN-1999
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ptersygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
(Dases 1 to 1001)
 Gaps
 ö
 ö
 Length 1001;
 Length 98;
 331 others
 Indels
 Indels
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/clone_lib="RPCI-98"
 ess
 2.4%; Score 61.2; DB 13; 25.4%; Pred. No. 0.017;
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 DB 11; I
2.8%; Scc. 100.0%; Pred. No. ... 0; Mismatches
 ų
 212
 fly), genomic survey sequence. AL066953
 /note="end : TET3"
148 c 151 g
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 prosophila melanogaster
 GI:4945517
 1001 bp
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catagtcaggttccttggatcaatggacagaaaaagcctctatatctttatggagctttc 420
 VERSION
KEYWORDS
SOURCE
ORGANISM
 481
 901
 441
 12
 CNS00FUH/C
 DEFINITION
 601
 681
 421
 661
 721
 781
 841
 ACCESSION
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 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
271 GRWITTWATTWWWTTWWTTACCYTAAWKGSGGKTWRRWRRGKKKWAWTTWRCCCC 212
 gtgattttactttccgaaagtttgatctaggtataatttcagcgttttaagtcaaatttt 838
 211 MAAARKTIWASKWWITIKGKIIWAAWIWAIKGIWAWKGKIIKGKIYCYWAAWYSKIIIIK 152
 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 03-JUN-1999
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
 503 others
 tataataaaactaaaagatttttattattttttgagttttta 940
 : ||:::||| :| :: :: ||:| : ::|| |
WITAWKRAAARSMATIKRAAWKRAWIWAWIITRAWIWWIIGA 50
 GSS
 melanogaster"
 ų
 202
 fly), genomic survey sequence.
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 Location/Qualifiers
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64 c 131 g
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 DEFINITION
 BASE COUNT
ORIGIN
 91
 ORGANISM
 RESULT 11
 TITLE
JOURNAL
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 REFERENCE
 FEATURES
 COMMENT
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COMMENT ö 241 gigaaaigiagigitgicgaciggaacacaitcgiicciicagaaacciccaciacagaa 300 aaagctgctacaaacgctatgaaatacaaatactgtgtttggcagtggctcgtcggaaag 360 .; DB 13; Length 1101; Score 60; DB 13; Pred. No. 0.03; Conservative 269;

Best Local Similarity Matches 119; Conserv

1041 301

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Web: www.genoscope.ons.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkely Drosophila denome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, WY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw sp, the same strain used for the BDGP's segref@genoscope.cns.fr Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr CNSOOFUH 996 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACK31021 of RPCI-98 library from Drosophila melanogaster (fruit 720 780 840 981 AGRRDGGRKRKDKKDRRDGDDRKGGKKKKAARAAKWATKWWDDWDWDKDDWKWDGAKDRK 922 480 GWADADWWIWDAAADDWWADDRWDAWAWKWDDAWAWGARTADRRDWGDRAGKRGGARKRR 802 099 fruit fly.
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera: Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. tggtttattggaggaactttagggggactcagaaaagctggagactggtctgccacagta ttaatgaaccetttagcaaaggetacgaagactacgttaaatggaaaagaaacctagct cgttatgagtatgtcgaagccttgtcagttccagaaatagatgtttcagggattggccgt ggtaatttattaaagttttggttcgcccaagcaattgctgctaactatgatcctaaagag tototatcattcagagettatggggettactccaaaccagcaaacgataaactcggcagt 621 AKWDWKTRADRWDRWAADTWTDARKADRDWAKARAWRARRDRARAARADRWTTKGKTTT fly), genomic survey sequence. taataaaactaaaagatttttattat 926 | |: ::|| |||||: ||:| TTTTWTWTTWWAATTATTTTWTTWT 416 GI:4951105 AL071063.1 Genoscope

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Similarity
 Unpublished
 Unpublished
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 Genoscope
 sequence.
 CNS04E5M
 AL286627
 91;
 Query Match
 Local
 source
 BASE COUNT
ORIGIN
 DEFINITION
 ORGANISM
 Matches
 783
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 ACCESSION
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CNSO4E5M
 VERSION
KEYWORDS
SOURCE
 REFERENCE
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 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton pBelobACII.
Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 GSS 26-JUL-1999
LLCSOPILIA melanogaster genome survey sequence SP6 end of BAC
BACN12P22 of DrosBAC library from Drosophila melanogaster (fruit
AL104456
 995 АААИТТТТТТТИАТАААААТИТТТТИИТИМТИАТТИМААААИТИАИАИАПИАМАТТИИТА 936
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 724 ctatcattcagagcttatggggcttactccaaaccagcaaacgataaactcggcagtgat
 935 ATTTBTTTBGGSSGSSSSGGGRRAAAAAAAAAAAAAWWWWATTTTTTWTWAAW
 784 tttactttccgaaagtttgatctaggtataatttcagcgttttaagtcaaattttaataa
 875 TITAARTTWRATTTWAWTAWWTTTTTTTTTTTTTTAATWDTTTWTTTTTTTW
 ö
 Length 996;
 197 others
 melanogaster"
 1. .987
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 132;
 Score 59.4; DB 13;
Pred. No. 0.04;
 ų
 48; Mismatches
 171
 Plasmid Drosophila melanogaster
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 Location/Qualifiers
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164 c 81 g
 AL104456.1 GI:5616067
 2.3%;
 Query Match 2:39
Best Local Similarity 38:19
Matches 111; Conservative
 Direct Submission
 æ
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 Genoscope
 383
 source
 source
 BASE COUNT
ORIGIN
 CNS014PQ/c
LOCUS
 DEFINITION
 664
 844
 ORGANISM
 TITLE
JOURNAL
 ACCESSION
 VERSION
KEYWORDS
SOURCE
 AUTHORS
 REFERENCE
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 COMMENT
 RESULT
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
 Fisher, C.,
 the
 Fisher, C.,
 Tetraodon nigroviridis genome survey sequence T7 end of clone
103P02 of library G from Tetraodon nigroviridis, genomic survey
 842
 911 МИЙНИТТТУНЫМИТИТТТТИМАТИМТТТИМАТИТИМАМУСУМТАТТТИТИММААМААТТ 852
 723 tetateatteagagettatggggettaetecaaaceageaaaegataaaeteggeagtga 782
 Gaps
 oŧ
 ttttactttccgaaagtttgatctaggtataatttcagcgttttaagtcaaattttaata
 2 (bases 1 to 976)
Socst-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fis
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.
Saurin, W. and Weissenbach, J.
 1 (bases 1 to 976)
30est-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fis
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
 Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
 ö
 Length 987
 245 others
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 GSS
 671 TTTTTATTCTAATTTWGTWWTKWTTKTTKTKKTKKGGGG 631
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 ų
 0.2;
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/note="end : SP6"
a 122 c 122 g
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Tetraodon nigroviridis.
Tetraodon nigroviridis
 65;
 2.2%;
 AL286627.1 GI:8025084
 976 bp
 (bases 1 to 976)
 Conservative
 Direct Submission
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 AU071789 240 bp mRNA EST 23-JUN-1999
AU071789 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSC524, mRNA sequence.
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1 151 c 137 g 327 t 118 others
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 869 attattagtgagagcttttttttttttttttataataaaactaaaagatttttattattt 928
 762 aaacgataaactcggcagtgattttactttccgaaagtttgatctaggtataatttcagc 821
 229 ATACAAAGAAAGAGTAATATTTTTTTTATAAATAATTTTACAATAGTAATTATAACAAA 170
 822 gittiaagicaaaititaataaaaittitaaaaaacaggcicgcaitaaitattagigaga 881
 Gaps
 Gaps
 Developmental cDNA in Dictyostellum discoideum (1999)
Unpublished (1999)
Contact: Hideko Urushihara
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: 4012hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostellum discoideum cDNA project in Japan.
 0;
 ;
 Score 52.4; DB 10; Length 240;
Pred. No. 1.3;
0; Mismatches 89; Indels 0
 2.1%; Score 52.8; DB 13; Length 976; 35.9%; Pred. No. 0.89; tive 46; Mismatches 77; Indels 0
 Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota; Mycerozoa; Dictyostellida; Dictyostellum.
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 AU071789.1 GI:5161978
 2.1%;
 Best Local Similarity 35.9
Matches 69; Conservative
 Best Local Similarity 53.9 Matches 104; Conservative
 tttgagttttta 940
 789 TTTTTTTTTA 800
 Urushihara, H.
 ď
 243
 109
 Query Match
 Query Match
 RESULT 15
AU071789/c
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 BASE COUNT
ORIGIN
 BASE COUNT
ORIGIN
 DEFINITION
 929
 ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
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 REFERENCE
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942 ggttaatcctatt 954

| ||| 49 GTTTATGGTTTTT 37

7, 2002, 21:32:10 completed: February ne: 20644 sec Search com AE001654 Chlamydia AE002165 Chlamydop AP002547 Chlamydop L23921 Chlamydia p AE001333 Chlamydia AE002357 Chlamydia U50732 Chlamydia AC015625 Homo sapi

Homo sapi Human DNA Homo sapi Human DNA Human Chr Human DNA

AXO83744 SAPO01118 PAC007091 PAL451103 PAC023295 PAL035251 PAL133485 PAL591431 PAL591431 PAX

Sequence Buchnera

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

nucleic search, using sw model

OM nucleic

Run on:

February

1472140 seqs, 8248589755 residues

Searched:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

US-09-391-606-2 651

Perfect score: Sequence: Scoring table: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries

gb\_ba:\* gb\_htg:\*

GenEmbl:\*

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

AC02541 Homo sapi AL52556 Homo sapi AE077537 Caenorhab AC068814 Homo sapi AC068127 Human BAC AC083885 Homo sapi AC036475 Homo sapi AC090213 Homo sapi AC0902406 Homo sapi AC0902406 Homo sapi AC007607 Genomic sapi AC007607 Genomic sapi AC007637 Genomic sapi AC007637 Genomic sapi AC009174 Human DNA AP013255 Human res AR089138 Sequence AF013255 Human res AC009174 Human DNA AC01328 Homo sapi AC019128 Homo sapi AC09128 Homo sapi AC09109823 Homo sapi AC09128 Homo sapi AC09128 Homo sapi AC09128 Homo sapi AC090526 Arabidops AC007296 Arabidops AC007296 Arabidops AC075110 AC00823 Homo sapi AC055114 Homo sapi

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_htg\_other:\*

em\_htg\_inv:\* em\_htg\_rod:\*

em\_htgo\_rod:\* em\_htg\_hum:\* em\_htgo\_hum:\*

em\_ro:\* em\_sts:\*

em\_sy:\* em\_un:\*

em\_p1:\*

em\_pat:\*

em\_fun:\* em\_hum:\*

em\_in:\* em\_om:\*

em\_or:\* em\_ov:\*

gb\_vi:\* em\_ba:\*

ap\_un:

\*:Ks\_dg

gb\_ro:\* gb\_sts:\*

gb\_pat: \* gb\_ph: \* gb\_pl: \* gb\_pr: \*

gb\_om:\*

SUMMARIES

Pasteur Limited (CA)
Location/Qualifiers
1. 2238
/organism="Chlamydophila pneumoniae"
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Patent: WO 0066739-A 7 09-NOV-2000;

Aventis

JOURNAL

source

FEATURES

PAT

University

BASE COUNT ORIGIN

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Direct Submission
Submitted (01-DEC-1998) Program in Infectious Diseases, Universit of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
 Hyman, R.W.
 Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
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 Shiral, M.

Direct Submission

Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.

Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.

Nutsunori Shiral, Yamnguchi University School of Medicine,

Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
75-805, Japan (E-mail:mshiraidepor cc. yamaguchi. u.ac.jp,

Tel:81-836-22-2227, Fax:81-836-22-2415)

On Sep 15, 2000 this sequence version replaced gi:617298

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 Direct Submission
Submitted (20-MAY-1998) Program in Infectious Diseases, University
of California, 235 Warren Hall, Berkeley, CA 94720-7360, USA
Location/Qualifiers
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Kalman,S., Mitchell,W., Marathe,R., Lammel,C., Fan,J., Hyman,R.W.,
Olinger,L., Grimwodd,J., Davis,R.W. and Stephens,R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
 Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis
Science 282 (5389), 754-759 (1998)
 Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

1 (bases 1 to 10954)
Stephens, R.S., Kalman, S., Lammel, C.J., Fan, J., Marathe, R.,
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Direct Submission
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Homo sapiens clone RP11-45J21, WORKING DRAFT SEQUENCE, 7 unordered
 Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 26, 2000 this sequence version replaced gi:6624051.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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 Center: Whitehead Institute/ MIT Center for Genome Research
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 Contact: sequence_submissions@genome.wi.mit.edu
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Unpublished
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site: http://www-seq.wi.mit.edu
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Quality coverage: 4.8 in Q20 base
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* consists of 7 contigs. The true order of the pieces
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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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 603 others
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 Shigenobu, S., Hattori, M., Watanabe, H., Toyoda, A., Yada, T., Sakati, Y. and Ishikawa, H.
Sakati, Y. and Ishikawa, H.
Direct Submission
Submitted (24-JAN-2000) to the DDBJ/EMBL/GenBank databases. Shuji
Shigenobu, University of Tokyo, Department of Biological Sciences;
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
(E-mail:shige@gsc.riken.go.jp, URL:http://buchnera.gsc.riken.go.jp,
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 Shigenobu, S., Watanabe, H., Hattori, M., Sakaki, Y. and Ishikawa, H. Genome sequence of the endocellular bacterial symbiont of aphids
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GAISSENCT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP databases can be found at the found at the found at the contigs of human was generated from part of bacterial clone contigs of human was generated from part of bacterial clone contigs of human and the found at the contigs of human and the found at the contigs of human and the found at
 chromosome \mathbf{X}, constructed by the Sanger Centre Chromosome \mathbf{X} Mapping Group. Further information can be found at
 derived from a single pUC clone. Restriction digest data confirm the assembly. Sequence from uni-directional primer reads only."
 http://www.sanger.ac.uk/HGB/ChrX
BY11-172M3 is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACG3.6
This sequence is the entire insert of clone RPI1-172M3 The true left end of clone RPI1-55869 is at 135984 in this sequence. The true right end of clone RPI1-417G14 is at 98898 in this sequence.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
 Db 104186 ACTAGGTTTGGGGGATTATTCTTGATTCCTCTTTCTGCTAGTAGAAATTTGAAGTACATG 104127
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 156142. 156163
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 Lawlor, S.
Direct Submission
Submitted (25-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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 Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
 Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108, USA
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On May 29, 1999 this sequence version replaced gi:4572701.
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2 (bases I to 179033)

S Birren, B. Lintcon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barnan, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Barown, A., Benkett, G., Campoplano, A., Castle, A., Boukhgalter, B., Brown, A., Darden, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArtellano, K., Devden, Domino, M., Doyle, M., Penestor, J., Ferreita, P., Fitzhigh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hadord, A., Horton, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Liev, I., Largocque, K., Lehoczky, J., Levine, R., McEwan, P., McGurk, A., McKarnan, K., McPheeters, R., Meldrim, J., McDwan, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGurk, A., McKarnan, K., McPheeters, R., Meldrim, J., Mebwan, D., Conner, T., O'Conner, T., O'Nesh, D., C., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stevers, M., Trigilio, J., Yessaliev, H., Viel, R., Vo, A., Wilson, B., Travers, M., Trigilio, J., Yeung, G., Zainoun, J., Zimmer, A. and
 AC023295 179033 bp DNA HTG 03-MAR-2000
Homo sapiens clone RP11-17P16, WORKING DRAFT SEQUENCE, 17 unordered
 Direct Submission

Direct Submission

Submitted (1-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
ON Mar 3, 2000 this sequence version replaced g1:7138910.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center clone name: 17_P16

Center clone name: 17_P16

Sequenciny vector: M13, M77815, 100% of reads
Sequenciny vector: M13, M77815, 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 170854 bases at least Q40

Consensus quality: 175131 bases at least Q30

Consensus quality: 175656 bases at least Q30

Consensus quality: 176656 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 177433; sum-of-contigs

Quality coverage: 4.8 in Q20 bases; sum-of-contigs
 * NOTE: This is a 'working draft' sequence. It currently * consists of 17 contigs. The true order of the pieces * is not known and their order in this sequence record is
 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-17P16
 AC023295.3 GI:7144963
HTG; HTGS_PHASE1; HTGS_DRAFT
 Center project name:
 Mammalia; Eutheria; Pr.
1 (bases 1 to 179033)
 Center code: WIBR
 Homo sapiens
 Unpublished
 AC023295
 human.
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JOURNAL
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AUTHORS
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 KEYWORDS
 COMMENT
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
 1058 1157: gap of 100 bp 1158 2610: contig of 1453 bp in length 2611 2710: gap of 100 bp 2611 2710: gap of 100 bp 2719: gap of 100 bp 2759 gap of 100 bp 2759 gap of 100 bp 2759 gap of 100 bp 2759 gap of 100 bp 2750: gap of 100
 37524: contig of 9523 bp in length 524: gap of 100 bp 48049: contig of 10425 bp in length 48049: contig of 10425 bp in length 149: gap of 100 bp 59544: contig of 11395 bp in length
 122861 122960: gap of 100 bp 122961 149152: contig of 26192 bp in length 149153 42525; gap of 100 bp 100 bp in length.
 p of 100 bp contig of 16951 bp in length
 59545 59644: gap of 100 bp
59645 72098: contig of 12454 bp in length
 2099 72198: gap of 100 bp
2199 87255: contig of 15057 bp in length
37256 87355: gap of 100 bp
 04307 104406: gap of 100 bp 122860: contig of 18454 bp in length
 56: gap of 100 bp 27901: contig of 6345 bp in length
 1057: contig of 1057 bp in length
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15949. .21456
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37625 48049: cont
 104306:
 21557 2790
27902 28001:
 87256 87355:
87356 10430
 21556:
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 FEATURES
 only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw.; SWISSPROT; Tr., TREMBL; Wp., WORNDEP; Information on the WORNDEP
 Submitted (09-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone by this sequence version replaced gi:4584645.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
 ö
 Db 135097 TTTTCTGATGAATTATATCGCTATGCACTGTATCAGTAATATGTTTTGCCTTAAAGTCT 135038
 Db 135037 GTTTTCTCTGTAGCTATACTAGCCTTCCTTTAGTCAGTATTTTCACAGAGTAACTTCTTT 134978
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (asses 1 to 16,1888)
Laird, G.
 429
 430 aatttattaaagtttttggttcgcccaagcaattgctgctaactatgatcctaaagaggct 489
 Gaps
 DNA PRI 18-MAR-2001 from clone RP4-70501 on chromosome 20q11.2 iSSs, complete sequence.
 370 tatgagtatgtcgaagccttgtcagttccagaaatagatgtttcagggattggccgtggt
 tttattggaggaactttagggggactcagaaaagctggagactggtctgccacagtacgt
 ;
0
 Length 179033,
 1601 others
 Score 38.8; DB 2; Length 1
Pred. No. 14;
0; Mismatches 127; Indels
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104407. 122860
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12961. 149152
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 Human DNA sequence from
Contains STSs and GSSs,
AL035251
 AL035251.11 GI:4585773
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 Query Match 6.0%;
Best Local Similarity 47.5%;
Matches 115; Conservative
 161888 bp
 Homo sapiens
 56286
 ||
| Db 134857 CT 134856
 HS70501
 human.
 misc_feature
 misc_feature
 misc_feature
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 RESULT 15
HS70501/c
LOCUS
 BASE COUNT
ORIGIN
 DEFINITION
 ORGANISM
 310
 TITLE
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KEYWORDS
SOURCE
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 AUTHORS
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20
 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
http://www.sanger.ac.uk/HGP/Chr20
FRP4-70501 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
 /note="L2 repeat: matches 2349. .2567 of consensus" 1919. .2158 //note="5 copies 48 mer 71% conserved" 1924. .2145 //note="74 copies 3 mer fra 73% corrections.
 .392 of consensus"
 3649. .3824
/note="8 copies 22 mer 84% conserved"
4351. .4734
470te="Lz repeat: matches 2292. .2734 of consensus"
5118. .5195
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 .114 of consensus"
 .211 of consensus"
 .145 of consensus
 This sequence is the entire insert of clone RP4-70501 Location/Qualifiers
 Jose of course for the conserved of course. The conserved of conserved
 8724. 9011
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9435. 9491
/note="MIR repeat: matches 83. 145 of con
 Noote="2 copies 48 mer 95% conserved"
8610. 8909
Noote="150 copies 2 mer ct 55% conserved"
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 3637, .8959
/note="19 copies 17 mer 58% conserved"
8649. .9032
 / Logic Matches 48. 114 o / hote="4 copies 49 mer 88% conserved" 816. 8311 / hote="2 copies 48 mor 8610. 8000
 66% conserved"
 ..userved
/.uue="8 copies 48 mer 61% conserved"
8689. .9031
//note="7 comion"
 63% conserved"
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 8637
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13930. .10440

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16441. .16586

/note="match: GSS: Em:AQ072870"

1744. .17261

/note="MLTIC repeat: matches 428. .534 of consensus"

18488. .18530

/note="Charlie6 repeat: matches 1128. .1171 of consensus charlie6 repeat: matches 1128. .1171 of consensus charlie6 repeat: matches 1128. .1171 of consensus charlie6 repeat: matches 9. .216 of consensus"

18554. .18760

/note="MERS8A repeat: matches 9. .216 of consensus"

18795. .19024
 10059. .22.09 men acco 30 concerned 11699. .21696. .22143 f. foote="match: STS: Em:G09929" 21766. .21916 f. foote="match: STS: Em:G09929" 21766. .21916 f. foote="militar repeat: matches 9. .189 of consensus" 24290. .24562 f. foote="militar repeat: matches 117. .385 of consensus" 24290. .26483 f. foote="Limitar repeat: matches -1390. .105 of consensus" 28153. .28259 f. foote="militar repeat: matches 36. .176 of consensus" 28986. .29396 f. mer cact 79% conserved" 30039. .30458 f. .30
note="MillH repeat: matches 432. .536 of consensus" 2346. .32575 note="MER20 repeat: matches 1. .218 of consensus"
 note="MLT1B repeat: matches 290. .390 of consensus'
 note="Alusg repeat: matches 13. 300 of consensus" 3820. 33911 note="Lz repeat: matches 2213. 2308 of consensus" 4001. 34100
 .2674 of consensus"
 18795. 19024

Anote="L2 repeat: matches 2338. .2581 of consensus" |
19440. 19473

Anote="L1P repeat: matches 503. .534 of consensus" |
19862. 19959

Anote="L2 repeat: matches 2581. .2702 of consensus" |
20808. .20855

Anote="12 copies 4 mer acac 89% conserved" |
 .2705 of consensus"
 0691. 30931

note="MIR repeat: matches 39. .256 of consensus"

10934. .31035
 Anote="727" copies 4 mer cctt 63% conserved" 32729. 33075 Anote="12 repeat: matches 2294. 2674 of complement(33076. 33152) Anote="match: GSS: Em:AQ489056" 33532. 33819
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1036. .31210
 /note="30 copies 2 mer tg 88% conserved" 34273. 34328
 34261. .34326
/note="3 copies 22 mer 86% conserved"
34267. .34326
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11447. 31520
note="L2 repeat: matches 2632.
12120. 32216
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34722. .34789
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36081. .36431
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36566. .36720
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/note="MIR Papeat: matches 1. .156 of consensus"
36723. .36972 repeat: matches 7. .260 of consensus"
37319. .38748
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37931. .38230
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38237. .38480
/note="MIR repeat: matches 47. .121 of consensus"
39183. .39480
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40048. .40218
/note="MIR repeat: matches 2. .297 of consensus"
/note="MIR repeat: matches 2. .297 of consensus"
/note="MIR repeat: matches 2. .297 of consensus"
/note="MIR repeat: matches 2. .297 of consensus"
/note="MIRII repeat: matches 245. .410 of consensus"
 94361 TCAAATTAGAATTCCAAAAAGCATGCTTGACTAGGAAACATCAGCAAGAAAGTTCCATTT 94302
 79 gttgtcgactggaacacattcgttccttcagaaacctccactacagaaaaagctgctaca 138
 139 aacgctatgaaatacaaatactgtgtttggcagtggctcgtcggaaagcatagtcaggtt 198
 19 gcttgggttgtagaagggattctcaatcgtttgcctaaacagtttttgtgaaatgtagt 78
 DB 9; Length 161888;
 Query Match
5.9%; Score 38.4; DB 9; Length 1
Best Local Similarity 48.2%; Pred. No. 18;
Matches 108; Conservative 0; Mismatches 116; Indels
 cettggatcaatggacagaaaaagcetetatatctttatggage 242
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Oligonucleotide D1 Oligonucleotide D2 Oligonucleotide D2 Oligonucleotide D1 Oligonucleotide D1 RSV isolate 2B w11 Nucleotide sequenc Nucleotide sequenc

DNA encoding the L RSV vaccine 2B33F RSV vaccine 2B33F RSV revertant 2B30 Nucleotide sequenc Nucleotide sequenc Nucleotide sequenc DNA encoding the L DNA encoding the L DNA encoding the L DNA encoding the L DNA encoding the L DNA encoding the L NA ```
Chlamydia pneumoniae lorf2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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                                 AAF58255
AAF58238
AAV18275
AAZ22909
AAZ22914
                                                                                         AAX35267
AAV18277
AAV18278
AAV18279
AAV18280
AAZ22911
                                                                                                                                                                          AAZ22913
AAX35269
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AAX35271
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AAV17552
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'SIDSZ/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                  hits satisfying chosen parameters:
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Database

Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

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647.8 647.8 647.8 87 87 87 87 87 87

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Score

Result Š.

Pred.

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WPI; 2000-350742/30. P-PSDB; AAY92716.

Canarypox virus Pv Canarypox virus DN C5 ORF from canary Canarypox Pvull fr Canarypox Pvull fr

Nucleotide sequenc DNA encoding the L

Canarypox virus C5 pRW764.5 (contq. C CDNA encoding fusi

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                                                                  This sequence encodes lorf2 protein of a strain of Chlamydia pneumoniae. Comparison of this sequence as to the recently published genome sequence of C. pneumoniae reveals that the sequence actually contains at least two open reading frames, a first one in the 5' portion and a second one in the 3' portion of the sequence. Despite the presence of the stop codon at the end of this sequence. C. pneumoniae does make a 76 kba product. It appears possible that C. pneumoniae is able to read through this stop codon and produce a full-length product terminated by the stop codon at the end of the second open reading frame. There is at least one in-frame ATG upstream of the start codon. This suggests that the first open reading frame may form part of one or more larger open reading frames. The lorf2 protein or DNA can be used as a vaccine for humans to treat or prevent disease caused by Chlamydia infection. The sequences or an antibody to lorf2 can be used to diagnose a Chlamydial infection.
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    ed polynucleotide encoding a Chlamydia polypeptide useful to diagnose and prevent disease caused by Chlamydia infection
                                                                                                                                                                                                                                                                                                             Score 647.8; DB 21; Length 1550;
Pred. No. 3.2e-183;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1550 BP; 472 A; 268 C; 317 G; 493 T; 0 other;
                                                 Claim 1; Fig 1A-C; 88pp; English
                                                                                                                                                                                                                                                                                                                    99.58;
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           Isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a 76 kDa protein from Chlamydia pneumoniae, useful for vaccinating against Chlamydia infections –
                                                                                                         76 kDa protein; bactericidal; diagnosis; prevention; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; truncation mutant; fusion gene;
                                                                                                                                                                                                                                                                                                                                                                           /note= "This part of the sequence is unrelated to
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                                                                                                                                                                                                                                                                    unrelated
                                                                                     C. pneumoniae 76 kDa protein truncation mutant fusion gene.
                                                                                                                                                                                                                                                                                                                     /product= "Truncated Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                     the sequence is
gene"
                                                                                                                                                                                                                                                                                                                                                                                       C. pneumoniae 76 kDa gene"
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1..665
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                                                                                                                                                                                                                                                                                                                                    76KDa protein"
2122..2238
/*tag= c
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           BP.
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766..2238
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           AAD02066 standard; DNA; 2238
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                                                                                                                                                                                            Chlamydia pneumoniae
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Best Local Similarity
Matches 649; Conserv
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30-JUN-1999;
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Claim 1;
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                                                                                                                                                                                                                                                                                              Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss.
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                acagaaaaagctgctacaaacgctatgaaatacaaatactgtgtttggcagtggctcgtc
                                                            ggaaagcatagtcaggttccttggatcaatggacagaaaaagcctctatatctttatgga
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97FR-0014673.
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21-NOV-1997;
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                                                                                                      The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY34584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        829363 ATGACAAAAAAACATTATGCTTGGGTTGTAGAAGGGATTCTCAATCGTTTGCCTAAACAG 829304
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                                                                                                                                                                                                                                                                                                                                                                 Length 1230025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atgacaaaaaaacattatgcttgggttgtagaagggattctcaatcgtttgcctaaacag
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                                                                                                                                                                                                                                                                                                                                                               Score 647.8; DB 20
Pred. No. 4.5e-182;
0; Mismatches 2;
                                  sequence of Chlamydia pneumoniae
                                                                          English.
                                                                      1912pp;
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                                                                        Page 291-611;
WPI; 1999-357842/30
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 649; Conserv
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WPI; 2001-159728/16
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                      group, useful as labels in allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acagaaaaagctgctacaaacgctatgaaatacaaatactgtgtttggcagtggctcgtc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.4%; Score 87; DB 22; Length 936; 0.9%; Pred. No. 3.9e-16; ive 386; Mismatches 251; Indels
                                                                        Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                                                      Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 127; 159pp; English
                                                                                                                                                                                                                                              (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                   26-JUL-2000; 2000WO-US20476
                                                                                                                                                                                                           99US-0145695
2000US-0190259
                         (first entry)
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                                                                                   gene expression; ss.
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nes 6; Conserv
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                         24-APR-2001
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                                                                                                             Synthetic.
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AAF58252;
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group, useful as labels in allowing repeat analyses on
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gene expression; ss.
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Best Local Similarity 0.9%; Pred. No. 3.9e-16;
Matches 6; Conservative 386; Mismatches 251; Indels
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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17-MAR-2000; 2000US-0190259
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                                                                     301 ctagcttggtttattggaggaactttagggggactcagaaaagctggagactggtctgcc 360
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                                   241 gctttcttaatgaaccctttagcaaaggctacgaagactacgttaaatggaaaagaaac 300
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17-MAR-2000; 2000US-0190259
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and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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Best Local Similarity 0.9%; Pred. No. 3.9e-16;
Matches 6; Conservative 386; Mismatches 251; Indels
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                                                                                                                                 Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other
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AAF58254 standard;
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                                                                                                                                                                                                              Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                        253;
                                                                                                                                                                                                                                                ; Pred. No. 2e-15
384; Mismatches
                                                                                                     Nucleic acids containing electron-transfer hybridization assays, e.g. for genotyping,
                                                                                                                                                                                                                                        Score 84.6;
red. No. 2e-
                                                                                                                                      Example 6; Page 127; 159pp; English
                                                    (CLIN-) CLINICAL MICRO SENSORS
                                                                                                                                                                                                                                         13.0%;
                            99US-0145695.
2000US-0190259.
           26-JUL-2000; 2000WO-US20476
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                                                                                                                        single surface
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17-MAR-2000;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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ilarity 0.9%; Pred. No. 2e-15;
Conservative 384; Mismatches 253;
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                                                                                                                                                                                                                Electron-transfer group, ETM; mismatch; gene expression; ss.
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17-MAR-2000; 2000US-0190259
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Pred. No. 2e-15;
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17-MAR-2000; 2000US-0190259
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hybridization assays, e.g. for genotyping, allowing repeat analyses
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17-MAR-2000; 2000US-0190259
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421 ggccgtggtaatttattaaagttttggttcgcccaagcaattgctgctaactatgatcct 480
                                                                                                                                                                                                                present invention relates to a composition comprising two nucleic
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                                                                                                                                                               541 acagattetetateatteagagettatggggettaetecaaaeceageaaegataaaete
                                                                                                         13.0%; Score 84.6; DB 22; Length 938; Similarity 0.9%; Pred. No. 2e-15; 6; Conservative 384; Mismatches 253; Indels 0
                                                                                                                                                                                                                                                                                                                                                                               601 ggcagtgattttactttccgaaagtttgatctaggtataattt 643
                                                                                                                                                                                                                                                                                                                                                                                                                                   Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Mulphy, Brian R.
APPLICANT: Collins, Peter L.
APPLICANT: Whitehead, Stephen S.
APPLICANT: Juhasz, Katalin
TILLE OF INVENTION: PRODUCTION OF ATTENUATED RESPIRATORY
TITLE OF INVENTION: STROYTAL VIRUS VACCINES FROM CLONED NUCLEOTIDE SEQUENCES
NUMBER OF SEQUENCES: 14
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                            US-09-001-141-1
US-09-532-803-1
US-08-136-743B-40
                                                                                                            US-08-136-743B-3
US-08-487-826B-13
                                                                                                                                                        US-08-169-927-1
US-08-232-463-14
US-09-016-000-8
US-09-006-636-1
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: Two Embarcadero Center, 8th Floor
San Francisco
                                                                                                                                                                                                                       S-09-006-632-1
S-08-714-918-34
S-09-265-315-34
S-09-265-315-34
                               US-09-211-631-1
US-09-265-628-1
                                                                                                                                       US-08-116-098-1
US-08-169-927-1
                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,634
FILING DATE: 23-MAY-1997
PRIOR APPLICATION NUMBER: US 60/046,141
APPLICATION NUMBER: US 60/046,141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-WAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,773
FILING DATE: 15-UUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08892403A Patent No. 5993824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFRENCE/DOCKET NUMBER: 17634
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
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TYPE: nucleic acid
STRANDEDNESS: single
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-105-483-220
US-08-105-483-220
US-08-224-391-90
US-08-224-391-90
US-08-224-657-39
US-08-458-101-220
US-08-458-101-220
US-08-458-101-220
US-08-417-210A-66
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US-08-460-736-68
US-09-085-273-27
PCT-US96-00547-27
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US-08-310-356-36
PCT-US92-06300-1
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                                                                                                       7, 2002, 15:53:24
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Maximum Match 100%
Listing first 45 summaries
                                                                         - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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2447 AGATAGAGGGCCCAAAGTAAATTACAAGGATGTTTACGGTTCTTCAGCTCTCCATAGAGC 2506
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                                                                                                                           348 agactggtctgccacagtacgttatgagtatgtcgaagccttgtcagttccagaaataga 407
                                                                                      taactatgatcctaaagaggctaatagttttacaaattataaaggattttccgctctata 527
  408 tgtttcagggattggccgtggtaatttattaaagttttggttcgcccaagcaattgctgc 467
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GENETICALLY ENGINEERED VACCINE
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/O William S. Frommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 12-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 220, Application US/08105483 Patent No. 5494807 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Frommer, William S. REGISTRATION NUMBER: 25.06 REFERENCE/DOCKET NUMBER: 45. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 220
SEQUENCE CHARACTERISTICS:
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ilarity 49.6%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Paoletti,
TITLE OF INVENTION: G
TITLE OF INVENTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 120; Conserva
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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PERITONITIS VIRUS, COMPOSITIONS THEREOF, AND METHODS FOR
MAKING AND USING THEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2446 AGATAGAGGGCCAAAGTAAATTACAAGGATGTTTAGGGTTCTTCAGCTCTCCATAGAGC 2505
                                                                                                                                                                                                                          8397 AGATGTTGGAGAAATTGTTGAGTGGCATCTAATAAGTTTTTAGGTGTCTCCAATGAATTTCA 8338
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Pred. No. 0.13;
0; Mismatches 119; Indels 3
                                                                                                 Length 15225;
                                                                                                                                           59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,398
FILING DATE: 01-DEC-1995
CLASSIFICATION: 424
                                                                                                 Score 36.6; DB 2;
Pred. No. 0.13;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 0.4
CLASSIFICATION: 424
ATYONER/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFRENCE/COKET UNBER: 454310-2880
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
FELEPAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
TENGTH: 3208 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curtis, Morris & Safford, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08566398 Patent No. 5858373
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Best Local Similarity 49.6%;
Matches 120; Conservative (
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                                                                                                   Query Match 5.6%;
Best Local Similarity 55.0%;
Matches 72; Conservative
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STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
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APPLICANT: Paoletti, Enzo
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8277 ATGTTTTTATG 8267
TOPOLOGY: linear
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US-08-566-398-51
                 ; MOLECULE TYPE:
US-08-892-403A-2
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STATE:

RESULT 2 US-08-566-398-51

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Length 3209

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APPLICANT: DAGLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: UCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS GB, GC, AND GD AND USES THEREFOR
                                                                   2624 ATATTAAAATATATAATAACTCTATTACTAATAACTCCAGTGGATATGAACATAATACG 2683
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COMPUTER: IEM PC compatible
OPERATUR SYTEM: PC-DOS/MS-DOS
SOFTWÄRE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.6; DB
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: CURTIS, MORRIS & SAFFORD, 530 FIFTH AVENUE, 25TH FLOOR W YORK
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ATTOMNEY AGENT INFORMATION:
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29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEW YORK
: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                  Sequence 62, Application US/08413118
Patent No. 5688920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25.506
REFERENCE/DOCKET NUMBER: 45.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 840-3333
(212) 840-0712
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Best Local Similarity 49.6%;
Matches 120; Conservative
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APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                                                               Patent NO. 3527.0.:
GENERAL INPORMATION:
APPLICANT: Limbach, Keith J.
APPLICANT: Limbach, Keith J.
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS GB, GC AND GD AND USES THEREFOR
TITLE OF SECULENCES: 91
                                                                                                                                        2624 ATATTAAAATATATAATAACTCTATTACTAATAACTCCAGTGGATATGAACATAATACG 2683
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2507 TGCTATTGGTAGGAAACAGG---ATATGATAAAGCTGTTAATCGATCATGGAGCTGATGT 2563
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                                       468 taactatgatcctaaagaggctaatagttttacaaattataaaggattttccgctctata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454310-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Curtis, Morris & Safford
530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/220,151
30-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          Sequence 62, Application US/08220151
Patent No. 5529780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Frommer, William S. REGISTRATION NUMBER: 25,50. REFERENCE/POCKET NUMBER: 4: TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEO ID NO: 62.
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.69
Matches 120; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-08-220-151-62
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2684 AA 2685
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US-08-220-151-62
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2624 ATATTAAATTATTAATAACTCTATTACTAATAACTCCAGTGGATATGAACATAATACG 2683
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                                                                                                                                                                                                                    APPLICANT: Paoletti, Enzo
APPLICANT: Pincus, Steven E.
TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 119; Indels
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PatentIn Release #1.0, Version #1.25
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us 07/729,800
                                                                                                                                                                                                                                                                                                                                                                                                                STATE: New York
COUNTRY: United States of America
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/08/224,391
                                                                                                                                                          Sequence 90, Application US/08484304
Patent No. 5744141
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERSTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Frommer, William S. REGISTRATION NUMBER: 25.06 REFERENCE/DOCKET NUMBER: 45. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Curtis, Morris
ADDRESSEE: C/O William S.
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 49.6%;
Matches 120; Conservative
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FILING DATE: 17-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: SEQUENCE: SEQUENCE: 3209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STREET: 53
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TOPOLOGY:
US-08-484-304-90
                                                             2684 AA 2685
                   588 aa 589
                                                                                                                                               JS-08-484-304-90
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                        2624 ATATTAAAATATATAATAACTCTATTACTAATAACTCCCAGTGGATATGAACATAATACT 2683
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528 tatgtatggcatcacagattctctatcattcagagcttatggggcttactccaaaccagc 587
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Pred. No. 0.13;
0; Mismatches 119; Indels 3
                                                                                                                                                                                                                                                            Patent No. 3. 4. 4. 4. 6 Education:

GENERAL INFORMATION:
APPLICANT: Paletti, Enzo
APPLICANT: Pincus, Steven E.
TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
TITLE OF INVENTION: PLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,391
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APPLICATION NUMBER: US 07/729,800
FILING DATE: 17-UL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Curtis, Morris & Saffors: c/o William S. Frommer 530 Fifth Avenue
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US-08-224-391-90
'Sequence 90, Application US/08224391
'Patent No. 5744140
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.6
Matches 120; Conservative
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MEDIUM TYPE: Floppy
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STRANDEDNESS: sing
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ADDRESSEE:
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US-08-224-391-90
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Length 3209;

DB 1;

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588 aa 589

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2507 TGCTATTGGTAGGAAACAGG---ATATGATAAAGCTGTTAATCGATCATGGAGCTGATGT 2563
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                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION: 424
                                                                                                                                                 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE TITLE OF INVENTION: STRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 119;
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0.13;
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Pred. No. 0.
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           Safford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-WAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORTIS & Saffo
ADDRESSEE: CVO William S. Frommer
STREET: 530 Fifth Avenue
                                                                Sequence 220, Application US/08709209
Patent No. 5762938
GNEFAL INFORMATION:
APPLICANT: Pacletti, Enzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.5%;
Best Local Similarity 49.6%;
Matches 120; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3209 base pairs
                                                                                                                                   Paoletti, Enzo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                         JS-08-709-209-220
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                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Pacietti, Enzo
APPLICANT: Partaglia, James
APPLICANT: Tartaglia, James
APPLICANT: Tartuction, Jil
TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE TITLE OF INVENTION: RECOMBINANTS
NUMBER OF SEQUENCES: 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,657
FILING DATE: 06-APR-1994
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Curtis, Morris & Safford, P.C
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454310-2550
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06-APR-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        Sequence 39, Application US/08224657
Patent No. 5756102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 4543
REFERENCE/DOCKET NUMBER: 4543
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 840-0712
TELEXAX: (212) 840-0712
TELEXAX: 42506 CURTMS
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
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NAME: Frommer, William S.
REGISTRATION NUMBER: 25,5
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STRANDEDNESS: single
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US-08-224-657-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036
2684 AA 2685
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                                                              RESULT 8
US-08-224-657-39
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2507 IGCIATTGGTAGGAACAGG---ATATGATAAAGCTGTTAATCGATÇATGGAGCTGATGT 2563
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2624 ATATTAAAATATTAATAACTCTATTACTAATAACTCCAGTGGATATGAACATAATACG 2683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                       APPLICANT: Tartaglia, James
APPLICANT: Cox, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
CORRESPONDENCE: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.6; DB 2; 1
Pred. No. 0.13;
0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: U9-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Frommer, Willam S.
REGISTRATION NUMBER: 25,506
REFRENCE/COCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPRENCE: (212) 840-3333
TELERA: 42506GURTMS
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   Curtis, Morris & Safford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          Sequence 68, Application US/08184009
Patent No. 5833975
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.5%;
Best Local Similarity 49.6%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         530 Fifth Avenue
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
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US-08-184-009-68
                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RY: USA
10036
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 53
                                                                                                  2684 AA 2685
                                                              588 aa 589
                                                                                                                                                            RESULT 11
US-08-184-009-68
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                                                                                                                                                                                                                                                                                                                                                                                                             CITY: N
STATE:
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Pred. No. 0.13;
0; Mismatches 119; Indels 3
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
TITING DATE: ....
A24
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION.

FILING DATE: 01-JUN-1,---
CLEASIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Frommer William S.
RRGIGTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-333
TELEFAX: (212) 840-0712
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 3209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Safford
                                                                                                                                                                                                            Tartaglia, James
No. 5766599ton, Elizabeth
Riviere, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Curtis, Morris & Saffo
ADDRESSEE: C/O William S. Frommer
STREET: 530 Fifth Avenue
                                                                                        Sequence 220, Application US/08458101 Patent No. 5766599
                                                                                                                                                                                                                                                                                     Limbach, Keith J.
Johnson, Gerard P.
Pincus, Steven E.
Cox, William I.
                                                                                                                                                                                                                                                                 de Taisne, Charles
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Best Local Similarity 49.6%;
Matches 120; Conservative (
                                                                                                                                                Paoletti, Enzo
Perkus, Marion E.
Taylor, Jill
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                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
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US-08-458-101-220
                                                            RESULT 10
US-08-458-101-220
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APPLICANT:
APPLICANT:
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RESULT

COUNTRY:

STREET:

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2447 AGATAGAGGGCCAAAGTAAATTACAAGGATGTTTACGGTTCTTCAGCTCTCCATAGAGC 2506
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                                                                                                                                           IMMUNODEFICIENCY RECOMBINANT POXVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35.6; DB 2;
Pred. No. 0.13;
0; Mismatches 119;
                                                                                                                                                                                                             SEE: CURTIS, MORRIS & SAFFORD, IS 330 FIFTH AVENUE IN YORK NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
| REFERÊNCE/DOCKET NUMBER: 454310-2690
TĒLECOMŅUNICATION INFORMĀTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/417,210A FILING DATE: 05-APR-1995
    Application US/08417210A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 68, Application US/08458356 Patent No. 5942235
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.5%;
Best Local Similarity 49.6%;
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                    APPLICANT: PAOLETTI, ENZO APPLICANT: TARTAGLIA, JAME APPLICANT: COX, WILLIAM ITITLE OF INVENTION: IMMUNG NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
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APPLICANT: Paolett
APPLICANT: Tartagl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FICATION:
                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA 2685
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                                                                                                                                                                                                                                TITLE OF INVENTION: RECOMBINANT POXVIRUS - RABIES
TITLE OF INVENTION: COMPOSITIONS AND COMBINATION COMPOSITIONS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2507 TGCTATTGGTAGGAAACAGG---ATATGATAAAGCTGTTAATCGATCATGGAGCTGATGT 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2624 ATATTAAAATATATAATAACTCTATTACTAATAACTCCAGTGGATATGAACATAATACG 2683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgtttcagggattggccgtggtaatttattaaagttttggttcgcccaagcaattgctgc 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,969
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.6; DB 2;
Pred. No. 0.13;
0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                             E: Curtis, Morris & Safford, P.C. 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                  RY: United States of America 10036
                                                                                                              Sequence 27, Application US/08486969 Patent No. 5843456 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY ACCENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25.506
REFERENCE/DOCKET NUMBER: 45.406
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 27.
                                                                                                                                                                                  APPLICANT: Paoletti, Enzo
APPLICANT: Maki, Joanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3209 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-486-969-27
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Matches 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                            New
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2684 AA 2685
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588 aa 589

528

2684

RESULT 13

Query Match

408

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RECOMBINANT POXVIRUS - CALICIVIRUS [RABBIT HEMORRHAGIC DISEASE VIRUS (RDHV)] COMPOSITIONS AND
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                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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0.13;
                                                                                                          ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISCHEATTON NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2650
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 840-3333
TELEPAX: (212) 840-313
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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Pred. No. 0.
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FILING DATE: 06-JUN-1995
                                                                                                                                                                                              United States of America
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illarity 49.6%;
Conservative
                                                                                                                                                                                                                                                                  Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
                    TITLE OF INVENTION: [R. TITLE OF INVENTION: US NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-08-471-025-27
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Best Local Similarity
Matches 120; Conserve
  FITLE OF INVENTION:
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APPLICANT: COX, William I.
TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
NUMBER OF SEQUENCES: 217
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,356
FILING DATE: US-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fronmer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
                                                                                   ADDRESSEE: Curtis, Morris & Safford STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:.
APPLICATION NUMBER: US 08/184,009
FILING DATE: 19-JAN-1994
ATTORNEY/AGENT INFORMATION:
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Patent No. 5989561
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Fischer, Laurent
APPLICANT: Legros, Francois-Xavier
                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066URTMS
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 3209 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 120; Conservative (
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US-08-458-356-68
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CNS04TMN
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942.878 Million cell updates/sec
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                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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ALIGNMENTS

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Tetraodon

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1M0309K12 1160 Gmax

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ENTIF21TF ENTEA18TF Drosophil

Drosophil QV1-BT063

AV398733

AW569587 474 bp mRNA EST 18-JUL-2000 si8bhlo.yl Gm-c1031 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1031-1820 5' similar to SW:TCPQ_HUMAN P50990 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;, mRNA sequence. A. Glaster, R. Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Mylle, T., Underwood, K., Steptoe, M., Theislang, B., Allen, M., Bowers, M., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Thi, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Eubic Soybean EST Project
Unpublished (1999)
Contact: Shomaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine ėukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Email: estëwatcon.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430.0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 AW569587.1 GI:7234248 (bases 1 to 474) Glycine max EST. soybean. Glycine. RESULȚ 1 AW569587 LOCUSȚ DEFINȚTION ORGANISM ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL COMMENT REFERENCE AUTHORS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_other:*

em_gss_vrt

gb_gss:* em_gss_tun:* em_gss_hum:*

gb_htc:*

em_gss_inv:* em_gss_pln:* em_gss_pro:* em_gss_rod:*

		Description	AW569587 s188h10.y	AQ769224 HS 3155 B	AK013338 Mus muscu	AZ933264 Gm_ISb001	BB173567 BB173567	AA184415 mt34907.r	AA185888 mt35c07.r	AZ017765 RPCI-23-2		AL108540 Drosophil		_
SUMMARIES		a		AQ769224	AK013338	AZ933264	BB173567	AA184415	AA185888	AZ017765	AA563513	CNS017V6	CNS0077X	CNS0039G
		88	10	13	12	13	10	10	10	13	10	13	13	13
		e Match Length DB I	474	498	1894	446	294	303	412	531	780	1101	914	1101
ø	Query	Match	9.0	5.9	5.8	5.8	5.7	5.7	5.7	5.7	5.7	5.7	5.6	5.6
		Score	39	38.2	37.8	37.6	37.2	37	37	37	36.8	36.8	36.6	36.6
	Result	. 80	1	c 0	3	4	c S	9	7	60	σ	10	c 11	c 12

FEATURES

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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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HS_3155_B2_G11_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3155 Col=22 Row=N, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
University of Washington
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@rasgen.com).
BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_plate=3155 Col-22 Row=N" /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: sperm; Vector: pBeloBAC11; BAC clones in E-Coli DH10B"
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 4.5;
0; Mismatches 123;
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1 (bases 1 to 498)
Mahairas, G.G., Wallace, J.C., Smith, K.,
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/db_xref="taxon:9606"
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Best Local Similarity 47.7%;
Matches 112; Conservative (
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Class: BAC ends
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//lab_nost="buildb"

//lab_nost
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0
                                                                                                                                                                                                                                                  /tissue_type="Williams seedlings, minus the cotyledons" /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 AAAATTTGCTGAAAGTTTTGAAATGATTCCTAGAACTTTGGCTGAGAATGCTGGGTTGAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347
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                                                                                                                                                          /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1031-1820"
                   info@genomesystems.com web site: www.genomesystems.com
Insert Length: 700 Std Error: 0.00
High quality sequence stop: 436.
Location/Qualifiers
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Best Local Similarity 50.8%; Pred. No. 2.7;
Matches 93; Conservative 0; Mismatches 90; Indels
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                                                                                         /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                  /note="putative"
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AZ933264.1 GI:13542581
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Best Local Similarity 60.0%;
Matches 63; Conservative (
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                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome research. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachl, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakwa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatu, N., Hizamoto, K., Hirsoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kato, H., Kawai, J., Kojima, Y., Konno, H., Rouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Sato, H., Sato, H., Sato, H., Sato, H., Sato, H., Sato, H., Sato, F., Sato, H., Sato, F., Sato, H., Sato, F., Shibata, Y., Shibata, R., Shibata, Y., Shibata, K., Shibata, Y., Shibata, K., Shibata, T., Yanamaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasuhishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand CDNA was prepared with the primer adapter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGACTCTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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The RIKEN Genome Exploration Research Group Phase II Team and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 (bases 1 to 1894)
clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                        1 (bases 1 to 1894)
Caralhot, P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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                        clone:2810453L12.
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Sequence on contig Gm_A685_ctg_a near unmapped duplicate of pA685.

For more information, see SoyBase at:
http://genome.cornell.edu/cgi.bin/webAcc/webace?db=soybase&class=Locus. Please see as an authority for the mapping/naming: Cregan P.B.
T. Jarvik, A.L. ush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSQVLFQQLVPLLVKCKDREERRGSVRVSIELQSLSNPVHRKDL
VRLTDDDTDPFLYNLVISEDFQSLKLKQGGLLVDFLAFPQKFIDLLQQQMQEHAKET
PRFLLQLLSSATLLENSPVLLNVVENPFKHITHLSIKLLPGNDVEIKKFLAGCUKCS
KEEKLSLTRSLDDVTRQLHITQFTLSEKMQELDKLRSEWASHTASLTNKHSQELTAEK
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DLNTLMGKIKLKNTVTOOEKLLAEKEEMLOKERKESODAGGFLRAKEGEVCRLOGEO
TTYOKLEESKOLLKNNEKLITWLNKELNENOLVRKODTLGTSATPHSTSNSTIRSGL
SPNLAVVDRLNYPSGIGYPVSALTFONAFPHVVAAKNTSHPISGPKVAKC"
397 c 1 others
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                                                                                                                                                /clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10, 11 days embryo"
132. .1814
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ELKAKLAGVEEELQRAKQEVLSLRRENCTLDTECHEKEKHINQLĢTKVAVLEQEIKDK
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Gm_ISb001_045_J24R ISU Soybean BAC Library (pBeloBAC11 HindIII)
Glycine max genomic clone Glycine max genomic, DNA sequence.
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Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St.
Tel: 612 625 2225
Fax: 612 625 9728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 gaygctaatagttttacaaattataaaggattttccgctctatat 528
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Danesh, D. and Young, N.D.
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Pred. No. 6.9;
0; Mismatches
                                                                                                       /db_xref="MGD:MGI:1905655"
/db_xref="MGD:MGI:1920026"
                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAB28799.1"
/db_xref="G1:12850640"
/organism="Mus musculus"
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                                                                      /db_xref="taxon:10090"
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Query Match
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci; A., P., Endo, T., Fukuda, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, I., Kojima, Y., Kondo, S., Kurihara, C., Kuchaka, Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Matsuyama, T., Miki, R., Mizuno, Y., Sato, K., Shibata, Y., Shibata, Y., Shingemoto, Y., Shinaqawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yasunishi, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yasunishi, H., Yakawa, A., Takahashi, F., Tominaga, N., Toya, Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yokota, T., Yoshida, K., Yoshida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anote—"Vector: pBelloBAC1; The ISU BAC library (Marek and Shoemaker, Genome 40:420, 1997) was constructed using the Hindiii site in pBeloBAC1! The library consists of approximately 40,000 clones with an average insert size of 150 Kb, equal to 4 haploid genome equivalents. Screening of the library is done by hybridization of high-density colony filters. Two high density filters, each containing 18,432 clones (doubly spotted) represent the portion of the library screened.
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кауа, т.т. VanToai, D.G. Lohnes, J. Chung, and J.E. Specht. 1999а.
An integrated genetic linkage map of the soybean genome. Crop Sci.
39:1464-1490.
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BB173567 RIKEN full-length enriched, adult male hypothalamus Mus
musculus cDNA clone A230046106 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3847"
/clone_lib="ISU Soybean BAC Library (pBeloBAC11 HindIII)
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                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max genomic clone"
/tissue_type="primary leaves"
/dev_stage="cotyledon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                               Seq primer: M13R
Class: BAC ends.
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Email: genome-reségsc.riken.go.jp,
URL:http://genome-reségsc.riken.go.jp,
URL:http://genome-reségsc.riken.go.jp,
URL:http://genome-reségsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunah,Y., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Haysahizaki,Y., Ozawa,Y., Muramatsu,M., Okazaki, Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
Highh-efficiency full-length CDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGGAGAAGCATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
177-22 Sublication Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Site_1: Sal1: Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 taatgaaccctttagcaaaggctacgaagactacgttaaatggaaaagaaaacctagctt 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 ggtttattggaggaactttagggggactcagaaagctggagactggtctgccacagtac 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.2; DB 10;
Pred. No. 7.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="hypothalamus"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="A230046106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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                                                                                                                Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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AA184415 303 bp mRNA EST 17-FEB-1997 INTAGO7.rl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:623004 AA184415
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:10090"
/clone="lwAGE:623004"
/clone_lib="Soares mouse 3NbMS"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 279.
Location/Qualifiers
1. 303
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J
                                                                                                        AA184415.1 GI:1768064
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                                                                                                                                                  house mouse.
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Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:383828
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JOURNAL
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                                                                                      ACCESSION
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KEYWORDS
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AALBSB88 412 bp mRNA EST 17-FEB-1997 mt35cO7.r1 Scares mouse 3NbMS Mus musculus cDNA clone IMAGE:623052 AALBSB88
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pyly3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and Mretina Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                         Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1990)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:623052"
/clone_lib="Soares mouse 3NbMS"
/sex="male"
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Pred. No. 9.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                         AA185888.1 GI:1772287
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                  SOURCE ORGANISM
                                                      DEFINITION
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AUTHORS
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JOURNAL
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KEYWORDS
             AA185888
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GSS.

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

DEFINITION

LOCUS

RESULT AZ017765

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                                                                                                                                                                                                                                                                                                       AA563513 780 bp mRNA EST 18-AUG-1997
JEO0F007.QF3 PME-SD.96 Schistosoma japonicum cDNA clone SJPF007 5',
mRNA sequence.
AA563513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 780)
Expr.J. and Brindley,P.J.
Expressed sequence tags (ESTS) from a cDNA library of Schistosoma
japonicum (Philippine strain) Egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma japonicum. Schistosoma japonicum. Schistosoma japonicum Bukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths; Rakaryota; Metazoa; Platyhelminthes; Rabditophora; Bulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosoma.
Contact: Brindley, P.J.
Molecular Parasitology Unit
Queensland Institute of Medical Research
300 Herston Road, Qeensland 4029, Australia
Tel: 61 7 3362 0413
Fax: 61 7 3362 0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Schistosoma japonicum"
/strain="Philippine strain"
/db_xref="taxon:6182"
/clone="SJPF007"
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/dev_stage="Egg"
/lab_host="Rabbit"
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                                                                              146 tgaaatacaaatactgtgtttggcagtggct 176
                                                                                                                 High quality sequence stop: 780.
Location/Qualifiers
1. 780
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/sex="Mixed sex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: paulB@qimr.edu.au
PCR PRimers
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Insert Length: 1100 S1
Seg primer: T3 Reverse
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AA563513
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Mouse BAC End Sequences from Library RPCI-23
Moublished (1999)
Other GSSs: RPCI-23-265B4.TJ
Contact: Shaying Javan, Canomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fex: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhaoettgr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 265 row: B column: 4
Seq primer: T7
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//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI: Site_2: ECORI: Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                A2017765 531 bp DNA GSS 25-FEB-2000 RPCI-23-265B4, TV RPCI-23 Mus musculus genomic clone RPCI-23-265B4,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 531)
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                        5.7%; Score 37; DB 13; Length 531;
ilarity 52.3%; Pred. No. 9.7;
Conservative 0; Mismatches 72; Indels
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/strain="C57BL/6J"
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/clone_lib="RPCI-23"
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Query Match Best Local Matches 7

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                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genome survey sequence T7 end of BAC BACN37U12 of DrosbAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                   taatttattaaagttttggttcgcccaagcaattgctgctaactatgatcctaaagaggc 488
                                                                                                                                                     452 TTATGTATTAGAGTTTTTGTTTTAGAAAAACTACAACTGACTATTCTGTAATAAACAT 511
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                                                                                                      489 taatagttttacaaattataaaggattttccgctctatatatgta
                                                DB 10;
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Pred. No. 12;
6; Mismatches 141;
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Pred. No. 12;
0; Mismatches
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/clone="BACN37J12"
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Similarity 59.0%;
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"Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo.Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: na bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                           GSS' 03\text{-JUN-1999} ne survey sequence T7 end of BAC # from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              829 ANN'TTAAAGGBWAAAWRRSAAAATWTKTGGGKTTKGSGAMAMAAAAAKGARAGGGGAAAA 770
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 914)
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                                     531 gratggcatcacagattctctatcattcagagcttatggggcttactccaaa 582
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38.9%; Pred. No. 13;
ive 27; Mismatches
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                                                                                                                                                                                  Drosophila melanogaster genome BACRISE13 of RPCI-98. library frefily), genomic survey sequence.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR15E13"
                                                                                                                                                                                                                                                                                                                                                              GI:4945392
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741 RAGTAGRKWRRTWKRRWKRRDTRWDDADADDTARDDRRRRGDDGADAGKGKKTGRKRRRR 682
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

By 191 91006 EYRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Nr. The library is named RPCI-98 and was constructed by partial EcoxI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library, or filters for hybridzation from the BACPAC Resource Center can be found at http://worper.end.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC \# BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db.xxef="texon:7227"
/clone_lib="RPCI-98"
/clone="BACRO8K10"
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ilarity 13.9%; Pred. No. 14;
Conservative 247; Mismatches 250;
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64 c 131 g
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Drosophila melanogaster
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  DEFINITION
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                                                                ACCESSION
                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                            AUTHORS
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre C'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence T7 end of BAC BACO BACO DrosbAC library from Drosophila melanogaster (fruit Lly), genomic survey sequence.
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DRATWDRTDAWWADAAWWTTTDTDTDDWDKRDRRRKGARRRRTTARAAWDWWTWKAWDW
                                                                                                   tetetateatteagagettatggggettaetteeaaaccageaaacgataaaeteggeagt
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/plasmid="PBeloBAC11"
/db.xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03K20"
/note="end: T7"
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                                                                                                                                                                                                                                                           561 ATWITWAARAAWWAWAWATTIAIWTITWITIT 525
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Entamoeba histolytica Sheared DNA Entamoeba histolytica
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1 (bases 1 to 846)
'Loftus, B., van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
                                                                             tygtttattggaggaactttagggggactcagaaaagctggagactggtctgccacagta 366
                                                                                                                        94 TGAGTGAACTTTTTAGCATAGAATTCTTAAGCAAATAAAATTTAAAACGTAAATTCCATAT 153
                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
       Pred.
                                                                                                                                                                                                                                                                     367 cúttatgagtatgtcgaagcettgt 391
                                                                                                                                                                                                                                                                                                                     214 TGGTTTTGGTTTTTCAAGACAGGGT 238
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  Best Local Similarity 53.1%;
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                              AZ324640 555 bp DNA GSS 29-SEP-2000
1M0046J11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0046J11 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 55)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Longarcers,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
Mouse whole genome scaffolding with paired end reads from 10kb
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Seg primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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Insert Length: 10000 Std Err
                                                  gtaatttattaaagttttggtt 449
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AZ324640.1 GI:10380569
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Fax: 801 585 7177
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TITLE

COMMENT

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/db_xref=_mailings
/db_xref=_faxon:5759"
/clone_lib="Entamoceba histolytica Sheared DNA"
/clone_lib="Vector: ph051; Site_1: BSt 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoceba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kD). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Email: entaetigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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/strain="HM1:IMSS"
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Pred. No. 17;
0; Mismatches
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High quality sequence stop: 832.
Location/Qualifiers
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Seq primer: M13-Forward
Class: shotgun
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Length DB ID Description	6 AX045137 1 CHT76KDA 6 AX045131	1 AE001654 1 AE002165 1 AP002547 6 AV0/5136	1852 6 AX045133 AX045133 Sequence 150 6 AX14067 AX14067 Sequence 816 6 AX105043 AX105043 Sequence 1200 6 AX052220 AX092220 Sequence	6 AX105044 6 AX105036 6 AX105037	12 AY029367 6 AX072889	6 E36262	6 E36259 6 AX001324	6 E3250 1 AE001333 6 AX019231 6 I66494	6 AX155814 1 MCU51235 6 AR077332	AKUU8322 ARO27306 ARO35771 ARO37631	6 AR079063 6 AR079063 6 AR070063	6 116740 6 170472	b 192332 1 STRSURPROA 6 AR083872	9 HSA225093 9 HSA225092 1 AE002357	913 6 AR054408 913 6 AX080641	ALIGNMENTS		2238 bp DNA	from Patent WO0066739.	1 GI:11343736	Chlamydophila pneumoniae. Chlamydophila pneumoniae	Hacceria; Chlamydiales; Chlamydiaceae; Chlamydophila. 1 (bases 1 to 2238) Murdin,A.D., Oomen,R.P., Wang,J. and Dunn,P. 1 (chlamydia) antigens and corresponding dna fragments and uses	-NOV-2000; CA)	12238 /organism="chlamydophila pneumoniae" /ar.worfe====================================	/db_xrei="taxon:bjjg"
Query e Match	93.	9 9 9 9	78 78 10 44	444	444	4 4	4 4 4	ա ο 4 4 1 4 α α α α . ω ο α ν . ι	m m m r	n m m m	. m m m		, w w	m m m					Sequence AX045137	X045137.1	hlamydop	acterla; (bases urdin,A.	thereof Patent: W Aventis P		
ult No. Score			8 1155.4 9 146.8 10 65														[.] -		DEFINITION S ACCESSION A		SM	REFERENCE 1 AUTHORS M TITLE	JOURNAL F	source	
Result No.		υυ		ů	1.			<u>.</u>			. 1		;				RESULT	AX045137 LOCUS	DEFI	VERSION KEYWORDS	SOURCE	REFEI AU' TI'	O.D E.A.R.		
GenCore version 4.5 Copyright (c) 1993 - 2000 Computer 1.td	using sw model	Run on: February 7, 2002, 19:27:24; Search time 12230.8 Seconds (without alignments) (Without alignments)	ו ו	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1472140 seqs, 8248589755 residues	Total number of hits satisfying chosen parameters: 2944280	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1: gb_ba:* 2: ch h+c.*	3: 9b_in:* 4: 9b_om:* 5: 9b ov:*	6: gb_pat:* 7: gb_ph:* 8: ch_ph:*	9: 95_pr:* 10: 95_ro:*						em_ro				35: cm_htg_inm:: 34: cm_htg_in:* 35: cm_htg_other:* 36: cm_htg_other:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	P

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CAGACAGATGCTACAGCGACACAGATAGAGAAAGATGGAAATGCGATTAGGGATGCATAT 1545
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L23921.1 GI:435961
76 kDa protein.
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Chlamydophila pneumoniae
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QQELAAQARAAKAGDDSAAAALADAQKALBAALGRAGQQGGILNALGGIASAAVVSA
GVLLAQVLWIRRAKYQAYVBQKLISEEDLNSAVDHHHHH"

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               protein
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   766. .2238
/note="unnamed
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/organism="Chlamydophila pneumoniae"
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1. .2148
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                                                                                                                                                          Length
                                                                                                                                                          DB 1;
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                         93.2%;
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Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila
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/db_xref="taxon:83558"
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/note="unnamed protein product"
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Sequence 1 from Patent WOU066739.
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REMADAWYCGAQITELAKRASDNOAILDSLGKLTSFDLLQAALLOSVANNIKABELL
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QQELAQARAKAGADSAAALADAOKALEAALGKAGQOQGILNALGQIASAAVSA
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NNVSTPALTRSVPRARTEARGPEKTDOALARVISGNSRTLGDVXSQVSALGSVWQIIQ
SLENGANNEEIRQKLTSAVTKPPQFGYPVQLSNDSTQKFIAKLESLFAEGSRTAAEIK
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Pred. No. 0;
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Chlamydophila pneumoniae CWL029
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
I (bases 1 to 10421)
Ralman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
                              Fan, J., Olinger
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Grimwood,J., Davis,R.W. and Stephens,R.S.
Direct Submission
Submitted (01-DEC-1998) Program in Infectious D
of California, 235 Earl Warren Hall, Berkeley,
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AE001654.1 GI:4377031
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.5%;
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MYQEANETVEGNCLTTANGAIQPDLGGFIREAMTWIGTVEADYVSRAQRILMEENTA
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                                                                                                                                                                4193 AACATAGATTCAGCTAAAGCAGCAATCGCTACTGCTAAGACAAAAAATAGCTGAAGCTCAG
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                        4793 AACAGCTCGTCTTCTACTAGCAGATCTGCAGACGTGGACTCAACGACGGGGCGACCGCACCT
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                                                                                                              gtcactaatataaaggatacagcggctactgatgaggaaaccgcaatcgctgcggagtgg
                                                                                                                                                                                                                                                 cagactgctcttctccaatctgtagcaaacaataacaaagcagctgagcttcttaaagag
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                                                                                                                                                                                                                                                                                                                                                                                                   cagacagatgctacagcgacacagatagagaaagatggaaatgcgattgggggtgcatat
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/translation="MLMMLMMIIGITGGSGAGKŢTLTQNIKEIFGEDVSVICQDNYYK
DRSHYTPEERANLIWDHPDAFDNDLLISDIKRLKNNEIVQAPVFDFVLGNRSKTEIET
IYPSKVILVEGILVFENQELRDLMDIRIFVDTDADERILRRWVRDVQEQGDSVDCIMS
RYLSWYKPMHEKFIEPTRKYADIIVHGNYRQNVYTNILSQKIKNHLENALESDETYYM
VNSK"
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hote="similar to SP:P31218 GB:X71492 PID:296947 GB:U00096 PID:1736770: identified by sequence similarity; putative" /codon_start=1
                                                                                                                                                                                                                                      Chlamydophila pneumoniae AR39.
Chlamydophila pneumoniae AR39
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (bases 1 to 12548)
Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., Mitte, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Read, T.D., Brunham, R.C., Shen, C., Gill, S.R., Heidelberg, J.F., White, O., Hickey, E.K., Peterson, J., Umayam, L.A., Utterback, T., Berry, K., Bass, S., Linher, K., Weidman, J., Khouri, H., Craven, B., Bowman, C., Dodson, R., Gwinn, M., Nelson, W., DeBoy, R., Kolonay, J., McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. McClarty, G., Salzberg, S.L., Eisen, J. and Fraser, C.M. Submission
Submitted (01-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
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30-MAY-2000
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LNRLEKQFFVKGSVVDMNTFVPSETSTTEKAATNAMKYKTCVWOMLVGKHSQVPWING
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AYGAYSKPANDKLGSDFTFRKFDLGIISAF"
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PPPTFDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEW
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GVPPAAASIGSSVKQLYKTSKSTGSDYKTQISAGYDAYKSINDAYGRARNDATRDVI
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ALSFETNSLFIQQVLVNIGSLYSGYLQ"
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NSISNIDSAKAAIATAKTQIAEAQKKFPDSPILOEAEOMVIQAEKDLKNIKPADGSDV
PNPCTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFROMIHMFNTENPDSQAA
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SGIYALRHLMARLQSENTWAALLNPNWIFPPTSWTDKKHSRPQASSPRAPSSOTPT
SUSAAALALVAVIDGGLAELVASVTEIDLGALSTISTVRQLMASYLGLTTLTABOEK
VVFSSSXVPSERNLLEHVQERAABIOAKQEETRAVLEAKGSFEEIBALKEYPDIY
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YLTDRQIAEYRGKITKVYQNSIQNLSETKRVVENNRSMLETQLSMFQQAQNCFVTWIS
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ATAYQPANETVEGNCLTTANGALQPDLGGFIREMATNVGTVEADVYSNAQRILNEFWTA
ATAYLQLQUQIAELQKADLDDGRASFTENRKFAVAMITSESLGDALISMILNSQ
LPKQERFLKPLIEBINENNLADANDALNSILQITNEFSTFGYYYSLSSYLVQSKTGQNLF
                                                                                                                                                                                                                                                                                                                      /translation-"MKKQVYQWLASVVLLALTISGYAELPLSEQKVKSHTYTTLDEVK
DYLSKRGFVETRKQDGVLRIAGDVRARWLYFREDIKNPSDKDKYNPLPVNRYRSEFYL
                                                                                                                                                                                                                                                                                                                                                                                     YIDYRAERNWLSSKMNWTAIAGGENTAAGVDINRAFLGYRFYKNPETRTDFFMEIGRS
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                                                                                             /note-"conserved hypothetical protein; identified by Glimmer2; putative"
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/protein_id="AAF37915.1"
/db_xref="G1:7188958"
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/db_xref="G1:7188956"
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/gene="CP0019"
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/db_xref="G1:7188957"
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                                                                                                                                                                                              /transl_table=11
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/transl_table=11
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/gene="CP0018"
7488. .9443
/gene="CP0018"
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/qene="CP0017"
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Best Local Similarity 99.5%;
Matches 1374; Conservative
                                 CDS
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                                                     EKLAQECDPETTPVAMYCTGGTRCELYSPVLLEKGFKEVYQLDGGVTAYGQQVGTGKW
LGKLFVFDDRLAIPIDESDPDVAPIAECCHCQTPSDAYYNCANTDCNALFLCCDECIH
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DCITLGISFVNFHPGAALKSSKEDCMNKIVSSFSQSAPLFDSSPPLVVLLETTAGQGT
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YLRAFHLNDSMFPLGANKDRHAPLGEGYIGKESFKFLMTDERTRKIPKYLETPGGPEN
GINGQFSGYEPHAELYMQWLKERPNFSKIKFKIHHIKENIFPRITVKYRKELAALGCE
                              /DLSKQAKHISPQEWHEKLQENRCLILDVRNNYEWKIGHFDNATLPDIQTFREFPEYA
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SDYGLQLEEKQKLKACYGMIMEKQLVKAFKEVIHKQGNVAQMFLERFECRLDNMVYRM
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VAAFWLGFRTVFFLRKILGGLILEQAFIPHFEFLRAQSLDRAAFFFRRFSRLIKGSTI
IFTLLIEAVLAVVLQYVEEGTYDMILLTMILLPCGIFLAMYNVNGALLHCENKFFGVG
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NIVLSLVLGRWVLKDVSGISYATSITAWVQLYFLWYYSSKRLPMYSKLLWESIRRSIK
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PID:405898 GB:U00096; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="conserved hypothetical protein; identified by Glimmer2; putative"
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M. Submitted (04-JUL-2000) to the DDBJ/EMBL/GenBank databases.

Mutsunori Shiral, Yamaguchi University School of Medicine,
Mutsunori Shiral, Yamaguchi University School of Medicine,
Department of Microbiology; 1-1-1 Minamikogushi, Ube, Yamaguchi
755-8565, Japan (E-mail:mshiral@po.cc.yamaguchi-u.ac.jp,
Tal:181-886-22-2227, Fax:81-8386-22-221, pax:81-836-22-215)

On Sep 15, 2000 this sequence version replaced g1:6172298
g1:6172300 g1:6172396 g1:6172398 g1:8978889.
AB033786-AB033787, AB033816-AB033817; Submitted (25-Oct-1999).

ES Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chlamydophila pneumoniae J138 (strain:J138) DNA.
Chlamydophila pneumoniae J138
Chlamydiales; Chlamydiaceae; Chlamydophila.
1 (sites)
Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K., Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T.
Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWLO29 from USA
                                                              8628 AIGTICAATACGGAAAATCCIGAITCICAAGCTGCCCAACAGGAGCICGCAGCACAAGCI 8687
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AP002547 AB033786 AB033787 AB033816 AB033817 BA000008 AP002547.2 GI:10176693
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complement(1358. .2917)
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Query Match Best Local Similarity

1081 gatgatgctgaaaatgagaccgcttccattttgatgtctgggtttcgtcagatgattcac 1111111111111111111111111111111111	Db 1241 ATGTTCAATACGGAAATCCTGATTCTCAAGCTGCCCAACAGGAGCTCGCAGCAGCT 1300	Oy 1261 getttagaageggetetaggtaaagetgggeaacaacagggeatacteaatgetttggga 1320 	<pre>Qy i321 cagatcgcttctgctgctgttgtgagcgcaggagt 1355 ,</pre>	AX045133	110N Sequence 3 110N Facent 110N AX045133.1 GI:11343732 DS GEORGE 3 1 GI:11343732	le. le Chlamydiacea	Murdin, A.D., Oomen, R.P., _i(chlamydia) antigens a thereof Patent: WO 0066739-A 3 0	Aventis Pasteur Limited (CA) FEATURES 1.0.0 (2011) (CA) Source 1.1852 (A) Agranism="Chlamydophila pneumoniae"	/db_xtel="taxon:83538" 10.1752 /note="unnamed protein product" /codon_start=1	/transl_table=11 /protein_id=(CAC1338.1" /db_xref="G1:1134333" /translation="MSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPTFDDYKT	QAQTAIDITTSTSLADIQAALVSLQDAYVNIKDYATDEETAAAABWEKNADAYKV GAQITELAKXASDNQAILDSCKLISFELQAALLQSVANNAKABLLKEMQDNPVVP GKTPAIAQSLVDQTDAATAYOIEKOGNAIRDAYFAQONASGAVENAKSNNSISNIDSAK AAIATAKTQIAEAQKKFPDSPILQEAEQWVIQAEKDLKNIKPADGSDVPNPGTTVGGS	RQQSSLGSILVSBILLDDAENETASILLMSGFRQMTHMFNTENDSQAAQQBELAAQARA ARAAGDDSAAAALADAQKALLEAALGKAGOQGGILNALGGIRASAVVSAGVPPAAASSI GSSVKQLYKTSKSTGSYTATSAGYDAYKSIINAYGRANDATROVINNYSTPALTR SVPRARTEARGPEKTDQALARVISGORSRTLGDVXSQVSALQSVWQITQSNPGANNEEI	ROKLTSATYRPPORGYPYVQLSNDSTOKFIAKLESLFAEGSRTAAEIKALSFETNSLF IQOVLVNIGSLYSGYLO" BASE COUNT 578 a 409 c 407 g 458 t ORIGIN	itch 78.6%; Score 1155.4; DB 6; Length 1852; al Similarity 99.4%; Pred. No. 9.3e-271;	Marches 11/0; Conservative U; Mismatches 6; Indels 1; Ga 205 atgagtctggcagataagctggtattgcttctagtaacagctcgtcttctactagcaga 	DD 1 ATGAGICTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
50; Conservative 0; Mismatches 5; Indels ggttaatcctattggtccaggtcctatagacgaacagaacgcacacctccg [IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 161 CTTCTGCTCAAGGACGCGAGTGCAGCAAATAAGAGTGCGGAAGTCTCAAAGAATA 220 Qy 121 gcaggtgcggaagctaaagcatcaagaacctaaagaacctaagaccgattctgtagagcgatggagcatc 180 Db 221 GCAGGTGCGGAAACTAAGCATAACAATTAACAATTCTAAGAACCAATGAACAATCAAAAATT	181 ttgcgttctgcagtgaatgctctcatgagtctgcagataagctgggtattgcttctgtt	.gcagacgtggactcaacgacagcgaccgc 	Oy 301 acgcctcccacccacttgatgattataagactcaagcgcaaacagcttacgatact 360	Oy 361 atcttacctcaacatcactagctgacatacaggctgctttggtgagcctccaggatgct 420	Oy 421 gtcactaatataaaggatacagcggctactgatgaggaaaccgcaatcgctgcggagtgg 480 	Oy 481 gaaactaagaatgccgatgcaattaaagttggcgcaaattacagaattagcgaaata 540 	Oy 541 gcttcggataaccaagcgattcttgactctttaggtaaactgacttcttcgaccttta 600 	Oy 601 cagactgctctcccaatctgtagcaaacaataacaagcagctgagcttcttaaagag 660	Oy 661 atgcaagataacccagtagtcccagggaaaacgcctgcaattgctcaatctttagttgat 720 	Oy 721 cagacagatgctacagcgacacagatagagaaagatggaaatgcgattggggatgcatat 780 	Oy 781 tttgcaggacagaacgctagtggagctgtagaaatgctaaatctaataacgtataagc 840 	Oy 841 aacatagattcagctaaagcagcaatcgctactgctaagacacaaatagctgaagctcag 900 	Oy 901 aaaaagttccccgactctccaattcttcaagaagcggaacaaatggtaatacaggctgag 960 	Qy 961 aaagatcttaaaaatatcaaacctgcagatggttctgatgttccaaatccaggaactaca 1020 D 1061 AAAGATCTTAAAAATATCAAACCTGCAGATGGTTCTGATGTTCCAAATCCAGGAACTACA 1120	Oy 1021 gttggaggctccaagcaacaaggaagtagtattggtagtattcgtgtttccatgctgtta 1080 1021 gttggaggctccaagcaacaaggaagtagtattggtagtattcgtgtttccatgctgtta 1080 1121 GTTGGAGCGCTCCAAGCAACAAGAAGTAGTAGTAGTAATTCGTGTTTCCATGCTGTTA 1180 1

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Qy Db	1165 961	tctcaagctgcccaacaggagctcgcagcacaagctagagcagcgaaagccgctggagat 1224
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Qy Dp	1345 1141	agcgcaggag-tcctcccgctgcagcaagttctatgg 1380

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Nucleic acid primers and probes for detecting Chlamydia pneumoniae
Patent: US 6210876-A 8 03-APR-2001;
Location/Qualifiers
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Agkistrodon contortrix.
Agkistrodon contortrix
Belazooa: Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
1 (bases 1 to 816)
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/db_xref="taxon:8720"
/note="Fragment of fibrolase of Agkistrodon contortrix"
a 219 c 168 g 209 t
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Sequence 19 from Patent W00125445.
AX105043
AX105043.1 GI:13921205
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/organism="unknown"
. 34 c 40 g
                                                    Sequence 8 from patent US 62
AR144067 GI:15105934
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                                                                                                                                                                                                                                                                  Unclassified.
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Ouery Match
4.4%; Score 65; DB 6; Length 816;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 65; Conservative 0; Mismatches 0; Indels

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Agkistrodon contortrix.
Agkistrodon contortrix

Agkistrodon contortrix

Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.

1 (bases 1 to 1620)

Boone, T. C. Li, H. and Mann, M.B.
Fibrinolytically active polypeptide
Patent: WO 0125445-A 12 12-APR-2001;
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a 329 c 291 g 358 t
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Coding sequence of native pro-fibrolase of Agkistrodon contortrix" 337 g 439 t
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J. 3.2e-05;
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complement(1. .1620)
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4.4%; Score 65; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 65; Conservative 0; Mismatches 0;
                                                                                                                                                                Query Match 4.4%; Score 65; DB Best Local Similarity 100.0%; Pred. No. 3.2 Matches 65; Conservative 0; Mismatches
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Sequence 12 from Patent WO0125445.
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Sequence 13 from Patent W00125445.
AX105037
Location/Qualifiers
1. .1373
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GRYRCSYQNGSLWALPESDQLELVATGVGPAFSELSAQPGPAVSGGGDVTLQCOTRYGEP
GFALXKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLE
AGPAROYTYGNGSKLISSEDATAELTVSFTETSRSITTSFKESDSP
AGPAROYTYGNGSKLISSEDATAELTVSFTHKVFTTFTSRSITTSFKESDSP
361 c 285 g 258 t
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Tandon, N., Sun, B., Nakamura, T. and Yamamoto, N.
Platelet membrane glycoprotein vi (gpvi) dna and protein sequences, and uses thereof
Patent: WO 0116321-A 36 08-MAR-2001;
OTSUKA PHARMACEUTICAL CO., LTD. (JP)
LOCATION/Qualifiers
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
1 (bases 1 to 1373)
Boone, T.C., Li, H. and Mann, M. B.
Fibrinolytically active polypeptide
Patent: WO 0125445-A 20 12-APR-2001;
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 3.2e-05;
1ve 0; Mismatches 0; Indels
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Sequence 36 from Patent WO0116321.
AX092220
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Sequence 20 from Patent WO0125445.
AX105044
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/db_xref="taxon:9606"
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Synthetic construct his-tagged human friend leukemia integration 1
transcription factor (FLII) gene, complete cds.
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artificial sequence.
1 (bases 1 to 6849)
Ubhi,B.T.S., Rainey,D.R. and Meredith,D.M.
Direct Submission
Submitted (09-APR-2001) Molecular Medicine Unit, Leeds University,
Beckett St, Leeds LS9 7TF, United Kingdom
Location/Qualifiers
1. 6849
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transcription factor"
/protein_id="AaK50442.1"
/db_xref="G1:14017401"
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Anti-coding sequence of native pro-fibrolase of
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                                  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; AgKistrodon.
1 (bases I to 1620)
Boone, T.C. Li, H. and Mann, M.B.
Fibrinolytically active polypeptide
Patent: WO 0125445-A 13 12-APR-2001;
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/gene="FLI1"
/note="ETS transcription factor; involved in the
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/db_xref="taxon:8720"
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100.0%; Pred. No. 3.1e-05;
Live 0; Mismatches 0;
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/db_xref="taxon:32630"
/chromosome="11"
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337 c    379 q    4
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/trans1_table=11
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Aqkistrodon contortrix
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959. .2398
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NMDGKELCKMNKEDFLRATTLYNTEVILSHLSYLRESSLLAYNTTSHTDGSSRLSVKE
DPSYDSVRRGAMGNNMNSGLNKSPPLGGAQTISKNTEQRPQPDPYQILGPTSSRLANP
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AHQQKVNYYPPHPSSARVYSSEFGAASQYWTSPTGGIYPNPNVPRHPNTHVDSHLGS
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1844 c 1734 g 1639 t
                                              PHKINPLPPQQEWINOPVRVNVKREYDHMNGSRESPVDCSVSKCSKLVGGGESNPMNY
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Gaps 1; Length 6849; Indels Score 64.2; DB 12; Pred. No. 4.6e-05; 0; Mismatches 13; Query Match 4.4%; Best Local Similarity 85.6%; Matches 83; Conservative

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7, 2002, 19:30:32 Search completed: February Job time: 13346 sec

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AAH56196
AAQ68903
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AAF31389
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AAT61725
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AAV33264
AAV39470
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

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pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; truncation mutant; fusion gene;
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/*tag= a
/*tote= "This part of the sequence is unrelated to C. pneumoniae 76 kDa gene"
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                                                                                      C. pneumoniae 76 kDa protein truncation mutant fusion gene.
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                                                                                                            76 kDa protein; bactericidal; diagnosis; prevention;
                    BP
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query

Score

Š. Result

/SIDS2/gcgdata/geneseq/geneseqn/NA1999_DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA2000_DAT:*/SIDS2/gcgdata/geneseq/geneseqn/NA2001_DAT:*

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Chlamydia pneumoni C. pneumoniae 76 k

Description

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                                                                                                                                   ; acids encoding a 76 kDa protein from Chlamydia pneumoniae, for vaccinating against Chlamydia infections -
                                                                                                                                                                               The present sequence is a DNA coding for a fusion protein comprituncated Chlamydia pneumoniae 76 kba protein and vector-encoded residues. C. pneumoniae 76 kba protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory diseases uch as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
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P-PSDB; AAY71957.
                          03-MAY-2000;
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                          76 kDa protein; bactericidal; diagnosis; prevention; treatment; phoeumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                respiratory
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          encoding DNA
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Chlamydia infections -
                                                                                                                        pneumoniae 76KDa
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         full-length protein
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llarity 99.5%; Pred. No. 0;
Conservative 0; Mismatches
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P-PSDB; AAY71954.
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Matches 1374; Conserv
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The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AAY3584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AXX34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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                                                                                                                                                 // disease; pneumonia; bronchitis; heart disease; sarcoidosis;
purulent otitis media; erythema nodosum; pharyngitis;
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Best Local Similarity 99.4%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches
                                                                                                                       Nucleotide sequence of the complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae
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                                                                                                                                                                                     vaccine; neutralising epitope; ss
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Chlamydia pneumoniae
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Nucleic acids encoding a 76 kDa protein from Chlamydia pneumoniae, useful for vaccinating against Chlamydia infections –
                                                                                                                                                                                    76 kDa protein; bactericidal; diagnosis; prevention; pheumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; couch; sore throat; hoarseness; fever; vaccine; immunisation; treatment; truncation mutant; ds.
                                                                                                                                                                                                                                                                                         /*tag= a/product= "3/-truncated Chlamydia pneumoniae 76Kpa protein" //fote= "The coding region does not include stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a DNA coding for 3'-truncated Chlamydia pneumoniae 76 kba protein. C. pneumoniae 76 kba protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory diseases uch as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
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                                                                                                                                                                  Chlamydia pneumoniae 76 kDa protein
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99.6%;
                                                                                                     DNA; 1456
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                                                                                                                                              (first entry)
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/*tag= a
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Best Local Similarity 99.6
Matches 1350; Conservative
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Synthetic.
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P-PSDB; AAY71956.
                                                                                                     AAD02065 standard;
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                                                  827217
                               1380
                                                                                                                                                                 3'-truncated
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gotttagaagoggototaggtaaagotgggcaacaacagggcatactcaatgotttggga 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a 76 kDa protein from Chlamydia pneumoniae, useful for vaccinating against Chlamydia infections –
                                                                                                                                                                                                                                                                                                                                                    sinusitis;
                                                                              agagcagcagaaagccgctggagatgacagtgctgctgcagcgctggcagatgctcagaaa
                                                                                                                                                                                                                                                                                                                                                                fever;
                                                                                                                                                                                                                                                                                                                   5'-truncated Chlamydia pneumoniae 76 kDa protein encoding DNA
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                                                                                                                                                                                                                                                                                                                                       76 kDa protein; bactericidal; diagnosis; prevention; pneumonia; upper respiratory tract disease; bronchitis; sin acute respiratory disease; cough; sore throat; hoarseness; vaccine; immunisation; treatment; truncation mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein is used in the diagnosis, prevention and treatment of C. pneumoniae diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kDa
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1..1752
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P-PSDB; AAY71955.
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30-JUN-1999;
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                                                                                                                                               gctactgatgaggaaaccgcaatcgctgcggagtgggaaactaagaatgccgatgcaatt
                                                                                                                                                                                                  aaagttggcgccaaattacagaattagcgaaatatgcttcggataaccaagcgattctt
                                           Length 1852;
normal chest sounds on auscultation). C. pneumoniae sequence also used as vaccines for immunising humans against diseases
                                                        Indels
                         T; 0 other;
                                           DB 21;
                                                        9
                         Sequence 1852 BP; 578 A; 409 C; 407 G; 458
                                           Score 1155.4;
                                                        0; Mismatches
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                                                  Pred. No.
                                            78.6%;
99.4%;
                                                          Conservative
abnormal chest sounds on
             caused by C. pneumoniae
                                                   Best Local Similarity
Matches 1170; Conserv
                                             Query Match
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Nucleic acids containing electron-transfer group, useful as labels in hybridiżation assays, e.g. for genotyping, allowing repeat analyses on
 482 aaactaagaatgeegatgeaattaaagttggegegeaattaeagaattagegaaatatg 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agactgetettetecaatetgtageaacaataacaaageagetgagettettaaagaga
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                                                                                                                                                                                                                                         mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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.9e-14;
hes 278;
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                                      515
                                                    taagaatgccgatgcaattaaagttggcgc
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                                                                                                                                                                                                                             er group; ETM; 1
ss.
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17-MAR-2000; 2000US-0190259
                                                                                                                                                                                   (first entry)
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Best Local Similarity 1.2%.
Matches 8; Conservative
                                                                                                                                                                                                            Oligonucleotide D1835
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                                                                                                                                                                                                                                       Electron-transfer
                                                                                                                                                                                                                                                     gene expression;
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                                                 1020
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tccattttgatgtctgggtttcgtcagatgattcacatgttcaatacggaaaatcctgat 960
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                                                                          Cysteine rich outer-membrane protein; OMP; 60 kDa OMP; 76 kDa OMP; hybridisation; amplification; assay; detection; ds.
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1.1e-32;
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                                                                                                                                                                                 Chlamydia pneumoniae derived oligonucleotides probes for specific and sensitive detection
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Pred. No. 1.1e·
0; Mismatches
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10.0%;
Best Local Similarity 98.7%;
Matches 148; Conservative
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group, useful as labels in allowing repeat analyses on
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                                                                                                                                                                                                                                                                   1082 atgatgotgaaaatgagaccgcttccattttgatgtctgggtttcgtcagatgattcaca 1141
                                                                                                                                                                             aagatettaaaaaatateaaaeetgeagatggttetgatgttecaaateeaggaaetaeag 1021
                                                                                                                                                                                                                         1022 ttggaggetccaagcaacaaggaagtagtattggtagtattcgtgtttccatgctgttag 1081
                                                                                                                                                                                               aaaagttocccgactctccaattcttcaagaagcggaacaaatggtaatacaggctgaga 961
                                                                                                                                              acatagattcagctaaagcagcaatcgctactgctaagacacaaatagctgaagctcaga 901
                                                                                                           agacagatgctacagcgacacagatagagaaagatggaaatgcgattggggatgcatatt 781
                      ttgcaggacagaacgctagtggagctgtagaaaatgctaaatctaataacagtataagca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ybridization assays, e.g. for genotyping, single surface
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids containing hybridization assays, e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide D1875.
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detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                                          Length 936;
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                                                Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                               278;
                                                                                      Score 83; DB 22;
Pred. No. 7.9e-14;
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Conservative 403;
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Best Local Similarity
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electron-transfer group, useful as labels in 
 3. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having
                                 aaactaagaatgccgatgcaattaaagttggcgcgcaaattacagaattagcgaaatatg 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                                                                                                                                                                                                                                                           ETM; mismatch; genotyping;
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; Pred. No. 7.9e-
403; Mismatches
                                                                                                                                  tgttcaatacggaaaatcctgattctcaa 1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Éxample 6; Page 128; 159pp; English
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17-MAR-2000; 2000US-0190259
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nes 8; Conservative
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gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
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Pred. No. 7.9e-14;
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                                                                                                                                                                            (CLIN-) CLINICAL MICRO SENSORS INC
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1.2%; P
                                                                                              26-JUL-2000; 2000WO-US20476.
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Les 8; Conserver
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Synthetic.
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Example 6; Page 128; 159pp; English.
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                                              tgcaagataacccagtagtcccagggaaaacgcctgcaattgctcaatctttagttgatc 721
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17-MAR-2000; 2000US-0190259.
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               two nucleic
                             acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                  Length 936;
             relates to a composition comprising
                                                                                                                                                                                                                                           Mismatches 278; Indels
                                                                                                                                              Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
                                                                                                                                                                                                    Score 83; DB 22;
Pred. No. 7.9e-14;
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                                                                                                                                                                                                                                           403;
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                                                                                                                                                                                                        Query Match 5.6%;
Best Local Similarity 1.2%;
Matches 8; Conservative 40
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                                                                                                               monitoring gene expression.
The present invention acids each contact
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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llarity 1.2%; Pred. No. 3.9e-13;
Conservative 402; Mismatches 281;
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                                                                                                                                                                                                                                                                                                                                                                                                    (CLIN-) CLINICAL MICRO SENSORS INC.
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ID AAF58252 standard; DNA; 936
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gene expression; ss.
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                                                    Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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Pred. No. 7.9e-14;
403; Mismatches 278;
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    Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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Pred. No. 3.9e-13;
02; Mismatches 281;
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                                                                                          Electron-transfer group; ETM; mismatch; genotyping;
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PITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING
NUMBER OF SEQUENCES:
OORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STREET: Illinois
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Pred. No. 3.2e-34;
0; Mismatches 2;
              US-08-273-146-36
US-08-273-146-38
US-08-273-146-40
US-08-448-418-96
US-09-1184-658-7
US-08-211-202-131
US-08-418-94
US-08-961-083-33
                                                                                                                                                                    PCT-US93-01901-30
US-09-260-527-4
US-08-072-610-1
US-08-719-822B-1
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US-08-627-151A-6
US-08-186-222-1
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LENGTH: 150 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA (C. pneumoniae)
US-08+659-473-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/659,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: 1111022
COUNTRY: USA
ZIP: 60064-13500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM 7.0.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08659473
Patent No. 6210876
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INPORMATION:
NAME: Paul D. Yasger
REGIESTRATION NUMBER: 37,477
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-2341
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98.7%;
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   Query Match
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Matches
Search time 243.49 Seconds (without alignments) 1367.295 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-411-329C-20

US-09-411-329C-12

US-09-411-329C-13

US-08-32-463-14

US-08-32-463-14

US-08-32-463-14

US-08-32-463-14

US-08-465-746-1

US-08-469-434-1

US-08-34-1

US-08-35-1

US-08-35-1

US-08-35-1
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                                                                                                                   February 7, 2002, 15:53:37
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Maximum Match 100%
Listing first 45 summaries
                                                                                     nucleic search, using sw model
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seq length: 2000000000
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1470
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Match Length
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Maximum DB
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Query Match
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US-09-411-329C-12
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LENGTH: 1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Fragment of fibrolase of Agkistrodon contortrix
US-09-411-329C-19
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Pred. No. 1.4e-09;
                                                                                                                                                                                               Sequence 19, Application US/09411329C

Patent No. 6261820

GENERAL INFORMATION:
APPLICANT: Boone; Thomas
APPLICANT: Mann, Michael

TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
FILE REFERENCE: A-596
CURRENT FILING APPLICATION NUMBER: US/09/411,329C

CURRENT FILING APPLICATION NUMBER: US/09/411,329C

CURRENT FILING APPLE: 1999-10-01

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 19

LENGTH: 816
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US-09-411329C-20
Sequence 20, Application US/09411329C
Sequence 20, Application US/09411329C
GENERAL INCORNATION:
APPLICANT: BORNATION:
TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
FILE REFERENCE: 4-56
CURRENT APPLICATION NUMBER: US/09/411,329C
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. ...
                                                                                               121 TAAGAATGCCGATGCAGTTAAAGTTGGCGC 150
                                                                            486 taagaatgccgatgcaattaaagttggcgc 515
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Best Local Similarity 100.0
Matches 65; Conservative
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Matches 65; Conservi
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LENGTH: 1373
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US-09-411-329C-19
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Gaps

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Indels

Conservative

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NAME/KEY: misc_feature
LOCATION: (1)..(1620)
OTHER INFORMATION: Complementary (antisense) strand of sense strand (See SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; OTHER INFORMATION: Coding sequence of native pro-fibrolase of Agkistrodon contor
US-09-411-329C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)..(1620)
OTHER INFORMATION: Complementary (sense) strand of antisense strand (See SEQ ID OTHER INFORMATION: 3
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100.0%; Pred. No. 2e-09;.
tive 0; Mismatches 0; Indels
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APPLICANT: Li, Huimin
APPLICANT: Mann, Michael
TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Boone, Thomas
APPLICANT: Li, Huimin
APPLICANT: Man, Michael
TITLE OF INVENTION: FIBRINOLYTICALLY ACTIVE POLYPEPTIDE
FILE REPERENCE: A - 596
CURRENT APPLICATION NUMBER: US/09/411,329C
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 29
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CURRENT APPLICATION NUMBER: US/09/411,329C
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 29
SOFWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 1620
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; Sequence 13, Application US/09411329C
; Patent No. 6261820
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: David W. Clough
: Marshall, O'Toole, Gerstein, Murray & Borun
: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25 (EPO)
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FILING DATE: 05-DEC-1994
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Williams, Samuel Cameron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/08350260A Patent No. 5962255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Han
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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              NAME/KEY: misc_feature

OTHER INFORMATION: Anti-coding sequence of native pro-fibrolase of Agkistrodon contc

OTHER INFORMATION: rtri

US-09-411-3296-13
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                                                                                                                                                                                                        Gaps
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                                                                                                                                DB 4; Length 1620;
2e-09;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 54.4; DB 1;
Pred. No. 6.6e-06;
18; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                  4.4%; Score 65;
100.0%; Pred. No.
:ive 0; Mismatc
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTONNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.78;
9.38; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 9.3%
Matches 43; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      Conservative
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Best Local Similarity
Matches 65; Conserva
OTHER INFORMATION: 2
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ZIP: 22313-0299
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US-08-232-463-14/c
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Sequence 1, Application US/08072070
Separation 1, Application US/08072070
GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Pred. No. 8.5e-06;
0; Mismatches 14;
              FILING DATE: 10-JUL. 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR.1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG WREGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 38,107
REFERENCE/DOCKET NUMBER: 38,107
REFERENCE/DOCKET NUMBER: 38,107
RELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: PCT/GB91/01134
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 80.8%;
Matches 59; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:
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US-08-072-070-1
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982 cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
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Patent No. 5679768
GENERAL INFORMATION:
APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: PROTEIN A
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 50.6; DB 1; Length 2085; Pred. No. 4.3e-05; 0; Mismatches 154; Indels. 3
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..2025, 2029..2031, 2035..2085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                APPLICATION NUMBER: US/07/656,773 FILING DATE: 15-FEB-1991 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 415-0810
APPLICATION NUMBER: US/07/835,698 FILLING DATE: 12-FEB-1992
                                                                                                                                         TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.4%;
Best Local Similarity 49.8%;
Matches 156; Conservative
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                           FILING DATE: 12-FEB-1
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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CLONE: JY2008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: Rx1
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LOCATION:
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; LOCATION:
US-08-072-070-1
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865 atcgctactgctaagacacaaatagctgaagctcagaaaaagttccccga---ctctcca 921
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  712 CAAAAAGTGGATGCTGAAGAAGTCGCTCCTCAAGCTAAAATCGCTGAATTGGAAAATCAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2085;
                                                                                                                                                                                                                                                                             APPLICANT: BRILES, DAVID E.
APPLICANT: YOTHER, JANET L.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
WUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  :: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
3.4%; Score 50.6; DB 1;
Best Local Similarity 49.8%; Pred. No. 4.3e-05;
Matches 156; Conservative 0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-WAR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
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FILING DATE: 17-MAR-1994
                                                                                                                                                                                                              Sequence 1, Application US/08214164
Patent No. 5728387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W.
REGISFRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 6
TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0813
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
                                              1042 ggaagtagtattg 1054
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127..1983
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ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-08-214-164-1
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                                                                                                                                                                                   US-08-214-164-1
                                                                                                                                                                RESULT
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                     Mattare, Ltd
Jefferson Davis Highway
                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,746
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION: 144
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/048,896
FILING DATE: 15-FEB-1991
PRIOR APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
FILING DATE: 12-FEB-1992
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 415-0810
TELEFA: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDEDNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                        3: Shoemaker and
Suite 1203, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(127..1984)
                                                                                                        COUNTRY: U.S.A.
21P: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
1..2085
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                                                                                     Virginia
                                                                 Arlington
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN: RX1
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                         FILING DATE
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY:
; LOCATION:
US-08-465-746-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE:
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                                                                                         652 AAACTAGAAGAAGCTAAAGCAAAATTAGAAGAGGCTGAGAAAAAAGCTACTACTGAAGCCAAA 711
                                                                                                                                                            922 attottoaagaagoggaacaaatggtaatacaggotgagaaagatottaaaaatatoaaa 981
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: Yother, Janet
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
OWNERS OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELERAX: (703) 521-0378
TELERAX: LUKPAT MASHINGTON
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,065
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/469,434
                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08469434 Patent No. 5753463 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                     1042 ggaagtagtattg 1054
                                                                                                                                                                                                                                                            772 GITCATAGACIAG 784
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LOCATION: 1..2085
FEATURE:
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982 cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
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                                                                                                                                                                                                                    745 atagagaaagatggaaatgcgattggggatgcatattttgcaggacagaacgctagtgga 804
                                                                                                                                                                                                                                                              472 ACAGACAAAGCCGCAAAAGACGCAGCAGATAAGATGATGATGAAGCTAAGAAACGCGAA 531
                                                                                                                                                                                                                                                                                                                                                     532 GAAGAGGCAAAAACTAAATTTAATACTGTTCGAGCAATGGTAGTTCCTGAGCCAGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                    865 atcgctactgctaagacacaaatagctgaagctcagaaaaagttccccga---ctctcca
                                                                                                                         Length 2085;
                  join(127..1983, 1987..1992, 1996..2007, 2011
..2025, 2029..2031, 2035..2085)
                                                                                                                           Score 50.6; DB 1; Length 2
Pred. No. 4.3e-05;
0; Mismatches 154; Indels
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Janet L
STRUCTURAL GENE OF PNEUMOCOCCAL
PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...
17-MAR-1994
N: 530
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08214222
Patent No. 5804193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                3.4%;
                                                                                                                                Query Match
Best Local Similarity 49.89
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Briles, David
APPLICANT: Yother, Janet
TITLE OF INVENTION: STRI
TITLE OF INVENTION: PROJ
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: Shoemaker a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    772 GTTCATAGACTAG 784
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) NAME/KEY:
; LOCATION:
; LOCATION:
US-08-469-434-1
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US-08-214-222-1
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982 cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                592 ITGGCTGAGACTAAGAAAAATCAGAAGAAGCTAAAACAAAAAGCACCAGAACTTACTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(127..1983, 1987..1992, 1996..2007, 2011
..2025, 2029..2031, 2035..2085)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yother, Janet L.
APPLICANT: McDaniel, Larry S.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%; Score 50.6; DB 2;
49.8%; Pred. No. 4.3e-05;
tive 0; Mismatches 154;
                                                                   NAME KOMALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERNCE/DOCKET NUMBER: 454312-2064
TELECOMMUNICATION IRFORMATION:
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae Rx1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08468718
Patent No. 5871943
GENERAL INFORMATION:
APPLICANT: Briles, David E
                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          TELEPAR. 212-588-0500
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 49.8
Matches 156; Conservative
                                                                                                                                                                                                                                                                          TYPE nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1042 ggaagtagtattg 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772 GTTCATAGACTAG 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE
CLONE: JY2008
                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
LOCATION:
US-08-467-852A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     712 CAAAAAGTGGATGCTGAAGAAGTCGCTCCTCAAGCTAAAATCGCTGAATTGGAAAATCAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08467852A
Patent No. 5856170
GENERAL INFORMATION:
APPLICANT: BRIES, David E.
APPLICANT: YOTHER, Janet L.
APPLICANT: WCDANIEL, LAITY S.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50.6; DB 1; Length 2
Pred. No. 4.3e-05;
0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                       join(127..1983, 1987..1992, 1996..2007,
2011
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SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,852A
                                                                                                                                                                                                                                                                                                                                                                   ..2025, 2029..2031, 2035..2085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 Fifth Avenue
                                                                                                              ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 156; Conservative
                     MOLECULE TYPE: protein HYPOTHETICAL: NO
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LOCATION: 1..2085
TOPOLOGY: linear
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Best Local Similarity
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                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                   CLONE: JY2008
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                                      HYPOTHETICAL:
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COCATION:
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                                                              ANTI-SENSE:
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US-08-467-852A-1
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712 CAAAAAGIGGAIGCIGAAGAAGICGCICCICAAGCIAAAAICGCIGAATIGGAAAAICAA 771
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APPLICANT: Paties, David E
APPLICANT: Yother, Janet L
APPLICANT: Wobaniel, Larry S
APPLICANT: Wo, Hong-Yin
TITLE OF INVENTION: PETTOPIC REGIONS OF PNEUMOCOCCAL SURFACE
TITLE OF INVENTION: PROTEIN A
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Slite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHWARE: Patentin 1.25/...25 SCHWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,636
FILING DATE: 20-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50.6; DB 2;
Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
PRIOR APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,896
FILING DATE: 20-APR-1993
TELEPHONE: 20-APR-1993
TELEPHONE: 20-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        Sequence 1, Application US/08246636
Patent No. 5965141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 415-0813
TELEEX: LORFAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC COM)
                                                     1042 ggaagtagtattg 1054
                                                                                               772 GTTCATAGACTAG 784
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Best Local Similarity
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ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virginia
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; LOCATION:
US-08-246-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                                                  RESULT 15
US-08-246-636-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(127..1983, 1987..1992, 1996..2007, 2011
..2025, 2029..2031, 2035..2085)
             ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,718
FILING DATE:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,068
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATE: US/07/656,773
FILING DATE: 15-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae
                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 415-0810
TELEFAX: (703) 521-0378
TELEX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                 COUNTRY: U.S.A.
ZIP: 22202-0286
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN: RX1
IMMEDIATE SOURCE:
                                                          Arlington
                                                                                   Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
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                                                                                                                                                                       MEDIUM TYPE:
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LOCATION:
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; LOCATION:
; LOCATION:
US-08-468-718-1
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is 156; Conservative 0; Mismatches 154; Indels 3; Gaps	745 atagagaaagatggaaatgcgattggggatgcatattttgcaggacagaacgctagtgga 804	472 ACAGACAAAGCCGCAAAAGACGCAGCAGATAAGATGATAGATGAAGCTAAGAAACGCGAA 531	cagtataag	532 GAAGAGGCAAAAACTAAAATTTAATACTGTTCGAGCAATGGTAGTTCCTGAGCCAGAGCAG 591	5 ategetactgetaagacacaaatagetgaageteagaaaagtteeegaeteteea 921	592 TTGGCTGAGACTAAGAAAAATCAGAAGAAGCTAAACAAAAAGCACCAGAACTTACTAAA 651	922 attetteaagaageggaacaaatggtaatacaggetgagaaagatettaaaaatateaaa 981	652 AAACTAGAAGGAGAGGAAAATTAGAAGGGCTGAGAAAAAGCTACTGAAGGCCAAA 711	ıttccaaa	712 CAAAAAGTGGATGCTGAAGAAGTCGCTCCAAGCTAAAATCGCTGAATTGGAAAATCAA 771	1042 ggaagtagtagtagt 1054	772 GTTCATAGACTAG 784
Matches												
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41.2 2.8 616 13 A2525704 AU075947 AU07969 AU0799 AU07969 39 2.7 904 13 AZ69254 39 2.7 904 13 CNS033D4 39 2.7 1013 10 AL564621 8.8 2.6 450 13 FR0025683 8.8 2.6 738 10 AV405991 AZ682538 861 bp DNA AZ682538 861 bp DNA AZ682538 10 AZ692538 AZ682538 AZ692538 AZ692538	Determination of clone HM1:MSS sheared DNA 1) Unpublished (2000) Contact: Brendan J Loft Department of Eukaryoti The Institute for Genom 972 Medical Center Dr. Tel: 301 838 0200 Fax: 301 838 0200 Whall: enta@ftigr.org Clones are derived from DNA library Seq primer: M13-Forwary Class: shotgun High quality sequence sign quality and proposed sequence sign quality and proposed sequence sign quality and proposed sequence sign quality and proposed sequence sign quality and proposed sequence sign quality seq	
0 0 0 00°°°°° 00 000 00 00 00 00 00 00 0	C 41 43 45 3 44 3 3 45 3 45 3 45 3 AZ682538/C LOCUS DEFINITION ACCESSION VERSION VERYWORDS SOURCE ONGANISM REFERENCE	JOURNAL COMMENT COMMENT FEATURES SOUL
4.5 Compugen Ltd. ; Search time 7419.31 Seconds (without alignments) 2129.079 Million cell updates/secaccatcatcatcatcatcat 1470sidues sters: 22703874		results predicted by chance to have a to the score of the result being printed, of the total score distribution. SUMMARIES SUMMARIES Description A2550193 A2550193 A2550193 A314486 BH132709 A4550193 A4550193 A4550193 A4550193 A4672611 BF865301 A263258 A263259 A263258 A263259 A263258 A263258 A263259 A263150 AZ68553 AZ691916 AZ691916 AZ691916
GenCore version 4 Copyright (c) 1993 - 2000 C leic search, using sw model February 7, 2002, 21:32:15; US-09-391-606-3 1470 1 atggttaatcctattggtcc IDENTITY_NUC Gapop 10.0, Gapext 1.0 11351937 seqs, 5372889281 res hits satisfying chosen paramet tength: 0 length: 0 length: 2000000000 Maximum Match 0% Maximum Match 100% Listing first 45 summaries	EST:* 1: em_estfun:* 3: em_estfun:* 4: em_eston:* 5: em_eston:* 6: em_eston:* 7: em_esto:* 7: em_esto:* 10: gb_est:* 11: gb_est:* 13: gb_htc:* 13: gb_htc:* 14: em_gss_hun:* 15: em_gss_hun:* 16: em_gss_ln:* 17: em_gss_ln:* 18: em_gss_ln:* 19: em_gss_ln:* 19: em_gss_ln:* 10: em_gss_ln:*	is the number of ter than or equal rived by analysis and the color of
OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Searched: Total number of Minimum DB seq J Maximum DB seq J Maximum DB seq J		Score and is deal and is deal and is deal and is deal and is deal and is deal and is deal and is deal and is deal and is deal and and is deal and and is deal and and and and and and and and and and

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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Waking small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing. A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ550193 906 bp DNA GSS 14-NOV-2000
ENTCZ54TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 906)
Loftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 AATGCCAGATGAAAATACTGAGATTAAGAAAAAAACAATTAAAAAAGTTACTACAACACG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   798 tagiggagetgiagaaaatgetaaatetaataacagtataageaacatagatteagetaa 857
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 13; Length 861; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 135; Indels
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High quality sequence start: 25
High quality sequence stop: 845.
Location/Qualifiers
1..906
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Contact: Brendan J Loftus
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AZ550193
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al Similarity 48.3%;
126; Conservative
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TITLE
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 484)

2 (J., Lee,N.H., Kirknes; E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee,N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O.S. Sutton, G. Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.D., Cline, T.R., Cotton, M.D., Earle-Hughes J., Fine, L.D., Fitzagerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedhlom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shriley, R., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Li, Y., Ulmke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,
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EST186534 Colon carcinoma (HCC) cell line II Homo sapiens CDNA 5'
AA314486
AA314486.1 GI:1967036
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48.3%; Pred. No. 0.37; i
tive 0; Mismatches 135; Indels
/organism="Entamoeba histolytica"
                      /strain="HM1:IMSS"
/db_xref="taxon:5759"
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Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
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                                                                expression patterns
                                                                                                                                                                                                                                 Fax: 3018699423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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ENTNG59TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 856)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="ArCC (inhost):111272"
/db_xref="taxon:9606"
/close_lib="colon carcinoma (HCC) cell line II"
/cell_type="KM12C"
/cell_line="KM12C"
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EcoRI; Site_2: XhoI"
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                                                        Initial assessment of human gene diversity and explassed upon 83 million nuclectides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                          The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Pred. No. 0.44;
); Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                                                                        Contact: Kerlavage, AR
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/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Site_l: BST i; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Dlamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77.450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Maxing small insert libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 460)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
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                                             Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 946 gtaatacaggetgagaaagatettaaaaatateaaaecetgeagatggttetgatgtteea 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    766 attiggggatgcatattttgcaggacagaacgctagtggagctgtagaaaatgctaaatct 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       826 aataacagtataagcaacatagattcagctaaagcagcaatcgctactgctaagacacaa 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 GAAGCAGTTCTTGTTATGGTTGGTTGTTATTATCTACTACTACAGCA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    886 atagetgaagetcagaaaaagtteeeegaeteteeaattetteaagaageggaacaaatg 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 CAAGCAGAATTAATTCAACAACTCCTAAAACTCTGAAACTGCGAGTGGTGTTCATAGAGAT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 AAAGAATATGCAGAGGAATTAATTAAAGCAGTAGAAGATGTTAAAAGTACTGCAATTGAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              706 caàtetttagttgateagaeagatgetacagegaeaeagatagagaaagatggaaatgeg 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408 AAAAAAGAAGCTGCTGAAGCAAGTGAAGATCCTAAACAAATTGTTGAAGCTACTTTACAA 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 856;
                                                                                                                                                                                                                                                                                                 1. .856
/organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.9%; Score 42.8; Dilarity 46.1%; Pred. No. 1.4; Conservative 0; Mismatches
Email: enta@tigr.org
Clones are derived from the Entamo
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 3
High quality sequence stop: 856.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         /strain="HM1:IMSS
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Mus musculus
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AZ632588/C
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SOURCE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T 3/); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer [5'
rgttaccaarctgaagtgggaggggggggaagggtffttttttttttt
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Chlamydomonas reinhardtii
Eukaryota: Viridiplantae: Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceee; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:585801
Seq primer: -28m13 rev2 ET from Amersham
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       Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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0
                                                                                                                                                                                                                                                                      Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 460;
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/db_xref="taxon:10090"
/clone="IMAGE:1054255"
/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79;
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53.3%; Pred. No. 1.3;
Live 0; Mismatches
                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 453.
Location/Qualifiers
1. 460
/organism="Mus musculus"
                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 g
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Best Local Similarity
Matches 90; Conserv
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JOURNAL
COMMENT
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/usgantame="Cintamygoumous reinintatuli"
/strain="Cc1690 wild type mt+ 21gr"
/db_xref="taxon:305"
/db_xref="taxon:305"
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/clone_lib="Cc. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK- pBluescript II Shr P (4hr, 4hr), Tap-S (30 min, 1hr, 4hr), Tap-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized.
The CDNA was directionally cloned into lambda Zap II (Stratagene) in Sk- plasmids were excised from the lambda ZAP clones by superinfection with Exhassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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1M0487L17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0487L17 F, DNA sequence.
          Lefebvre, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomnonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 3
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Duke University
Duke University
Driam, NC 27708-1000
Tel: 919 613 8159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agctgtagaaaatgctaaatctaataacagtataagcaacatagattcagctaaagcagc 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aatcgctactgctaagacacaaaatagctgaagctcagaaaaagttccccgactctccaat 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744 gatagagaaagatggaaatgcgattggggatgcatattttgcaggacagaacgctagtgg 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hauser, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.9%; Score 42; DB 11; Length 62. Best Local Similarity 46.3%; Pred. No. 2.1; Matches 138; Conservative 0; Mismatches 160; Indels
Grossman, A., Davies, J., Federspiel, N., Harris, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..624
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                                                                                                                                                                                                                                                                                                                                                                                                            Email: chauser@duke.edu
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REFERENCE

JOURNAL

COMMENT

TITLE

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Genome Research Group
National Institute of Radiological Sciences
National Institute of Radiological Sciences
Marayawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: Kmita@hirs.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Petrygota; Neoptera; Bidoptera; Bidoptera; Bidoptera; Bidoptera; Bombycoidea; Bombycoidea; Bombycoidea; Bombycoidea; Bombywoidea; Bombywoidea; Bombyw.

1 (bases 1 to 850)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.

Unpublished (2000)
                                                                                                                   AV406016 Bombyx mori wing disk C108 5th-instar day-3 larva Bombyx mori cDNA clone wdV30506 T3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Bombyx mori wing disk C108 5th-instar day-3 larva"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (5' -> 3')
Project='Silkworm Genome Program in MAFF, and Research for the Project='Silkworm Genome Program in JSPS', see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for whole ESTdb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697 gcaattgctcaatctttagttgatcagacagatgctacagcgacacagatagagaaagat 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 ggaaatgcgattggggatgcatatttgcaggacagaacgctagtggagctgtagaaat 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579 TCACCAATTAAAGAAATTGAAGAAACTACAAAAGAAGCTACACCTGTTCCTGTAGATAAT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          877 aagacacaaatagctgaagctcagaaaaagttccccgactctccaattcttcaagaagcg 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519 GAAGCAGACACCATTGAAACATCTGAAAAGTAAAGGAGACTAGTCCTGTTAAAGAAAAC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="wing disk"
/dev_stage="5th-instar day-3 larva"
149 c 189 g 190 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.8; DB 10;
Pred. No. 2.6;
0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female/male mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bombyx mori"
/strain="C108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                937 gaacaaatggtaatacaggctgagaaaga 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699 CAAAATTTGGTTGGAGATGAAGCAAAGA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:7091"
/clone="wdV30506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                   AV406016.1 GI:6910104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.24
Matches 127; Conservative
                                                                                                                                                                                                                                                                                      domestic silkworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mita K
                                                                                                                                                                                                                                                                                                                 Bombyx mori
  29 AACACAAGC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322
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ORIGIN
                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwWa(2 (gil4732)14) gb]RE129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10°Gold (Stratagene) cells and selected for ampicillin resistance."
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0
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 586)
Dunn,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-"
/note="Vector: PWH042nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                    SIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1011 aggaactacagttggaggctccaagcaacaaggaagtagtattggtagtattcgtgtttc 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1071 catgotgttagatgatgctgaaaatgagaccgottccattttgatgtctgggtttcgtca 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1131 gatgattcacatgttcaatacggaaaatcctgattctcaagctgcccaacaggagctcgc 1190
                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AGAAGGAAGACGAGGAAGCAACAACAGCTAGGGCAGAAGAACTGGAACTTGAAGCCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
Unpublished (2000)
Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC1M0487L17"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 586;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.8%; Score 41.8; DB 13;
51.3%; Pred. No. 2.3;
tive 0; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0487 row: L column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 0487 row: L column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: plasmid ends
High quality sequence stop: 586.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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source

FEATURES

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Gaps

BASE COUNT ORIGIN

Matches

셤 ò 셤

g ò

03-NOV-2000

from Entamoeba histolytica

REFERENCE AUTHORS

SOURCE

FEATURES

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/strain="HM1:IMSS"
/db.ref="taxon:5759"
/dlone_lib="taxon:5759"
/clone_lib="taxon:5759"
/clone_lib="tentamoeba histolytica Sheared DNA"
/rote="vector: pH031; Site_l: Bst I; Constructed at The
//note="vector: pH031; Site_l: Bst I; Constructed at The
//note="vector: pH031; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TiGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to give a
// 450.). The DNA was mechanically sheared to genome
Sequencing a Prescional Approach, eds. M. Vaudin and B.
// Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
AZ536150 842 bp DNA GSS 03-NOV-2000
ENTDB92TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Pel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                  Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HMI:IMSS sheared DNA library
                                                                                                                                                                                                                               Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 842)
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High quality sequence stop: 775.
Location/Qualifiers
1..842
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                                                         genomic, DNA sequence.
AZ536150
AZ536150.1 GI:11093097
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Entamoeba histolytica
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Matches 117; Conservative
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0
                                                                                                                                                         Glycine max
Marayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 TCAGTTGGATAAACATAAAATTCTGGGTTGATGCCTGATATTGAGGCTAAACTAGCTTC 468
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2.8%; Score 41.6; DB 10; Length 762;
Best Local Similarity 47.7%; Pred. No. 2.8;
Matches 122; Conservative 0; Mismatches 134; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
TT: 519 457 1470
Fax: 519 457 3997
                                                                                                                                                                                                                                                                                                                         Harris, N., Chapman, B.P. and Gijzen, M. Gene expression in developing soybean seed coats Unpublished (2000)
               GmaxSC Glycine max cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Seed coats"
/lab_host="E. coli strain XLOLR"
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/db_xref="taxon:3847"
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Location/Qualifiers
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155 c 17
         724 GmaxSC Glycine max
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BE661568.1 GI:9987460
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1 (bases 1 to 762)
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AZ536150/c
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            DEFINITION
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                                                                                           880 acacaaatagctgaagctcagaaaaagttccccgactctccaattcttcaagaagcggaa 939
                                                                                                                                                                418 GCACATITAAATGAATGIATTAAAAGICAGIGAATIAGAAGITAITCAIGAAGAAGIT 359
                                                                                                                                                                                                                   940 caaatggtaatacaggctgagaaagatcttaaaaaatatcaaacctgcagatggttctgat 999
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                                    Gaps
                                    ö
 Length 842;
                                    Indels
Score 41.4; DB 13;
Pred. No. 3.3;
                                    0; Mismatches 126;
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Matches 117; Conservative
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/db xref="taxon:5759"
/db xref="taxon:5759"
/clong-lib="Entamoeba histolytica Sheared DNA"
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/note="Vector: PH621; Site_1: Bst I; Constructed at The
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/note="Vector: PH621; Site_1: Bst I; Constructed at The
/note="Vector: PH621; Site_1: Bst I; Construction Construction: Bst Ph621; Phe A t in method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                        A268553 845 bp DNA GSS 14-DEC-2000 ENTMN43TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                        Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 845)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                     Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 20
High quality sequence stop: 759.
Location/Qualifiers
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Matches 117; Conservative
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Seq primer:
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                RESULT 11
AZ685553/c
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TITLE
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/db_xref="max.mag."
/db_xref="tax.mag."
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/clone_lib="Vector: pH051; Site_1" BSt i; Constructed at The
Institute for Genomic Research (TiGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a
method for Isolate dentification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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AZ691916 876 bp DNA GSS 14-DEC-2000
ENTJK22TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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1 (bases 1 to 876)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HMI: MSS sheared DNA library

Unpublished (2000)
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48.1%; Pred. No. 3.4;
Live 0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 16
High quality sequence stop: 801.
Location/Qualifiers
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                                                                                                                                            AZ691916.1 GI:11829182
                                                                  genomic, DNA sequence.
AZ691916
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Entamoeba histolytica
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/note="Weetor: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: ECORV; Site_2: ECORV; Genomic DNA was prepared from asynchronous blood stage forms of the cloned ANKA isolate of P. berghei grown in laboratory Swiss white mice. The DNA was purified from contaminating host DNA by Hoechst Dye 33258-CsCl ultracentrifugation and precipitated. Purified DNA was ultracentrifugation and precipitated. Purified DNA was digested with mung bean nuclease in the presence of 36-38% formamide at 50 C, as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988 Nucleic Anids Research 16:6883-6896). The ends of the digestion fragments were polished using T4 DNA polymerase, and the fragments size selected in the range 500-2000 bp. These were ligated into the ECORV-cleaved and dephosphorylated pBluescript SK(+) vector. Recombinant plasmids were used to transform E.
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/strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
/db_xraf="taxon:5821"
/clone_lib="Pb MBN #21"
/dev_stage="asexual blood forms"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Entaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium. Enkaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium. Entaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium. Sariton, J. M. R. and Dame, J. B. Cariton, J. M. R. and Dame, J. B. The Plasmodium vivax and P. berghei gene sequence tag projects The Plasmodium vivax and P. berghei gene sequence tag projects. In Parasitol. Today 16 (10), 409 (2000)

Contact: Dame JB

Dept. of Pathobiology, College of Veterinary Medicine
University of Florida
2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA Tel: 352 392 4700

Fax: 352 392 9704

Email: damejémail.vetmed.ufl.edu
Seg primer: Mi3(-20) forward
Class: shotgun.
                                                                                                                                                                                                                                                                                           AZ525704 616 bp DNA GSS 07-MAY-2001
247PbC05 pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
AZ525704
1000 gitccaaaiccaggaactacagitggaggciccaagcaacaaggaagiagiagitggiagi 1059
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Pred. No. 3.4;
0; Mismatches 73; Indels 0
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Best Local Similarity 53.8%;
Matches 85; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                            AU075947 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSA185, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:44689"
/clone="SSA185"
/clone_lib="Dictyostellum discoideum SS (H.Urushihara)"
/dev_stage="slug"
1 109 c 87 g 288 t
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              15-JUL-1999
                                                                                                                                                                                                                                                                          University of Tsukuba
3-3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan
Emali: d402hubasakura.cc.tsukuba.ac.jp
PROJECT - Dictyostellium discoideum cDNA project in Japan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 737;
                                                                                                                                                                                                    Developmental cDNA in Dictyostelium discoideum (1999)
Unpublished (1999)
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1 (bases 1 to 737)
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/organism="Dictyostelium discoideum"
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                          Contact: Hideko Urushihara
Institute of Biological Sciences
                mRNA
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Dictyostelium discoideum
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                                                                                    AU075947.1 GI:5498843
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Best Local Similarity 51.1%;
Matches 97; Conservative
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be http://image.libr.gov

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Http://image.libr.gov

High quality sequence start: 12

High quality sequence stop: 594.

Location/Qualifiers

1. .1000

Arganism="Homo sapiens"

Abb_raref="Taxon:9606"

Alone="Index" 151906"

Alone indirectionally: oligo-dT primed.

Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH-MGC Library."

Note: this is a NIH-MGC Library."

Note: this is a NIH-MGC Library."
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     National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%;
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Sequence:

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Location/Qualifiers
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/*tag= a /*tag= a /*tag= This part of the sequence is unrelated to C. pneumoniae 76 kDa gene"
766..2238
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76kDa protein"
2122..2238
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/note= "This part of the sequence
C. pneumoniae 76 kDa gene"
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AAX02012
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AAH54630
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                                                                                                                                                                                                                                                                                     The present sequence is a DNA coding for a fusion protein compristruncated Chlamydia pneumoniae 76 kDa protein and vector-encoded diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinustits and acute respiratory tract disease, bronchitis, clinital contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract o
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 pneumonia; upper respiratory tract disease; bronchitis; sinusitis acute respiratory disease; cough; sore throat; hoarseness; fever;
                                                                                                                                                                                                                                                                                                                      The present sequence is a DNA coding for Chlamydia pneumoniae 76 kba protein. C. pneumoniae 76 kba protein of sused in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
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useful for vaccinating against Chlamydia infections
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P-PSDB; AAY71954.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;
                                                                                                                                                                  sarcoidosis;
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                                                                                                                                                        Respiratory disease; pneumonia; bronchitis; heart disease; sarcc sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; ss.
                                                                                                                               Nucleotide sequence of the complete genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae seque is also used as vaccines for immunising humans against disc
                                                                                                      kDa protein encoding
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Sequence 1852 BP;

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                                                                                          76 kDa protein; bactericidal; diagnosis; prevention; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; truncation mutant; ds.
pneumoniae
                                  agagcagcgaaagccgctggagatgacagtgctgctgcagcgctggcagatgctcagaaa
                                              diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases caused by C. pneumoniae.
                                                                                                                                                                                                                                                                            protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a /*tag= a //trancated Chlamydia pneumoniae //product= "5'-truncated Chlamydia pneumoniae //tkna protein" //transl_except= (pos:1489..1491, aa:Ile)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kDа
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a 76 kDa protein from Chlamydia against Chlamydia infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for 5'-truncat
C. pneumoniae
                                                                                                                         5'-truncated Chlamydia pneumoniae 76 kDa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a DNA coding Chlamydia pneumoniae 76 kDa protein. Oprotein is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2b; Page 97-99; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                          вР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang J,
                                                                                                                                                                                                          DNA; 1852
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for vaccinating
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                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae
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P-PSDB; AAY71955.
                                                                                                                                                                                                          AAD02064 standard;
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30-JUN-1999;
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                                                                      gattataagactcaagcgcaaacagcttacgatactatctttacctcaacatcactagct 384
                                               tetgeagaegtggaeteaaegaeagegaeegeaeetaegeeteeteeaeeegtetgat 324
            Gaps
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                                                                                                                                  241 getactgatgaggaaaccgcaatcgctgcggagtgggaaactaagaatgccgatgcagtt
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                                  1 atgagiciggicagataagcigggiatigcitciagtaacagcicgicitciactagcaga
                        atgagtctggcagataagctgggtattgcttctagtaacagctcgtcttctactagcaga
1852;
Length
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21;
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DB
Score 1155.4;
Pred. No. 0;
            Mismatches
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83.2%;
99.4%;
            Conservative
     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents part of the gene encoding the 76 kDa cysteine rich outer-membrane protein (OMP) of Chlamydia pneumoniae. Novel oligonucleotides AAV16195-206 can function either as PCR primers or probes. They are used to detect C. pneumoniae in a sample. Oligonucleotides V161202-04 are specific for the present sequence. The oligonucleotides can be used in a hybridisation or amplification based assay for the detection of C. pneumoniae in a test sample.
                                                                                               1081 gctgggcaacaacagggcatactcaatgctttaggacagatcgcttctgctgctgttgtg 1140
961 tctcaagctgcccaacaggagctcgcagcacaagctagagcagcgaaagccgctggagat 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tacctcaacatcactagtgacatacaggctgctttggtgagcctccaggatgctgtcac 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                                                                                                                                                                                                                                                                                                                 Cysteine rich outer-membrane protein; OMP; 60 kDa OMP; 76 kDa OMP; hybridisation; amplification; assay; detection; ds.
                      Chlamydia pneumoniae derived oligonucleotides - used as primers probes for specific and sensitive detection
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                                                                                                                                                                                                                                                                                          Part of the gene encoding the 76 kDA cystein rich OMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 150 BP; 43 A; 34 C; 40 G; 33 T; 0 other;
                                                                                                                          1345 agcgcaggag-tcctcccgctgcagcaagttctatgg 1380
                                                                                                                                       taagaatgccgatgcaattaaagttggcgc 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 24; 28pp; English
                                                                                                                                                                                                                BP.
                                                                                                                                                                                                               AAV16207 standard; DNA; 150
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Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
Example 6; Page 127; 159pp; English
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                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                                 Oligonucleotide D1835
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                                                                                                                                                                                                                                                                                                                                                                         gene expression; ss
                                                                                                                                                AAF58252 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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5 T; 776 other;

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Sequence 936 BP; 4 A; 144 C; 7

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                                                    962 aagatettaaaaatateaaaeetgeagatggttetgatgtteeaaateeaggaaetaeag 1021
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841
                                                            902 aaaagttccccgactctccaattcttcaagaagcggaacaaatggtaatacaggctgaga 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                    782 ttgcaggacagaacgctagtggagctgtagaaaatgctaaatctaataacagtataagca
                                                                                                                               842 acatagattcagctaaagcagcaatcgctactgctaagacacaaatagctgaagctcaga
                                                                                                                                                                                                                                                                                                                           Electron-transfer group; ETM; mismatch; genotyping;
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17-MAR-2000; 2000US-0190259.
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AAFS824/C
1D AAFS824/C
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XX AAFS82
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 Length 936;
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6.0%; Score 83; DB 22;
ilarity 1.2%; Pred. No. 7.4e-14;
Conservative 403; Mismatches 276
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ID AAF58257 standard; DNA; 936
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agactgetettetecaatetgtageaaacaataaeaaageagetgagettettaaagaga
                                      Length 936;
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Similarity 1.2%; Pred. No. 7,4e-14;
8; Conservative 403; Mismatches 27
                                                                         1142 tgttcaatacggaaaatcctgattctcaa 1170
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                                                                                                      CLIN-) CLINICAL MICRO SENSORS INC.
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17-MAR-2000; 2000US-0190259
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6.0%; Score 83; DB 22;
Best Local Similarity 1.2%; Pred. No. 7.4e-14;
Matches 8; Conservative 403; Mismatches 278
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                                                                                                                           (CLIN-) CLINICAL MICRO SENSORS INC.
                                  26-JUL-2000; 2000WO-US20476
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                               Gaps
different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                    Ouery Match
Best Local Similarity 1.2%; Pred. No. 7.4e-14;
Matches 8; Conservative 403; Mismatches 278;
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Nucleic acids containing electron-transfer group, useful as labels in hybridication assays, e.g. for genotyping, allowing repeat analyses on a single surface
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gene expression; ss.
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17-MAR-2000; 2000US-0190259
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Pred. No. 7.4e-14;
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17-MAR-2000; 2000US-0190259
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Best Local Similarity 1.2%; Pred. No. 3.7e-13;
Matches 8; Conservative 402; Mismatches 281;
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Example 6; Page 127; 159pp; English
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Pred. No. 3.7e-13;
02; Mismatches 281; Indels
                                                            Electron-transfer group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                          (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative 402;
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17-MAR-2000; 2000US-0190259.
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                Oligonucleotide D1954.
                                                                                    gene expression; ss.
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Run on:

Sequence:

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Sequence 1, Appli
Sequence 1032, Ap
Sequence 533, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 2, Appli
Sequence 2, Appli
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5171843
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                                                     Sequence 71, Appl
Patent No. 5352450
                                                                                           Sequence 63, Appl
Sequence 63, Appl
Sequence 190, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: M. B. Cerney
TTLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 abbott Park Road
CITY: Abbott Park
STREET: 111inois
COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 146.8; DB 4;
Pred. No. 9.8e-35;
0; Mismatches 2;
                                                                                                         US-09-005-069-63
US-08-998-416-190
US-09-998-416-103
US-08-998-416-533
US-08-998-416-533
US-08-998-416-53
US-08-998-416-886
US-08-469-8038-4
                                                                                                                                                                                                                                                             US-08-469-802B-5
US-08-267-803B-5
US-08-469-802B-2
US-08-267-803B-2
                                                     JS-08-961-083-71
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                                                                       5352450-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDLUM FYEE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.0.1
SOFWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08659473
Patent No. 6210876
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37,477
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 708/937-2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 150 base pairs
TYPE: nucleic acid
TYRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
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illarity 98.7%;
Conservative
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NAME: Paul D. Yasger
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
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Matches 148; Conserv
JS-08-659-473-8
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-732-463-14
US-08-72-466-1
US-08-465-746-1
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US-08-246-434-1
US-08-469-434-1
US-08-467-491-1
US-08-247-491A-1
US-08-247-491A-1
US-08-312-949-1
US-08-119-125A-2
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-08-913-942-3
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ATTLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE DOCKET NUMBER: 30472/114 IMMU FELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                             121 TAAGAATGCCGATGCAGTTAAAGTTGGCGC 150
                                                                            486 taagaatgccgatgcaattaaagttggcgc 515
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                               Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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STRANDEDNESS: sing
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Best Local Similarity
Matches 43; Conserva
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SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                  RESULT 2
US-08-232-463-14/C
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ggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaaggaagtagt 1050
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gaaaatgctaaatctaataacagtataagcaacatagattcagctaaagcagcaatcgct 870
                                                                                                                                                                                  gaagcggaacaaatggtaatacaggctgagaaagatcttaaaaaatatcaaacctgcagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCRMATION:
APPLICANT: Briles, David E
APPLICANT: Yother, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                 1051 attggtagtattcgtgtttccatgctgttagatgctg 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US/07/656,773
APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,070
FILING DATE: 1993663
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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CITY: Arlington
STATE: Virginia
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982 cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.6%; Score 50.6; DB 1;
Best Local Similarity 49.8%; Pred, No. 3.1e-05;
Matches 156; Conservative 0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
APPLICATION NUMBER.
FILING DATE: 12-FEB-1994
TELECOMGUNICATION INFORMATION:
TELEPHONE: (703) 521-0378
TELERX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
LENGTH: 2085 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-214-164-1
Sequence 1, Application US/08214164
Patent No. 5728387
GENERAL INFORMATION:
APPLICANT: BRILES, DAVID E.
APPLICANT: YOFHER, AMET E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(127..1984)
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MOLECULE TYPE: protein
HYPOTHEFICAL: NO
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LOCATION: 1..2085
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STATE: Virginia
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                   Rx1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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FEATURE
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-465-745-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 GAAGAGGCAAAAACTAAATTTAATACTGTTCGAGCAATGGTAGTTCCTGAGCCAGAGCAG 591
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APPLICANT: Briles, David E
APPLICANT: Vother, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: RPITOPIC REGIONS OF PNEUMOCOCCAL SURFACE
TITLE OF INVENTION: PROTEIN A
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                 Length 2085;
                                                                                                                                                           join(127..1983, 1987..1992, 1996..2007, 2011
..2025, 2029..2031, 2035..2085)
                                                                                                                                                                                                                                                                          Score 50.6; DB 1; Length 2 Pred. No. 3.1e-05; 0; Mismatches 154; Indels
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Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22202-0286
ZIP: 22202-0286
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: US 07/656,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/048,896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08465746
Patent No. 5679768
                                                                                                                                                                                                                                                                               3.6%;
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                                                                                                                                                                                                                                                                             Query Match 3.6
Best Local Similarity 49.8
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1042 ggaagtagtattg 1054
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1..2085
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CLASSIFICATION:
                            CLONE: JY2008
                                               FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                      ) NAME/KEY:
; LOCATION:
; LOCATION:
US-08-072-070-1
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US-08-465-746-1
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Length 2085;

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745 atagagaaagatggaaatgcgattggggatgcatattttgcaggacagaacgctagtgga 804
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..2025, 2029..2031, 2035..2085)
McDaniel, Larry S
VENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
VENTION: PROTEIN
                                                                                                                    ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.6%; Score 50.6; DB 1; I Best Local Similarity 49.8%; Pred. No. 3.1e-05; Matches 156; Conservative 0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,065
FILING DATE: 03 JUNE 1993
APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/656,773
FILING DATE: 15-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,434
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: LUKPAT WASHINGTON INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 2085 base pairs
APPLICANT: McDaniel, Lay
TITLE OF INVENTION: STR
TITLE OF INVENTION: PROYING
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                          Arlington
                                                                                                                                                                                                   Virginia
                                                                                                                                                                                                                                            22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rx1
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
; LOCATION:
US-08-469-434-1
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                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                       CITY:
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                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,164
FILING DATE: 17-MAR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.6; DB 1;
Pred. No. 3.1e-05;
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,773
FILING DATE: 15-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                  6102-137
                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 1, Application US/08469434
; Patent No. 5753463
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  REPERENCE/DOCKET NUMBER: 6102
REFERENCE/DOCKET NUMBER: 6102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0813
TELEX: LUKRAT WASHINOTON
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W.
REGISTRATION NUMBER: 22,651
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.6%;
Best Local Similarity 49.8%;
Matches 156; Conservative
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  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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127..1983
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LOCATION:
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US-08-214-164-1
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Length 2085;

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                                                                                                    472 ACAGACAAAGCCGCAAAAGACGCAGCAGATAAGATGATAGATGAAGAAGCTAAGAAACGCGAA 531
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APPLICANT: BRILES, David E.
APPLICANT: YOTHER, Janet L.
APPLICANT: MCDANIEL, Larry S.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
     0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: KOWALSKI, Thomas J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2064
TELECPHONICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: Streptococcus pneumoniae Rx1
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/467,852A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08467852A Patent No. 5856170
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      745 Fifth Avenue
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     Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid.
EDNESS: double
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ADDRESSEE: FROMMER L
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                                                                                            982 cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
922 attetteaagaageggaacaaatggtaatacaggetgagaaagatettaaaaatateaaa 981
                                                                                                                              652 AAACTAGAAGAAGCTAAAGCAAAATTAGAAGAGGCTGAGAAAAAAGCTACTGAAGCCAAA 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
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..2025, 2029..2031, 2035..2085)
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Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 3.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12 FEB-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELET: LUFPAT WASHINGTON
INFORMATION FELEX: LUFPAT WASHINGTON
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
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FILING DATE: 17-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08214222
Patent No. 5804193
GENERAL INFORMATION:
APPLICANT: Billes, David E
APPLICANT: Yother, Janet L
TITLE OF INVENTION: STRUCTURAL GEN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Shoemaker
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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LOCATION:
FEATURE:
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COCATION:
COCATION:
US-08-214-222-1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) (1)
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; LOCATION:
US-08-468-718-1
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                                                                                                                              join(127..1983, 1987..1992, 1996..2007, 2011
..2025, 2029..2031, 2035..2085)
                                                                                                                                                                                                                                               Score 50.6; DB 2; Length 2
Pred. No. 3.1e-05;
); Mismatches 154; Indels
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APPLICANT: Other, Janet L
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL
TITLE OF INVENTION: STRUCTURAL
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Shoemaker and Mattare, Ltd
Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/07/835,698
FILING DATE: 12-FEB-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/07/656,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/072,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08468718 Patent No. 5871943
                                                                                                                                                                                                                                             3.68;
                                                                                                                                                                                                                                                                                            Matches 156; Conservative
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                                                                                                                                                                                                                                                                         Best Local Similarity
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                                          NAME/KEY:
LOCATION:
                                                                                                                                 CCATION:
CCATION:
US-08-467-852A-1
                                                                                                                   NAME/KEY:
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APPLICANT: McDaniel, Larry S
APPLICANT: McDaniel, Larry S
APPLICANT: Wu, Mong-Yin
TITLE OF INVENTION: BPITOPIC REGIONS OF PNEUMOCOCCAL SURFACE
TITLE OF INVENTION: PROTEIN A
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%; Score 50.6; DB 2; Length 2085; 49.8%; Pred. No. 3.1e-05; Live 0; Mismatches 154; Indels 3
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.2025, 2029..2031, 2035..2085)
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Suite 1203, 2001 Jefferson Davis Highway
                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae
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Patent No. 5965141
GENERAL INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 521-0378
TELEFX: LUKPAT WASHINGTON
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICANT: Briles, David E
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                                                                                                                                                                                                               linear
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CLONE: JY2008
                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Str
                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: N
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745 atagagaaagatggaaatgcgattggggatgcatattttgcaggacagaacgctagtgga 804
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49.8%; Pred. No. 3.1e-05;
Live 0; Mismatches 154; Indels 3
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BRIES, David E.
APPLICANT: YOTHER, Janet L.
TITLE OF INVENTION: STRUCTURAL GENE OF PNEUMOCOCCAL PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
join(127..1983, 1987..1992, 1996..2007, 2011
..2025, 2029..2031, 2035..2085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,491A FILING DATE: 23-JUN-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, Thomas J. REGISTARTION UNMBER: 32,147
REFERENCE/DOCKET NUMBER: 454312-2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROMMER LAWRENCE & HAUG LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN: Streptococcus pneumoniae Rx1
MMEDIAȚE SOURCE:
                                                                                                                                                                                                                                                   Sequence 1, Application US/08247491A Patent No. 5965400 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 Fifth Avenue
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Best Local Similarity 49.8'
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
1042 ggaagtagtattg 1054
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                                                                    772 GTTCATAGACTAG 784
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COUNTRY:
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                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,636
                                                                                                                                                                                                                                                                                                                                          PAPLICATION NUMBER: US/46,636
FILING DATE: 20-MAY-1994
CLASSIPICATION 1435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 15-FEB-1991
PROR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US 07/835,698
FILING DATE: 20-APR-1993
FILING DATE: 20-APR-1993
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                                                                                                                                                                                                         COMPUTER: IBM PC compatible
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                                                                                                                                        COMPUTER READABLE FORM:
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LOCATION: 1..2085
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                                  Virginia
                                                                COUNTRY: U.S.A.
ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE
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; LOCATION:
US-08-246-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                              Query Match
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                   982 cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
                                                                                                                                                                                                                                                                                                                                                      712 CAAAAAGTGGATGCTGAAGAAGTCGCTCCTCAAGCTAAAATCGCTGAATTGGAAAATCAA 771
    652 AAACTAGAAGAAGCTAAAGCAAAATTAGAAGAGGCTGAGAAAAAAGCTACTGAAGCCAAA 711
                                                                                                                         922 attottoaagaagoggaacaaatggtaatacaggotgagaaagatottaaaaaatatoaaa 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08319795

Sequence 1, Application US/08319795

GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: Yother, Janet L.
APPLICANT: McDaniel, Larry S

TITLE OF INVENTION: Epitopic Regions of Pneumococcal Surface
TITLE OF INVENTION: Protein A
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sheomaker and Mattare, Ltd.
STREET: 1203 Crystal Plaza Bldg. 1, 2001 Jefferson
STREET: Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,795
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,636
FILIND DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,896
FILIND DATE: 20-APPR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698
FILIND DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US 07/656,773
FILIND DATE: 15-FEB-1991
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 115-0813
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE: DATA OF SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC IN SEC I
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ZIP: 22202-0286
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IMMEDIATE SOURCE:
CLONE: JY4313
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MOLECULE TYPE: pr
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US-08-319-795-1
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982 cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
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Epitopic Regions of Pneumococcal Surface
Protein A
                                                                                                                                                                                        Length 2085;
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Pred. No. 3.1e-05;
0; Mismatches 154; Indels
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APPLICANT: Yother, Janet L.
APPLICANT: Yother, Janet L.
APPLICANT: McDaniel, Larry S
TITLE OF INVENTION: Pritchin A
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheomaker and Mattare, Ltd.
STREET: 1203 Crystal Plaza Bldg. 1, 2001 Jefferson
STREET: Davis Highway
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                                                                                                                                                                                        3.6%;
                                                                                        join(127..1984)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US
FILING DATE: 20-MAY-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                        Conservative
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APPLICATION NUMBER:
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               1..2085
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nes 156; Conserva
intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                 NAME/KEY:
                                                                                           . LOCATION:
US-08-319-795-1
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TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR MUCOSAL ADMINISTRATION OF TITLE OF INVENTION: PREUMOCOCCAL SURFACE PROTEIN A (PSPA)
FILE REFERENCE: 454312-2018
CURRENT APPLICATION NUMBER: US/08/446, 2018
CURRENT FILING DATE: 1995-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cctgcagatggttctgatgttccaaatccaggaactacagttggaggctccaagcaacaa 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 GAAGAGGCAAAAACTAAATTTAATACTGTTCGAGCAATGGTAGTTCCTGAGCCAGAGCAG 591
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                                                                                                                                                                                                                    SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50.6; DB 3;
Pred. No. 3.1e-05;
0; Mismatches 154;
                Morris & Safford, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                        454312-2049
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/312,949
FILING DATE: 30-SEP-1994
CLASSIFICATION: 424
                                                                                                    United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2 Application US/08446201B Patent No. 6042838
                                                                                                                                                                                                                                                                                                                                                                       NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                   E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 840-3333
TELEFRAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LEWATH: 2086 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
US-08-312-949-1
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Best Local Similarity 49.8%;
Matches 156; Conservative (
                                     530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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APPLICANT: BRILES, David E.
APPLICANT: WU, HONG-Yin
                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                              COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                    New York
                                                                                                                                                                                                                                                                                                        FILING DATE: 3C
                                                          New York
                                                                                                                           10036
                                                                                                    COUNT'RY:
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US-08-446-201-2
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US-08-312-949-1
Sequence 1, Application US/08312949
Sequence 1, Colory 14
Setent No. 6027734
SERERAL INFORMATION:
APPLICANT: Briles, David E.
TAPLICANT: Wu, Hong-Yin
TITLE OF INVENTION: MUCOSAL ADMINISTRATION OF
TITLE OF INVENTION: PNEUMOCOCCAL ANTIGENS
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50.6;
Pred. No. 3
FILING DATE: 20-APR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/835,698

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,773

FILING DATE: 15-FEB-1991

TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 415-0813

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: NUCLEic acid
STRANDEDNESS: double
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Best Local Similarity 49.8
Matches 156; Conservative
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MOLECULE TYPE:
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US-08-468-985-1
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EARLIER APPLICATION NUMBER: 08/312,949
EARLIER FILING DATE: 1994-09-30
EARLIER APPLICATION NUMBER: 08/246,636
EARLIER FILING DATE: 1994-05-20
EARLIER FILING DATE: 1993-04-20
EARLIER PILING DATE: 1993-04-20
EARLIER PILING DATE: 1993-02-12
EARLIER PILING DATE: 1991-02-15
EARLIER PILING DATE: 1991-02-15
SEARLIER PAPLICATION NUMBER: 07/656,773
EARLIER PILING DATE: 1991-02-15
SEARLIER PAPLICATION NUMBER: 07/656,773
EARLIER PAPLICATION NUMBER: 07/656,773
EARLIER PAPLICATION NUMBER: 06
EARLIER PAPLICATION NUMBER: 07/656,773
EARLIER PAPLICATION NUMBER: 07/656,773

TOFFE: DATE: 2086

TYPE: DATE: 2086

SEQ ID NO 2

LENGTH: 2086

TYPE: DATE: 100-12
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Score 50.6; DB 3; Length 2086; Pred. No. 3:1e-05; 0; Mismatches 154; Indels 3
 Query Match 3.6%;
Best Local Similarity 49.8%;
Matches 156; Conservative
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Search completed: February 7, 2002, 15:54:07 Job time: 361 sec

AZ676761 ENTHP32TF BG893782 K155CQ+.y AQ227560 HS_2019_B AL103838 Drosophil AL067752 Drosophil AL49765 T3 end of AL05906 Drosophil R1537 yf90C02_r1 B60448 CTT-HSP-200 BE783140 601470746 BG339626 602437485 BB444826 BB454826 BI394077 pgpin.pk0 AZ667395 ENTLHISTR AIZ18089 GHZ5D01.x

B1394077 pgpln.pk0 AZ667395 ENTLH15TR A1218089 qh22b01.x R03975 pkl3e11.rl BE217675 MD0305 Me

Scoring table:

Searched:

Database

score:

Title: Perfect :

Sequence:

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on:

ENTIO70TR ENTES80TR ENTDD36TF

ENTLC06TF

AZ688493 AZ548883 AZ693152 AZ549589 AZ522521 BG602389

SP_0175_A ENTLG27TF

Tetraodon

BG124392 AZ136778 AZ692954 AL225985 AL564621 AL018519 AV405991

AL564621

EST501479

207PbG07

F.rubripe AV405991

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Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
72: 13 80 0208
Fax: 301 838 0208
Email: entaftigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 14-DEC-ZUUU
DNA Entamoeba histolytica
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Entamoeba histolytica.
1 (bases 1 to 861)
Loftus, B., van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
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Entamoeba histolytica Sheared
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High quality sequence stop: 813.
Location/Qualifiers
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AV405991
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BG291509
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BG893782
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   ENTIA11TF
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38.
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AZ682538/c
LOCUS
DEFINITION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
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AA314486 EST186534
BH132709 ENTUG59TF
AA672611 VO59H01.r
PF865301 963058F02
AZ632588 1M0487L17
AV406016 AV406016
BE661568 724 GMAXS
AZ536150 BNTDM43TF
AZ65553 ENTUM43TF
AZ691916 ENTUK22TF
                                                                                                      Search time 7419.31 Seconds (without alignments)
2011.762 Million cell updates/sec
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                                                                                                                                                                                                 1 atggttaatcctattggtcc.....aagttctatggatccgagct 1389
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                           11351937 segs, 5372889281 residues
                                                                                                                                                                                                                                                                                                       Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                       7, 2002, 21:32:23
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Maximum Match 100%
Listing first 45 summaries
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AZ691916
                                                                         nucleic search, using sw model
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Maximum DB seq length: 200000000
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Result Š. /organism="Entamoeba histolytica"

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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing A Practical Approach, eds. M. Vaudin and B. Barell, Oxiord University Press, 1999)."
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Eukaryota: Entamoebidae; Entamoeba.

Eukaryota: Entamoebidae; Entamoeba.

E. 1 (bases 1 to 906)

E. Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica
HMI-IMSS sheared DNA library

L. Unpublished (2000)

Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208

Fax: 301 838 0208

Email: enta@tigr.org
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ENTCZ54TR Entamoceba histolytica Sheared DNA Entamoceba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 13; Length 861; Pred. No. 0.36;
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AZ550193
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Best Local Similarity 48.3%;
Matches 126; Conservative
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δ

High qualitý sequence start: 25 High quality sequence stop: 845. Location/Qualifiers 1. 906

source

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 484)

2. Loe,N.H., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

3. C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

3. C.J., Lee,N.H., Kirkness,E.F., Weinstock,R.G., Catayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

3. L.M., Fitzhugh,M.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Gnehm,C.L., Hamnam.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
/strain="HM1:IMSS"
/db.ref="taxon:5759"
/dlone_lib="Entamocba histolytica Sheared DNA"
/clone_lib="Entamocba histolytica Sheared DNA"
/clone_lib="Entamocba histolytica Structed at The
/note="vector: PHOS1: Site_l: Bst i; Constructed at The
Institute for Genomic Research (TIGR). Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S. (1993) Entamocba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
fight size distribution (-2 kb). The v +1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.2%; Score 45; DB 13; Length 906;
48.3%; Pred. No. 0.36;
tive 0; Mismatches 135; Indels
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1006 aatccaggaa 1015
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AA672611/c
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Wel.Y.F., Wing.J., Xu.C., Yu.G.L., Ruben,S.M., Dillion,P.J., Fannon
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
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                                                         Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: MI3 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH132709 856 bp DNA GSS 07-AUG-2001
ENTNG59TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Determination of clone end sequences from Entamoeba histolytica
HMI:LMSS sheared DNA library (2001)
Unpublished (2001)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1231 gctgctgcagcgctggcagatgctcagaaagctttagaagcggctctaggtaaagctggg 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1171 gctgcccaacaggagctcgcagcacaagctagagcagcgaaagccgctggagatgacagt 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_typ6="KM12C"
/cell_line="KM12C(HCC)-parental human colon carcinoma;
bukes B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI" 61 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 GCTGCTGGAGCTGGGGGGAGCTGCTGCTGGTGGTGCTGCTGCTGCTGGTGGAACT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 GCTGCTGCAGGGCATGCTGCTGCTGAAAGGGCTGGAGCTGCTGCTGAGGGCGATGCAGCT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Colon carcinoma (HCC) cell line II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 484;
                                                                                                                                                                               The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1291 caacaacagggcatactcaatgctttgggacagatcgcttctgctg 1336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.2%; Score 44.4; DB 10;
ilarity 54.2%; Pred. No. 0.43;
Conservative 0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="ATCC (inhost):111272"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 856)
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="colon"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                        Contact: Kerlavage, AR
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BH132709
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                                                                                                                                                             Bioinformatics
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Best Local Sim
Matches 90;
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/GLZAID="THAT.THAT."
//STEAD="LAZON:5759"
//Clone_lib="Entamoeba histolytica Sheared DNA"
//Clone_lib="Detamoeba histolytica Sheared DNA"
//Clone_lib="Entamoeba histolytica Sheared DNA"
//Clone_lib="Entamoeba histolytica in Stitute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica:
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kD). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             706 caatctttagttgatcagacagatgctacagcgacacagatagagaaagatggaaatgcg 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 CAAACTGTTACTAGTGAAATAGATTCTATTTATAAAGATATGCAAAAAGACATCCAAGCT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        766 attggggatgcatattttgcaggacagaacgctagtggagctgtagaaatgctaaatct 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAAGAAGCTGCTGAAGCAAGTGAAGATCCTAAAAAATTGTTGAAGCTACTTTACAA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         886 atagctgaagctcagaaaagttccccgactctccaattcttcaagaagcggaacaaatg 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 CAMGCAGAATTAATTCAACAACTCCAAAACTCTGAAACTGCGAGTGGTGTTCATAGAGAT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 AAAGAATATGCAGAGGAATTAATTAAAGCAGTAGAAGATGTTAAAAGTACTGCAATTGAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 voS9h01.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone tMAGE:1054225 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   826 aataacagtataagcaacatagattcagctaaagcagcaatcgctactgctaagacacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 GAÄGCAGTICTIATATGTTATGGTTGATCTATTATTATCTACTACTACAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                         /organism-"Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.8; DB 13;
Pred. No. 1.4;
                                                               DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 3
High quality sequence stop: 856.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    /strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA672611.1 GI:2644828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.1%;
Best Local Similarity 46.1%;
Matches 143; Conservative
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house mouse
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                                                                                                                                                                                                                                                                    source
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
AZ632588/c
     REFERENCE
                       AUTHORS
                                                                                                           JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF865301 624 bp mRNA EST 963058F02.yl C. reinhardtii CC-1690, Stress condition I, normalized Lambda 2ap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pharmacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmaci) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                  Contact: Marra M.Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1158 tectgatteteaagetgeecaacaggagetegeageacaagetagageagegaaageege 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1218 tggagatgacagtgctgctgcagcgctggcagatgctcagaaagctttagaagcggctct 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 recretrecrecretrecregaecrerecrescrecreserecresascrecrecrecrecres 152
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1278 aggtaaagctgggcaacaacagggcatactcaatgctttgggacagatc 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090" 
/clone="twAGE:1054225" 
/clone_lib="Soares_mammary_gland_NbWMG" 
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 GGACGATGCAACTGCTGCTGAGGGTGTAATGGTTGCTGTGGAACGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.6; DB 10;
Pred. No. 1.3;
0; Mismatches 79;
                                                                                                                                                                                                                                                        MOI:58501
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 g
                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.3%;
Matches 90: Concernia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonaldo."
162 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
BF865301/c
LOCUS
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                                                                  TITLE
JOURNAL
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VERSION
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SOURCE
                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                      COMMENT
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/clone_lib_caxon_solution in crefego, Stress condition I, normalized, Lambda Zap II"
/note="Vector: Bluescript II SK-; Site_1: ECORI; Site_2:
XhoI: This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from Cc-1690 cells grown to mid-log phase in TAP-N (30 min, lhr, 4hr), TAP-S (30 min, lhr, 4hr) and NH4 to NO3 (30min, lhr, 4hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the ECORI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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1M0487L17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0487L17 F, DNA sequence.
1 (bases 1 to 624)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 3
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  804 agctgtagaaaatgctaaatctaataacagtataaagcaacatagattcagctaaagcagc 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864 aatcgctactgctaagacacaaatagctgaagctcagaaaagttccccgactctccaat 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 AGARARGARARARGARARGARARARGGARARARARARGAGARARGGARARARGGARARA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744 gatagagaaagatggaaatgcgattggggatgcatattttgcaggacagaacgctagtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.0%; Score 42; DB 11; Length 624; Best Local Similarity 46.3%; Pred. No. 2; Matches 138; Conservative 0; Mismatches 160; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: chauser@duke.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ632588
AZ632588.1 GI:11754778
                                                                                                                                                                                                                                                                                     Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, .624
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REFERENCE AUTHORS

JOURNAL TITLE

COMMENT

FEATURES

us-09-391-606-4.rst

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyridae; Bombyridae; Bombyridae; Mitya; I (bases 1 to 850)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
                                                                                                                 AV406016 850 bp mRNA EST 06-FBB-2U00 AV406016 Bombyx mori wing disk Cl08 5th-instar day-3 larva Bombyx mori.cDNA clone wdV30506 T3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Bombyx mori wing disk C108 5th-instar day-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project='Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for whole ESTdb. Location/Qualifiers
1. 0850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              697 gcaattgctcaatctttagttgatcagacagatgctacagcgacacagatagagaaagat 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         757 ggaaatgcgattggggatgcatatttgcaggacagaacgctagtggagctgtagaaat 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         817 gctaaatctaataacagtataagcaacatagattcagctaaagcagcaatcgctactgct 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1877 aaqacacaaatagetgaagetcagaaaaagtteeeegaeteteeaattetteaagaageg 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459 GANATAGCTGAAGAAACCTCCCAAGAAACAGAAACTACAGCGGAAAAAGCAGAAAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="wing disk"
/dev_stage="5th-instar day-3 larva"
149 c 189 g 190 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41.8; DB 10;
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female/male mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaacaaatggtaatacaggctgagaaaga 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          699 CAMAATTTGGTTGGAGATGAAGCAAAAGA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:7091"
/clone="wdV30506"
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                                                                                                                                                                                                            AV406016.1 GI:6910104
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Unpublished (2000)
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                                                                                                                                                                                                                                                             domestic silkworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                   Bombyx mori
    29 AACACAAGC 21
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                                                                                                                                       DEFINITION
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AUTHORS
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BE661568
LOCUS
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AV406016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jaxs.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to electrophoresis. Vector DNA was prepared from a derivative of pwW42 (gil473114 [jab] AB1230721], a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                          SIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1131 gatgattcacatgttcaatacggaaaatcctgattctcaagctgcccaacaggagctcgc 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1011 aggaactacagttggaggctccaagcaacaaggaagtagtattggtagtattcgtgtttc 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 AGAAGGAAGACGAAGGAAGCAACAACTAGGGCAGAAGAAGAGCTGGTGGAACTTGAAGCCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 GGTACTGGGCATGAGTAGGGAGCCTAGAAATTCTGCTCAAGACACCCAAGACCAGATCTC 30
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                                                                                                                                                                                                                                                                                                          S. 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M04BL17"
/clone=lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41.8; DB 13;
Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0487 row: L column: 17
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 586.
Location/Qualifiers
Chordata;
Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.0%;
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 586)
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Matches 97; Conserv
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Gaps

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152

BASE COUNT ORIGIN

Query Match

g ò g ò g 06-SEP-2000

us-09-391-606-4.rst

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE AUTHORS REFERENCE

COMMENT

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/strain="HM1:IMSS"
/db.xref="taxon:5759"
/db.xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PH031; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Dlamond (Clark,
C.G., and Dlamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Waudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
842 bp DNA GSS 03-NOV-2000
Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1000 gitccaaaitccagaactacagitggaggitccaagcaacaaggaagtagitatiggitagi 1059
                                                                                                                                                                                                                                                                                                          from Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                880 acacaaatagctgaagctcagaaaaagttccccgactctccaattcttcaagaagcggaa 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   940 caaatggtaatacaggctgagaaagatcttaaaaatatcaaacctgcagatggttctgat 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ATAAAAGAAATTIGIGAACAATTIAAAGTIAITIGITIAAGAGAACAAAATGITGTICCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       820 aaatctaataacagtataagcaacatagattcagctaaagcagcaatcgctactgctaag 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41.4; DB 13; Length Pred. No. 3.2; 0; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .842
/organism-"Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                             Determination of clone end sequences HM1:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                  Entamoeba histolytica.
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 842)
Loftus, B., Van Aken, S. and Fraser, C.
                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Brendan J Loftus
Department of Bukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
High quality sequence start: 32
High quality sequence stop: 775.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: M13-Forward
                                                                                                                 GI:11093097
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Best Local Similarity 48.1%;
Matches 117; Conservative (
                                                    genomic, DNA sequence
AZ536150
                                                                                                                 AZ536150.1
                               ENTDB92TF
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                               DEFINITION
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                                                                                                                    VERSION
KEYWORDS
SOURCE
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/note="Vector: put. strain another
/note="Vector: put. strain another
from green seed coats in mid to late developemental stage
from green seed coats in mid to late developemental stage
, average fresh weight 250 mg per seed. Traces of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an Xhol-poly(dT)
linker-primer. EcoRI adopters were ligated to the
bluut-ended cDNA fragments and the products were digested
with Xhol for directional cloning into lambda ZAP Express
vector. This lambda library was amplified once using E.
coli host strain XLI Blue MRF'. Inserts were then
subcloned by mass excision using ExAssist helper phage for
strain XLOIR."
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                                                                                                                                                   Glycine max
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae, eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         741 acagatagagaaagatggaaatgcgattggggatgcatattttgcaggacagaacgctag 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 TGTTGAGAAGAGGATTATGTCAGATGAGTCTCTTATGAAAGTTAAAGAGGCTAGGGTACA 348
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                                                                                                                                                                                                                                                                                                          Harvis, N., Chapman, B.P. and Gijzen, M.
Gene expression in developing soybean seed coats
Unpublished (2000)
Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 397
Email: gijzenm@em.agr.ca.
Location/Qualifiers
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           724 GmaxSC Glycine max cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Seed coats"
/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="GmaxSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 g
                                                                  BE661568.1 GI:9987460
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155 c
                                                                                                                                                                                                                                                                                      (bases 1 to 762)
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/strain="HMI:IMSS"
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/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Straintute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of B. Histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)

Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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                                                                                                                                                                                                                     AZ691916 876 bp DNA GSS 14-DEC-2000
ENTJK22TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Eukaryota; Entamoebidae; Entamoeba.

I (basses 1 to 876)
Loftus, B., Yan Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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48.1%; Pred. No. 3.3;
Live 0; Mismatches 126;
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High quality sequence stop: 801.
Location/Qualifiers
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Seq primer: M13-Forward
Class: shotgun
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AZ691916
AZ691916.1 GI:11829182
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Matches 117; Conservative
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                                                           100 ATT 98
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/db.ref="taxon:5759"
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/note="vector: pH051; Site_l: Bst I; Constructed at The
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/note="vector: pH051; Site_l: Bst I; Constructed at The
/note="vector: pH051; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
// *1450.) The DNA was mechanically sheared to give a
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                      845 bp DNA GSS 14-DEC-2000
Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                     Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 845)
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Seq primer: M13-Reverse
Class: shotgun
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                                                                                                                                                  genomic, DNA sequence.
AZ685553
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/strain="ANKA clone 15cyl (clone of the ANKA 8417 clone)"
/db.xref="texon:5821"
/clone_lib="pb MBN #21"
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/lab_nostage="asexual blood forms"
/lab_nostage="asexual blood forms"
/lab_nostage="asexual blood forms"
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247PbC05 Pb MBN #21 Plasmodium berghei genomic 3', DNA sequence.
AZ525704
                                1000 gitccaaaiccaggaactacagitggaggciccaagcaacaaggaagtagtagii 1059
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Bukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 616)

Carlton, J.M.-R. and Dame, J.B.

The Plasmodium vivax and P. berghei gene sequence tag projects parasitol. roday 16 (10), 409 (2000)

Contact: Dame JB

Dept. of Pathobiology, College of Veterinary Medicine University of Florida

2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA Tel: 352 392 4700
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3.0%; Score 41.2; DB 13; Length 616;
Best Local Similarity 53.8%; Pred. No. 3.3;
Matches 85; Conservative 0; Mismatches 73; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: damej@mail.vetmed.ufl.edu
Seq primer: M13(-20) forward
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1000)
NIH-MGC http://mgc.ncl.nih.gov/.
                AU075947 737 bp mRNA EST 15-JUL-1999
AU075947 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSA185, mRNA sequence.
AU075947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG291509 1000 bp mRNA EST 21-FEB-2001 602385708F1 NIH_MGC_93 Homo sapiens CDNA clone IMAGE:4514905 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             878 agacacaaatagctgaagctcagaaaagttccccgactctccaattcttcaagaagcgg 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             818 ctaaatctaataacagtataagcaacatagattcagctaaagcagcaatcgctactgcta 877
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                                                                                                                                                                                                             Developmental cDNA in Dictyostelium discoideum (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Bmail: d402hu(sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
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                                                                                                                                Dictyostellum discoideum.
Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 737)
Urushihara,H.
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/organism="Dictyostelium discoideum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
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109 c 87
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BG291509
BG291509.1 GI:13049457
                                                                                                                                                                                                                                                                                                                                                                                                          /strain="AX4"
                                                                                                  GI:5498843
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Best Local Similarity 51.1°
Matches 97; Conservative
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/clone_lib="NIH_MGC_93"
/tlssue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMY-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Site_1 sall; Clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov ocolumn: 02
High quality sequence start: 12
High quality sequence stop: 594.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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/organism="Homo sapiens"
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                US-08-680-326-38
US-09-425-383-2
US-08-633-768A-1
US-09-036-987A-2
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3-07-689-008-2
3-08-248-629A-1
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US-09-370-700-2
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US-09-043-123-2
US-08-445-050-5
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Best Local Similarity 23.4%; Pred. No. 0.8;
Matches 57; Conservative 28; Mismatches
                                                                                                                                                                                                                                       US-08-451-932-1
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                    Sequence 82, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PET
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 309-8504
TELERAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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5-08-816-105A-1
5-07-985-458-3
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Maximum Match 100%
Listing first 45 summaries
                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COMPOSITIONS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1627 LDFML-----PRKTSLSSDSNKTFCMIGHCLSSQEEFLQLAGKWDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.6%; Score 77.5; Dest Local Similarity 22.2%; Pred. No. 37; Matches 41; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 NTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVP
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: *...
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
FEGISTRATION NUMBER: 7853-062-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                         E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                           CURRENT APPLICATION DOS
CURRENT APPLICATION DATA
FILING DATE: 21-MAR-1997
APPLICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08822445
Patent No. 595223
GENERAL INFORMATION:
APPLICANT: Kaplan, Jerry
APPLICANT: Perou, Charles
APPLICANT: Moore, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1668 -----GNLLLFNGAKVGSO---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                               IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3672 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-08-822-445-12
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                                                                                                                                                        ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                              New York
                                                                                          New York
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                                            ADDRESSEE:
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                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-822-445-10
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                                                                                                                                       COUNTRY:
                                                                                        CITY: N
STATE:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                         ----QAIAANYDPKEANSFTNYKGFSALY----MY 178
                                                                                                                                                                                549 DKTRYVTMGADKFRFGNGSGGHEKIADELDAVGFNY----SEDNYKALRAKHPKWLIY 602
                                                                                                                                                                                                                                                          603 GSETSSATRTRGSYXRPERELKHSNGPERNYEQSDYGNDRVGWGKTATASWTFDRDNAGY 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       870 --KTTVADLVNLNIKKNL---IGSAMAGSIGGFNAHASDILTSIFLATGQDPAQNVESSM 924
--LVQEEAFDTWYGG-KKP-YDYGRFFEKDATHPE 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KYCVWQWLVGKHSQVPWINGQKKPL----YLYGAFLMNPLAK 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF CHEDIAK-HIGASHI SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.9%; Score 81; DB 4; Length 1091; 22.4%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 WV--VEGI------LNRLPKQFFVKCSVVDWNTFVPSETST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   925 CMTLMEAVNDGKDLLITCSMPAIECGTVGGGTFL 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OJIMA, KAZUYUKI
APPLICANT: SETOGUCHI, YULAKA
TITLE OF INVENTION: ISOPRENOID PRODUCTION
FILE REPERENCE: ISOPRENOID PRODUCTION
CURRENT APPLICATION NUMBER: US/09/306,595C
CURRENT FILING DATE: 1999-05-06
PRION APPLICATION NUMBER: 98108210
PRION FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08822445 Patent No. 5952223 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09306595C Patent No. 6284506
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APPLICANT: Percu, Charles
APPLICANT: Moore, Karen
TITLE OF INVENTION: COMPOS
TITLE OF INVENTION: AND TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Phaffia rhodozyma
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 22.4 Matches 48; Conservative
443 THNPASEQTLQIAAELGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: HOSHINO, Tatsuo
                                                                                                                                       136 DVSGIGRGNLLKFWFA--
                                                                                                                                                                                                                                 179 GITDSLSFRAYGAYSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 ATNAMKY---
                                                                                                                                                                                                                                                                                                                                                                           663 AGQF 666
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US-09-306-595C-7
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RESULT

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APPLICANT: Knuth, Mark W.
APPLICANT: Knoche, Kimberly K.
APPLICANT: Schame, Susanne
APPLICANT: Hartnett, James R.
TITLE OF INVENTION: ISOLATED AGARASE ENZYMES FROM
TITLE OF INVENTION: FLAVOBACTERIUM SP. STRAIN NR19, CLONED GENES THEREFOR, AND
TITLE OF INVENTION: EXPRESSION THEREOF IN TRANSFORMED HOST CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 VPWINGOK -- KPLY ----- LYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 -WSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPK-EANSFTNYKGFSAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AWROPIFYPYMHA-----SVYGRGESLKPLIS-----SPKYDCSDFTDVPYVDAA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 NRLPKQFFVKCSVVDWNTFVPSETSTTE--KAATNAMK-YKYCVWQWLVGKHSQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 77; DB 3; Length 500; 23.1%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 YMYG-ITDSLSFRAYGAYSKPANDKLGSDFTFRKFD 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :| ::|: | |::: | |: | 410 VYSEEEETLTIFAV----NKAEDQMETEISLRGFE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: DeWitt Ross & Stevens S.C.
8000 Excelsior Drive, Suite 401
                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-089 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 313-164
TELER: 133-21
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . OTHER INFORMATION: /product- "abfa" US-08+926-842B-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/655,704B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                     : 500 amino acids amino acid
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Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wisconsin
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COUNTRY: U.S.A.
ZIP: 53717-1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-08-655-704B-17
                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 EIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLSFRAYGAYS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64, Application US/08926842B
Patent No. 6030807
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sa No. 6030807ueira, Isabel
APPLICANT: de Lencastre, Herminia
TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,842B
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 NTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVP-
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                                                                                             OCTANAME: ESSEND VECSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,445
FILING DATE: 21-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 783-062-99
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3801 amino acids
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STREET: 411 Hackensack Avenue
CITY: Hackensack
                                     MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 22.2
Matches 41; Conservative
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COMPUTER READABLE FORM:
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: USA
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US-08-926-842B-64
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156 HHSFIRTPFTDYQPK------DWNSWYNDNRVTA-----NYGWGDWCWNNGNRR 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 YMRMGVYWVGPKHFEYYIDGOLVRVMYHNATATKVNGTWEYQYF--NAMNGOFPANNANG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 YTAVTTYTTSSTYSFPTIQAASNNSNGISVIDPGNFQGGAGFTKAMDIIINVEXQQWLAL 316
                                                                                                                                                                                                                                                                                                                                                                            5 HYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLV3KHS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INFORMATION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    DB 3; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 WSATVRYEYVEALSVPEID-----VSGIGRGN----
                                                                                                                                                                                                                                                                                  Query Match 6.6%; Score 76.5; L
Best Local Similarity 19.7%; Pred. No. 1.7;
Matches 37; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Human Genome Sciences, Inc
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSDOS version 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,37:
REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (301) 309-850
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: (
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                                                                                                 367 amino acids
                          TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-107-755-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                    TYPE: amino acid STRANDEDNESS:
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CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 NYDPKEAN 164
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317 NHTPSDAD 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20850
         TELEPHONE:
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                                                                                                 LENGTH:
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APPLICANT: Knoche, Kimberly K.
APPLICANT: Selman, Susanne
APPLICANT: Hartnett, James R.
TITLE OF INVENTION: ISOLATED AGARASE ENZYMES FROM
TITLE OF INVENTION: FLAVOBACTERIUM SP. STRAIN NR19, CLONED GENES THEREFOR,
TITLE OF INVENTION: AND EXPRESSION THEREOF IN TRANSFORMED HOST CELLS
                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 HHSFIRTPFTDYQPK------DWNSWYNDNRVTA------NYGWGDWCWNNGNRR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 YMRMGVYHVGPKHFEYYIDGQLVRVMYHNATATKVNGTWEYQYF--NAMNGQFPANNANG 256
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                                                                                                                                                                                                                                                                                                                                                       Length 367;
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,755
                                                                                                                                                                                                                                                                                                                                               Score 76.5; DB 2;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 WSATVRYEYVEALSVPEID-----VSGIGRGN---
                                                                                                                                                                                                                                                                                                                                                                                               24; Mismatches
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8000 Excelsior Drive, Suite 401
30,492
ER: 34506.036
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APPLICATION NUMBER: 08/655,704
FILING DATE: 03-JUN-1996
REGISTRATION NUMBER: 30,492
REFERENCE/POCKET NUMBER: 34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
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                                                                                        TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 19.7%;
Matches 37; Conservative 2
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ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                          LENGTH: 367 amino acids TYPE: amino acid
                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-655-704B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 53717-1914
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317 NHTPSDAD 324
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                                                                                                                                                                                                          STRANDEDNESS:
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US-09-107-755-17
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COURVALIN, PATRICE
VENTION: POLYPEPTIDES IMPLICATED IN THE
VENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
VENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
VENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
VENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                         123 RYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSAL--YMYGI 180
                                                                                                                                                                                                                                                                                                                                                                                         OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                6.3%; Score 73.5; DB 2; 23.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                               18; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/980,357
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY AGENT INFORMATION:
NAME: Oblon, NO. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08980357
Patent No. 6013508
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
TELEFAX: (703) 413-2220
TELEX: 24865 OPAT UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 988 amino acids
                                                                                                                                                                                                                                                      Query Match 6.3%
Best Local Similarity 23.0%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COURVALIN, P. TITLE OF INVENTION: EXPLITLE OF INVENTION: EXPLITLE OF INVENTION: IN TITLE OF INVENTION: THE NUMBER OF SEQUENCES: 54 CORRESPONDENCE ADDRESS:
                                                                                                                                                                MOLECULE TYPE: protein US-08-286-819A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | |: : |: : : : 291 TQELTDKAFEIHDR 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TDSLSFRAYGAYSK 194
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MEDIUM TYPE: Floppy
                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN. PARRICE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GIXCOPEPTIDES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLECTIDE SEQUENCE CODING FOR NUMBER OF SEQUENCES: 54
CORRESPONDENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                            8;
                                                                                                                                                                                                                 113 -- RKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYK 170
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                            43;
                                                                                             Length 241;
                                                                                                                                                                                           ---GAFLMNPLAKATK-TTLNGKENLAWFIGGTLGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC_DOS/NG-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                DB 4;
                                                                                           Ouery Match 6.4%; Score 74.5; D. Best Local Similarity 24.7%; Pred. No. 1.5; Matches 37; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660-060-0 PCT
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APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-Aug-1992
CLASSIFTCATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PROR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY, AGGNT INFORMATION:
NAME: Oblon, NO. 58791910man F.
PRESISTATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                            171 GFSALYMYGITDSLSFRAYGAYSKPANDKL 200
                                                                                                                                                                                                                                                                                                                                                                                                          :|| :| :| :| 184 --TAL----LDDSFKPSDYGIVTKKSNTEL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/286,819A FILING DATE: 05-AUG-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/08286819A Patent No. 5871910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MC-
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FELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
protein
                                                                                                                                                                                      69 INGOKKPLYLY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
; MOLECULE TYPE:
US-08-961-083-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-08-286-819A-19
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ADDRESSEE:
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130 ---LSVPEIDVSGIGRGNLLKFWFAQAIAANYD---PKEANSFTNYKGFSALYMYGITDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 -RNFPAEAGTS-----GLSPALKFGAIG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UPN-1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/272,255
FILING DATE: 08-JUL-1994
                                                                                                                                                                                                                                                                       Sequence 13, Application US/08272255 Patent No. 5824859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 475 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-272-255-13
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                287 ETYQLFLSYS 296
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Matches 36; Conserv
                                                                                                                                          184 LSFRAYGAYS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-08-272-255-13
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                                                                                                                                                                                                                                                                                                                                                                         234 RLEYIRGMDLETVQISHLHRNRLLQL---SRLGSRYEPYAFRDFQENKRYSILTIYLLQL 290
                                                                                                                                                                                                                                                                                                5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Patrea L. Pabst
2800 One Atlantic Center, 1201 West Peachtree
Street
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: FILAPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,492
FILING DATE: 15-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGRNT INFORMATION:
NAME: PADAIL PATORIES: 31,284
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sims, Peter J.
TITLE OF INVENTION: C9 Complement Inhibitor
UMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 72.5; D;
; Pred. No. 8.9;
20; Mismatches
                                                                                                                                                                                                                                                         Query Match 6.3%; Score 73.5; D. Best Local Similarity 23.0%; Pred. No. 16; Matches 17; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08559492
Patent No. 5843884
GENERAL INFORMATION:
  TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENTH: 988 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.23
Matches 34; Conservative
                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-980-357-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                 181 TDSLSFRAYGAYSK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 TQELTDKAFEIHDR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 28
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US-08-559-492-12
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55 VWQWLVGKHSQVPWINGQKKPLYLYGAFLMN------PLAKATKTTLNGKENL---AW 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 LWDQLL--HSPDQILSGSGNPYSVYGPFWKNWQAQPKPTPVATPTELVDLSPEQLTAIAP 184
SEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5824859ris: One Liberty Place, 46th floor
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 475;
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cashmore, Anthony R.
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods
TITLE OF INVENTION: Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATIVE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 71.5; DB 2;
24.3%; Pred. No. 9.1;
iive 19; Mismatches 60;
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84 MNPLAKA-TKTTLNGKENLAWFIGGTLGGLRKAGDWSATV--

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68 WINGOKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGG------TLGGLRKAGDWS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gall, Jaso...
APPLICANT: Kovesdi, Imre
APPLICANT: Wickham, Thomas J.
TITLE OF INVENTION: CHIMBRIC ADENOVIRAL COAT PROTEIN AND
TITLE OF INVENTION: METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   623 FLVRAENTOGISVPS-----GLSNVIK-----TIEADFDAASANDLS 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 ATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 44;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 71.5;
       US/09/540,245A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHICAGO
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                                    2000-03-31
BER: 60/065,544
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 56, Application US/08816346 Patent No. 6127525 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Drosophila melanogaster
05-09-540-245A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Crystal, Ronald G.
APPLICANT: Falck-Pedersen, Erik
CURRENT APPLICATION NUMBER: US/O
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/06
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: 60/09
PRIOR FILING DATE: 1998-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNE / AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 67
TELECOMMUNICATION INFORMATION
TELEPHONE: 312/616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56:
                                                                                                                                                                                                                                                     Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 24.1% Matches 26; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILLINOIS
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ZIP: 60601-6780
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US-08-816-346-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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TYPE: amin
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-08-816-346-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                   SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 FIGGTLGGLRKAG-DWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PLAKATKTTLNGKENL---AW 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 LLLSELPTLKQLGFDWDGGFPVEPGETAAIARLQE------FCDRAIADYDPQ- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                   APPLICANT: Cashmore, Anthony R. APPLICANT: Ahmad, Margaret
APPLICANT: Ahmad, Margaret
APPLICANT: Lin, Chentao
TITLE OF INVENTION: Blue Light Photoreceptors and Methods of
TITLE OF INVENTION: Using the Same
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessler-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
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; Pred. No. 9.1;
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICKATION DATA:
PRICKATION NUMBER: US 08/272,255
FILING DATE: US -04/2194.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: UN-1795
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (215) 568-3100
TELEFRAX: (215) 568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 ANSFINYKGFSALYMYGITDSLSFRAYG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 -RNFPAEAGTS----GLSPALKFGAIG 253
                                 Sequence 13, Application PC/TUS9508565
GENERAL INFORMATION:
APPLICANT: Cashmore, Anthony R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09540245A
Patent No. 6270984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk COMPUTER: IBM PC COMPALIBLE ODERATING SYSTEM: PC-DOCAMO SOFTWARD OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF THE ODERATION OF T
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Best Local Similarity 24.3%;
Matches 36; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 475 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-540-245A-15
; Sequence 15, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-08565-13
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	56; Gaps	:GG 107	739	NY 158	VNY 789	1 214	IL 835	
		NLAWFI		AQAIA	LVQMLA	F-DLG	YQQVG]	
Query Match 6.0%; Score 70; DB 3; Length 967;	<pre>best bocal similarity 20.7%; rich. No. 30; Matches 37; Conservative 25; Mismatches 61; Indels</pre>	56 WOWLVCKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGG 107	IIV	108 TLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANY 158	740FDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFLVQMLANY 789	159 DPKEANSFINYKGFSALYMYGITDSLSFRAYGAYSKPANDKLGSDFTFRKF-DLGII 214	790 NIGYQGFYIPESYKDRMYSFFRNFQPMSRQVVDDTKYKEYQQVGIL 835	
3; L	61;	NPLAKA	HTFKK	58 -	EGYNVA	KPANDK	PMSRQ	
; DB	tches	GAFLM	GTFYL	VSGIGE	RSVDG	AYSI	FFRNE(
ore 70	Misma	1 1	SIPYLD	EIL	NEFEIR	SFRAYG	KDRMYS	
8; SC	5; F1 25;	LYLY	YYTYSG	EALSVP	DRLLTP	GITDSL	-IPESY	
9.00	ative	NGOKKP	SSGYDP	VRYEYV	VSWPGN	SALYMY	Т	
4	arity onserva	IQMLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATF	: : KETPSL	GDWSAT	FDSS	TNYKGE	IGYQGF	
h 	37; C	WLVGKH	FTRLKT	GGLRKA	!	KEANSF	:	
Matc	oca I	10M 9	3 WA	98 TL(0	Pag 69	· N 0	
ery	sst L	Ŋ	69	10	7.4	15	79	
2.5	MG	Qy	QΩ	ΟŊ	QQ	ΟŊ	qq	

Search completed: February 7, 2002, 21:36:13 Job time: 20482 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

US-09-391-606-7 1166 1 MTKKHYAWVVEGILNRLPKQ......DKLGSDFTFRKFDLGIISAF 217 Title: Perfect score: Sequence:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	conserved hypothet	CHLPN 76 kDa homol	hypothetical 76K p		Ψ	chitinase-like pro	٠	hypothetical prote	o)	hypothetical prote	ice nucleation pro	translation elonga	peptide methionine	threonine synthase	hypothetical prote	oligopeptide-bindi	conserved hypothet	hypothetical prote	probable outer mem	lysosomal traffick	isp4 protein homol	chlorophyll a/b-bi	vacJ lipoprotein h	glutamyl-tRNA (Gln	ubiquinolcytochr	alpha-L-arabinofur	carbohydrate kinas	probable ferric si	DNA ligase (ATP) (
SUMMARIES	Π	E72042	F86581	140729	H71490	G69723	T17672	A44054	F71062	A54760	G83558	T18042	JC5117	S74663	D70354	T35670	H75141	A82416	T02355	C71895	T18514	T08925	S14306	F64012	T44293	T39619	C69580	C69415	D81976	LQBYPX
	DB	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	~	~	7	~	~	7	7	7	~	7	7	н
	Query Match Length	422	422	715	446	667	830	810	743	449	268	1176	449	214	409	469	644	195	482	499	3796	753	250	250	476	228	200	505	725	755
æ	Query	7.66	99.7	99.1	66.7	7.9	7.6	7.2	7.1	7.1	7.1	7.0	7.0	6.9	6.9	6.9	6.9	6.8	6.8	8.9	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9
	Score	1162	1162	1156	778	92	88.5	84	ന	82.5	82.5	82	81.5	80.5	80.5	80.5	80			79	78.5	78	77.5	77.5	77.5	77	77	. 77	76.5	76.5
	Result No.	-	7	e	7	S	9	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29

181 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 217

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	hypothetical prote	hypothetical prote	ligand gated chann	probable glutamate	probable ligand-ga	probable ubiquitin	probable sodium-tr	hypothetical prote	TonB-dependent rec	ribonucleotide red	hypothetical prote	carboxylesterase (mannosyl-glycoprot	threonine synthase	hypothetical prote	gene 112 protein -	
	D64618	T28034	T51133	T51132	A84550	T37964	G72022	A86601	н81030	T43215	D85742	JN0438	A56390	G75080	н86189	T03319	
	7	~	7	~	~	~	~	~	~	~	~	~	~	ď	ď	7	
	499	906	925	951	975	3227	431	431	725	1740	254	542	1311	394	580	653	
	6.5	6.5	6.5	6.5	6.5	. 6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	
	16	97	97	16	97	97	75.5	75:5	75:5	75, 5	75	75	75	74.5	74.5	74.5	
6-	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
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ALIGNMENTS

	RESULT 1	
	L/2042 Conserved hypothetical protein CP0017 [imported] - Chlamydophila pneumoniae (st. N;Alternate names: chipn 76 kda homolc, 1.2 (ct623); hypothetical protein CPn0729 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (C) Date; 23.Apr. 1999 #sequence_revision 23.Apr. 1999 #text_change 28-Jul-2000	Chlamydophila pneumoniae (strains hypothetical protein CPn0729 moniae #text_change 28-Jul-2000
	C, ACCESSION: E/2042; C61023 R; Malan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Cenet 21 385-389 1909	n, J.; Olinger, L.; Grimwood,
	A.Title: Comparative genomes of Clamydia pneumoniae and C. A.Reference number: A72000; MUID:99206606	C. trachomatis.
	A, ACCESSION: E/2042 A, Molecule type: A, Residues: 1, -412 < ARN>	
	A;Cross-references: GB:AE001654; GB:AE001363; NID:94377031; PIDN:AAD18868.1; PID:943 A;Experimental source: strain CWL029	031; PIDN:AAD18868.1; PID:943
	R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hick, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzb	elberg, J.F.; White, O.; Hick onay, J.; McClarty, G.; Salzb
	Nucleic Acids Res. 28, 1397-1406, 2000 A.Title Genome seminences of Chlamydia trachomatis Mobr and Chlamydia promise AR3	and Chlamydia chommoniae AR3
	A; Reference number: A81500; MUID:20150255	construction of the state of th
	A) Status: preliminary A, Wolf and a three controls the control of	
	A, Residues: 1-422 < REA>	0.0000000000000000000000000000000000000
	A; Septimental source: strain AR39, HL cells.	1
	PIR:H71490).	comologous to part of a sequen
	C;Genetics: A;Gene: CPn0729; CP0017 C;Superfamily: Chlamydia trachomatis hypothetical protein CT62	in Cr623
_		
	Ouery Match 99.7%; Score 1162; DB 2; Len Best Local Similarity 99.5%; Pred. No. 3.6e-97; Matches 216; Conservative 0; Mismatches 1; In	;; Length 422; ; 1; Indels 0; Gaps 0;
	Qy 1 MTKKHYAWVVEGILNRLPRQFFVKCSVVDWNTFVPSFTSTTEKAATNAMKYKYCVWQWLV	TNAMKYKYCVWQWLV 60
	DD 206 MTKKHYAMVVEGILNELPROFFVKCSVVDWNTEVPSETSTTEKAATNAMKYKYCVWDWLV	
	Qy 61 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSA	GGTLGGLRKAGDWSA 120
	Db 266 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLKRGDWSA	
	QY 121 TVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGI	FTNYKGFSALYMYGI 180
•	Db 326 TVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANGFTNYKGFSALYMYGI	

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hypothetical protein CT623 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
Nylternate names: chlpn 76kda homolog CT623
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 28-Ju1-2000
C;Accession: H71490
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch R;Stephens, R.S.; Kalman, S.; Kalman, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch R;Stephens, R.S.; Kalman, S.; Kalman, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephens, R;Stephe
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CiSpecies: Bacillus subtilis
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CiSpecies: Bacillus subtilis
CiSpecies: Bacillus subtilis
CiSpecies: Bacillus subtilis
CiSpecies: Bacillus Subtilis
Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be
Rikunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Errington, J.; Fabret, C.; Ferrari,
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin,
A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma
A.Authors: Lauber, W.; Rocha, E.; Rocha, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Stato, T.; Scan,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan,
A.Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANS 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Genetics:
A,Gene: CT623
C;Superfamily: Chlamydia trachomatis hypothetical protein CT623
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                                                                                                                                                                                                                                                                                                                         26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 WQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAK---
                                                                                                                                                                                                                                                                                     TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISA
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C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
C; Accession. 140-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
C; Accession. M.; Kuo, C.
Infect. Immun. 62, 880-886, 1994
A; Perez-Melgosa, M.; Kuo, C.
Infect. Immun. 62, 880-886, 1994
A; Perez-Melgosa, M.; Kuo, C.
A; Perez-Melgosa, M.; Kuo, C.
Infect. Immun. 62, 880-886, 1994
A; Perez-Melgosa, M.; Kuo, C.
A; Perez-Melgosa, M.; MulD:94156481
A; Accession: 140729
A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                   CHLPW 76 kDa homolog_2 (CT623) [imported] - Chlamydophila pneumoniae (strain J138) C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C; Caccession: F86581 R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000 A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A; Reference number: A86491; MUID:20330349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Comment: This is the hypothetical translation of a sequence that was reported as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 MIKKHYAWWVEGILNRLPRQFFVKCSVVDWNTFVPSETSTTERAATNAMKYKYCWWQWLV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSA 325
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C;Superfamily: Chlamydia trachomatis hypothetical protein CT623
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99.1%; Score 1156; DB 2;
Best Local Similarity 99.5%; Pred. No. 2.4e-96;
Matches 215; Conservative 0; Mismatches 1;
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Pred. No. 3.6e-97;
0; Mismatches 1;
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                    386 TDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIISAF 422
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Best Local Similarity 99.5%;
Matches 216; Conservative
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A; Residues: 1-715 <RES>
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A; Molecule type: DNA
A; Residues: 1-422 <STO>
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C; Species: Junonia coenia densovirus
C; Species: Junonia coenia densovirus
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C; Accession: A44054 #sequence A.M.; Bergoin, M.
R; Dumas, B.; Jourdan, M.; Pascaud, A.M.; Bergoin, M.
Virology 191, 202-225, 1992
A; Title: Complete nucleotide sequence of the cloned infectious genome of Junonia coe A; Reference number: A44054; MUID:93033112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVG 61
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-810 < DUM>
A; Cross-references: GB: S47266; NID: 9257675; PIDN: AAB23698.1; PID: 9257676
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Best Local Similarity 25.8%; Pred. No. 12;
Matches 61; Conservative 22; Mismatches 59
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18.5%; Pred. No.
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les 42; Conserv
                                                                                                             101 NQIL--PLVGK--
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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yasumoto, Yas
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T17672
Chitinase-like protein - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17672
R;Graves, M.V.; Van Etten, J.L.
R;Graves, M.V.; Van Etten, J.L.
A;Reference number: Z18806
A;Reference number: Z18806
A;Stetus: preliminary; translated from GB/EMBL/DDBJ
A;Stetus: DNA
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-830 <GRA>
A;Residues: 1-840                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 SNKTTIKNAGDFTA------VDYSG------KNFWFGVREFAMGAALN---- 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 ENFTWFSEGDLVRKGNKVTMIPK------DWNWSIPAGTTKIIPFGGVKALPGNLKY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 VWQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNG-KENLAWFIGGT--LGG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFW-----FAQAIAANYDPK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KHYAWVVEGILNR-----LPKQFFVKCSVVDWNTFVPSETSTT-----EKAATNAMKY 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 7.9%; Score 92; DB 2; Length 667; Best Local Similarity 22.9%; Pred. No. 1.9; Matches 50; Conservative 32; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96549.2
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: A181/182R
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Best Local Similarity 22.4%
Matches 38; Conservative
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Qy 9 VVEGILNRLPRQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPW 68 1:1 1 1 1 1 Db 314 IIEEELRAAVPKGFEIVEVSGTREI	C; Species: Pseudomonas aeruginosa C; Species: Is-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: G83558 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; J. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic p. A; Reference number: A82950; MUID:20437337 A; Accession: G83558 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-568 «STO>
RESULT 9 A54760 Lianslation elongation factor eEF-1 alpha chain - Trypanosoma brucei C; Species: Trypanosoma brucei C; Species: Trypanosoma brucei C; Species: Trypanosoma brucei C; Accession: A54760; C49394 C; Accession: A54760; C49394 A; Title: Protein translation elongation factor-lalpha from Trypanosoma brucei binds calm A; Reference number: A54760; MUID:94364999 A; Reference number: A54760; MUID:94364999 A; Status: preliminary	Query Match Best Local Similarity 23.4%; Pred. No. 11; Matches 29; Conservative 19; Mismatches 39; Indels 37; Gaps 5; QY 102 AWFIGGLGGLRKAGDWSATVRYEVVEDEDVSCIGRGNLLKFWFAQALAANY 158
A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-239, 'TCT', 243-449 < KAU> A; Cross-references: GB:U10562; NID:9507782; PIDN:AAA57476.1; PID:9507783 A; Cross-references: GB:U10562; NID:9507782; PIDN:AAA57476.1; PID:9507783 B; Baldauf, S.L.; Palmer, J.D. Proc. Natl. Acad. Sci. US.A. 90, 11558-11562, 1993 A; Title: Animals and fungi are each other's closest relatives: congruent evidence from mA; Reference number: A49394; MUID:94089672 A; Reference number: A49394 A; Residues: Dreliminary: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 18-415 < ABL> A; Cross-references: GB:L25868; NID:9438909; PIDN:AAA16602.1; PID:9438910 C; Superfamily: translation elongation factor Tu translation elongation factor Tu homology cETU> C; Reywords: calmodulin binding; GTP binding; nucleotide binding; P-loop E; 8-1567Domain: translation elongation factor Tu homology cETU> E; 14-217 Regidon: nucleotide-binding motif A (P-loop)	Oy 214 ISAF 217 Db 565 NTRF 568 RESULT 11 T18042 Ice nucleation protein homolog A540L - Chlorella virus PBCV-1 C;Species: Chlorella virus PBCV-1 C;Species: Chlorella virus PBCV-1 C;Species: Chlorella virus PBCV-1 C;Species: Chlorella virus PBCV-1 C;Species: Chlorella virus PBCV-1 C;Accession: T18042; E46352 R;Graves, M.V.; Van Etten, J.L. submitted to the EMBL Data Library, May 1999 A;Reference number: 218806 A;Accession: T18042 A;Accession: T18042
Ouery Match Ouery Match Ouery Match Dest Local Similarity 21.6%; Pred. No. 8.3; DB 2; Length 449; Best Local Similarity 21.6%; Pred. No. 8.3; Matches 42; Conservative 26; Mismatches 71; Indels 55; Gaps 9; QY 19 KQFFVKCSVDWNTFVPETTTEAATNAMKYXCVWGWLVGKH 63	A; Status: preliminary Lanstaced Lion Of Lanstaced Lion Of Lanstaced Lion Of Lanstaced Lion Of Lanstaced Lion Of Lanstaced Lion Of Lanstaced Lion Of Lanstaced Lion Of Residues: 1-1176 <gra> A; Residues: 1-1176 <gra> A; Cross-references: EMBL: U42580; NID: 94028896; PIDN: AAC96907.1 R; Schuster, A. M.; Graves, M.; Korth, K.; Ziegelbein, M.; Brumbaugh, J.; Grone, D.; M. Virology 176, 515-523, 1990 A; Richard Lion and Sequence studies of a 4.3-kbp fragment from a ds-DNA euka A; Reference number: A46352; MUID: 90266467 A; Accession: E46352 A; Status: preliminary A; Status: preliminary A; Molecule type: DNA A; Residues: 885-1176 <sch> A; Cross-references: GB: M33758; NID: 9323370; PIDN: AA666404.1; PID: 9807598</sch></gra></gra>
Qy 115 AGDWSATVRYEYVE	Ouery Match 7.0%; Score 82; DB 2; Length 1176; Best Local Similarity 23.0%; Pred. No. 29; Matches 43; Conservative 26; Mismatches 61; Indels 52; Gaps 10; Matches 43; Conservative 26; Mismatches 61; Indels 52; Gaps 10; Oy 59 LVGKHSQVPWINGQKKPLYLYGAFLWNPLAKATKTTLNGKENLAWFIG

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A; Molecule type: DNA
A; Residues: 1-214 <KAN>
A; Residues: 1-214 <KAN>
A; Residues: 1-214 <KAN>
A; Residues: 1-214 <KAN>
A; Once: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Genetics: marA
A; Gene: marA
A; Start codon: GTG
C; Superfamily: peptide methionine sulfoxide reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 26-May-2000
C;Accession: D70354
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NID:92983224; PIDN:AAC06822.1; PID:92983225; GB:AE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666
A;Accession: D70354
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-409 <AQF>
A;Cross-references: GB:AE000698; NID:92983224; PIDN:AAC06822.1; PID:92983225; GB:A;Genetics:
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C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35670
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: thrCl.
C;Superfamily: threonine dehydratase
C;Keywords: carbon-oxygen lyase; phosphoprotein; pyridoxal phosphate
F;109/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 LYGAFLMNPLAKATKTTLNGKENLAWFIGGTLG-----GLRK-AGDWSATVRYEYVEAL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||: | |: | : |
|-----KGFNELKKVGLIDEVKTR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 IIGSLVFNPTVVAVEGNYDDVNRLCSEIANDLGWAFVNINIRPYYAEGSKTLAFEVAEQL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S--VPEIDVSGIGRGNL-LKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLSFR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GSFLISPFSKVIPDPVVDINPVSTTARGTEK-AVFAGGCFWGLEAMFEEVRGVKDVQTGY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 AGDWSATVRY-----EYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEAN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        threonine synthase (EC 4.2.99.2) thrCl [similarity] - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                        Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein SC7B7.02 SC7B7.02 - Streptomyces coelicolor
                           A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            80 GAFLMNPLAKA-----TKTTLNGKENLAWFIGGTLGGLRK-
                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                     6.9%; Score 80.5; DB 2;
24.6%; Pred. No. 5.1;
ive 16; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.9%; Score 80.5; Dilarity 23.2%; Pred. No. 11; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 GWRAPDVVVAPAASGSLYTKIW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| :: : | || MYGAQAEGCSPIAQAWREGRDF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AYGAYSKPAND----KLGSDF 204
                                                                                                                                                                                                                                                                                                                        Query Match 6.9°
Best Local Similarity 24.6°
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V.
Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 33; Conserv
  874663
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Best Local Si
Matches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131
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Spyt63
Spyt64
Spyt66
Spyt66
Spyt66
Spyt66
Spyt66
Spyt166
Spyt67
Species: Synechocystis sp. (strain PCC 6803)
Spyt74
Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis sp.
C; Species: Synechocystis
S; Shimpo, S; Takeuchi, C; Wada, T; Watanabe, A.; Yamada, M.; Yasuda DNA Res; 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: GB:L76077; NID:g1929444; PIDN:AAC01751.1; PID:g1929445; Comment: This protein plays roles in genetic control of cell death and nuclear process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation elongation factor Tu homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Billaut-Mulot, O.; Fernandez-Comez, R.; Loyens, M.; Ouaissi, A.
Gene 174, 19-26, 1996
A;Title: Trypanosoma cruzi elongation factor 1-alpha: Nuclear localization in parasites
A;Reference number: JC5117; MUID:97017123
A;Accession: JC5117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                       C;Species: Trypanosoma cruzi
C;Date: 02-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 02-Feb-2001
C;Accession: JC5117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 KQMVVCCNKMDDKSVNFAQERYDEIVKEVSAYLKKVGYNVEKVRFIPISGWOGDNMIDKS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLG-------GLRK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 ENMPWYKG---PILLEALDMLEPPVRPSDKPLRLPLQDVYKIGG-IGTVPVGRVETGTMK 261
SVAIGRCAGLNTISGSNNVWVGSDSGSFAATAK----ETVAIGA--KAGYNAGNSLQSVF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KQFFVKCSVVD------WNTFVPSETSTTEKAATNAMKYKYCV---WQW--LVGKH 63
                                                                                   282 V-GRSAGYNGGGTSTFIGYEA----GYGATDSSLYNTFVGY-KTGNIRTGSFNTIMGAD
                                                    AQAIAANYDPKEANSFINYKGFSALYMYGITDSLSFRAYGAYSKPANDKLGSDFTFRKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ALSVPEIDVSGIGRGNLLKFWFAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 PGDVVTFAPANVTTEVKSIEMHHEQLAEATPGDNVGFNVKNVSVKDIRRGNVC-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: translation elongation factor Tu; translation elc
C;Keywords: GTP binding; nucleotide binding; P-loop
F;8-156/Domain: translation elongation factor Tu homology <ETU>
F;14-21,91-94,153-156/Region: GTP binding #status predicted
F;14-21/Region: nucleotide-binding motif A (P-loop)
F;162-181/Region: actin binding #status predicted
F;230-266/Domain: tRNA binding #status predicted <TRN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                            RESULT 12
JC5117
translation elongation factor eEF-1 alpha - Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Scoll 21.6%; Pred. No. 10, 10, 14.e. 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S74322; MUID: 97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGD-----WSATVRYEYVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.0%
Best Local Similarity 21.69
Matches 42; Conservative
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316 NSKNDPPKEAADFT 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-449 <BIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: EF-lalpha
                                                                                                                                                         211 LG 212
                                                                                                                                                                                                              335 AG 336
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                                                    151
228
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submitted to the EMBL Data Library, November 1997
A;Reference number: 221586
A;Recession: T35670
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: DNA
A;Residues: 1-469 <MUR>
A;Residues: 1-469 <MUR>
A;Cross-references: EMBL:AL009199; PIDN:CAA15782.1; G$PDB:GN00070; SCOEDB:SC7B7.02
C;Genetics:
A;Stoperimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC7B7.02
                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 NGQKKPLYLYGAFLMNPLAKATKT------TLNGKENLAWFIGGTLGGLRKAGDWS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 ATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 -----EPFIVPKQGKNPAGGKEVLRAMLSEKAAANFS-KTKLAPTIVKGTVPADGYG 396
                                                                                                                                                                                                                                                                                                                                                                      68; Indels 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 10 VEGILNRLPROFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVPWI 69
                                                                                                                                                                                                                                                                                                               Query Match
6.9%; Score 80.5; DB 2; Length 469;
Best Local Similarity 24.2%; Pred. No. 13;
Matches 45; Conservative 20; Mismatches 68; Indels 5:
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Search completed: February 7, 2002, 21:38:03 Job time: 7092 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 7, 2002, 21:32:46 ; Search time 76.51 Seconds
(without alignments)
103.990 Million cell updates/sec Run on:

US-09-391-606-7 1166 1 WTKKHYAWVVEGILNRLPKQ.....DKLGSDFTFRKFDLGIISAF 217 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 Total number of hits satisfying chosen parameters:

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	tion	bacillus su	junonia coe	trypanosoma	methanopyru	arabidopsis	haemophilus	bacillus ha	homo sapien	schizosacch		bacillus th	saccharomyc	galleria me	chlamydia p	drosophila	drosophila	streptococc	hansenula a	drosophila	drosophila	escherichia	caenorhabdi	chlamydia t	odontella s	enterococcu	schizosacch	schizosacch	rattus norv	cyanidium c	oryctolagus	staphylococ	diatraea sa	homo sapien
	Description	P45694	090053	P41166	032864	P56785	P44042	0x6z60	869660	009154	P94531	Q9x682	P04819	090125	092723	005487	P11995	P49610	P06835	004047	P11996	P34210	P45971	084252	P49479	006238	009788	Q9ut18	P22789	019915	P48747	P11162	071155	Q9y210
																		•																
SOMMAKIES	ID	TKT_BACSU	COAT_JCDNV	EF1A_TRYBB	MTRD_METKA	YCF1_ARATH	VACJ_HAEIN	GATB_BACHD	LYST_HUMAN	UCRI_SCHPO	ABFA_BACSU	CSAA_BACTF	DNLI_YEAST	COAT_GMDNV	NORF_CHLPN	ESTS_DROVI	LP1A_DROME	STRH_STRPN	BGLS_HANAN	NONA_DROME	LP1B_DROME	OMPP_ECOLI	OST4_CAEEL	DNA1_CHLTR	PSAA_ODOSI	TNP6_ENTFC	YA9A_SCHPO	YFYA_SCHPO	SUHA_RAT	THIG_CYACA	CO9_RABIT	PTLB_STAAU	COAT_DSDNV	TRP6_HUMAN
	DB	-	Н	ч	Н	Н	Н	Н	-1	,				-	Н	Н	-	-	-	~	.–ι	-		7		-	Н	-	-	н	٠.	-	-	7
	Length	667	810	449	225	1786	250	476	3801	228	200	1109	755	811	431	542	789	1311	825	700	789	315	445	456	752	988	530	591	283	291	557	572	809	931
æ (Match	7.9	7.2	7.0	6.9	6.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.3	6.3	6.3		6.3			٠	6.2	6.2	6.2	6.2
	Score	92	84	81.5	80	80	77.5	77.5	77.5	77	77	`	76.5	7	75.5	75	75	^	74.5	74	7	73.5	e.	73.5	m.	73.5	73	73			72.5		72.5	72.5
1000	NO.	1	7	m	4	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

12;

68; Gaps

1 MTKKHYAWVVEGILNRLPKOFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKY----C 54

ð . අ

7.9%; Score 92; DB 1; Length 667; 22.9%; Pred. No. 0.57; Live 32; Mismatches 68; Indels

Query Match 7.9% Best Local Similarity 22.9% Matches 50; Conservative

Q9x114 thermotoga P44847 haemophilus P38712 saccharomyc P06525 bacteriopha P46607 arabidopsis O88700 mus musculu Q9jzq5 nelsseria m P05327 synechococc P45848 escherichia P11997 drosophila Q61143 mus musculu P18150 streptomyce	PRT; 667 AA. d) equence update) nnotation update) nnotation update) by: Bacillus. C., Hederstedt L.; EMBL/GenBank/DDBJ databases. EMBL/GenBank/DDBJ databases. HEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE HORPHATE + D-XYLULOSE 5-PHOSPHATE. H-PHOSPHATE + D-XYLULOSE 5-PHOSPHATE. H-PHOSPHATE + D-XYLULOSE 5-PHOSPHATE. H-PHOSPHATE are no restriction on its fions as long as its content is in no way is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/ isb-sib.ch). toolase. 11. ASE_1; 1. ASE_2: 1. A
1 RS11_THEMA 2 SUFI_HABIN 1 RRP3_YEAST 1 DPOL_BEPSP2 1 HGL2_ARATH 1 BLM_MOUSE 1 METX_NEIMB 1 PHR_STNLE 1 YCIQ_ECOLI 1 YCIQ_ECOLI 1 LP1G_DROME 1 TRP6_MOUSE 1 TRP6_MOUSE 1 APHE_STRGR ALIGNMENTS	MANA SERVICE OF THE S
6.2 130 6.2 311 6.2 543 6.2 745 6.2 1416 6.1 379 6.1 631 6.1 772 6.1 930 6.1 272	STANDARD; el. 32, Cre el. 35, Lase el. 40, Las el. 40, Las (EC 2.2.1.] lis. lises licutes; Bac ylococcus g 3; N.A. n K.; n K.; n Wachenfel 1-667 FROM n Wachenfel 1-667 FROM librory is E D-RIBOG THIBOG THIB
336 336 337 337 337 337 337 337 34 337 317 317 317 317 317 317 317 317 317	PACSU PACSU PACSU PACSU PACSU PASSO O1-NOV-1995 (Rel. 32, C. O1-NOV-1997 (Rel. 35, L. 20-AUG-2001 (Rel. 40, L. TRANSKETOLASE (EC 2.2.1 TRANSKETOLASE (EC 2.2.1) TRANSKETOLASE (EC 2.2.1) TRY OR TWAN. Bacillus subtilis. Bacteria; Firmicutes; Bacteria; Firmicutes; Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID-1423; [1] SEQUENCE FROM N.A. STRAIN-168; SCHOINT T., VON WACHENFO STRAIN-168; SCHOINT T., VON WACHENFO STRAIN-168; SCHOINT T., VON WACHENFO STRAIN-168; SCHOINT T., VON WACHENFO STRAIN-168; SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT T., VON WACHENFO SCHOINT STRAINS THIS SWISS-PROT ENTRY SUBMEL; Z3334; CAA97616 EMBL; Z3334; CAA97616 EMBL; Z3334; CAA97616 EMBL; Z3334; CAA97615 EMBL; Z3334; CAA97615 EMBL; Z3334; CAA97615 EMBL; Z3334; CAA9765 EMBL; Z3334; CAA9766; EMBL; ZAA9766; EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 KQFFVKCSVVD-----WNTFVPSETSTTEKAATNAMKYKYCV---WQW--LVGKH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     !- SUBCELLULAR LOCATION: CYTOPLASMIC.
!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLIND=94089672; PubMed=8265589;
Baldauf S.L., Palmer J.D.;
"Animals and fungi are each other's closest relatives: congruent evidence from multiple proteins.";
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=LVH;75,USAMRU-K/18;
MFDLINE-9436499999; PubMed-8083206;
Kaur K.J., Ruben L.,
"Protein translation elongation factor-1 alpha from Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 90:11558-11562(1993).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING
-AMINOACYL.TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
BIOSYNTHESIS.
                                               155 ----AANYDPKEANSFINYKGFSALYMYGITDSLSFRAYGAYSKPANDKLGSDFTF
                                                                                535 TATSAPKYEP--ITGTTGYRGMIADY-YG-ADSTNDAAFGNAGNYPHHQVGS-FTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CT -> DVY (IN REE, 2).
F21113FB80A5116A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor; Protein biosynthesis; GTP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                                                                                    01-FEB-1996 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) ELONGATION FACTOR 1-ALPHA (FF-1-ALPHA).
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11.5%; Pred. No. 3.5;
.ve. 25; Mismatches
                                                                                                                                                                   449
                                                                                                                                                                                                                                                                                                                                                                                                                                   brucei binds calmodulin.";
J. Biol. Chem. 269:23045-23050(1994).
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00301; EFACTOR_GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000795; GTP_EFTU.
                                                                                                                                                                                                 31, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00009; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L25868; AAA16602.1; -. EMBL; U10562; AAA57476.1; -.
21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                     Trypanosoma brucei brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                  STANDARD;
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156
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449 AA;
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                 01-FEB-1995 (Rel. 01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                    Eukaryota; Eugler
NCBI_TaxID=5702;
                                                                                                                                                                EF1A_TRYBB
P41166;
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CONFLICT
SEQUENCE
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                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                           326 AEQLELAIKGELPKDWDQEVPVYEKGSSLAS--RASSGEVLNGLAKKIPFFVGGSADLAG 383
                                                                                                   413 TKSH-KFMIFGLAN------- 446
               55 VWQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNG-KENLAWFIGGT--LGG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --AEIPW---QKLPLYMNQSEFDLLPPGSRVVECNVKVIFRTNRIAFETSSTATKQATLN 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKENLAWFIGGTLGGLRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAI -- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Last annotation update)
COAT PROTEIN VP1 (STRUCTURAL PROTEIN VP1) [CONTAINS: COAT PROTEIN VP
CSTRUCTURAL PROTEIN VP2); COAT PROTEIN VP3 (STRUCTURAL PROTEIN VP3);
COAT PROTEIN VP4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHSQVPWINGQKKPLYLYGA------FLWPLA-----KATK-TTLN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parvoviruses.";
Virology 191:202-222(1992).
-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
OF A COMBINATION OF VP4, VP3, VP2 AND VP1 (BY SIMILARITY).
-!- ALTERNATIVE PRODUCES: THE FOUR DIFFERENT COAT PROTEINS ARE
PRODUCED BY ALTERNATIVE INITIATION.
                                                                                ----LRKAGDWSATVRYEYVEALSVPEIDVSGIGRGNLLKFW-----FAQAIAANYDPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93033112; PubMed=1413502;
Dumas B., Journdan M., Pascaud A.M., Bergoin M.;
"Complete nucleotide sequence of the cloned infectious genome compute nucleotide sequence of the cloned infectious genome Junonia coenia densovirus reveals an organization unique among
                                                                                                                                                                                                                                                                                                                                                                                                                  Junonia coenia densovirus (JCDNV).
Viruses; ssDNA viruses; Parvoviridae; Densovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0D618F04ADD04DE4 CRC64;
                                                                                                                                              162 EANSFINYKGFS---ALYMYGITDSLSFRAYGAYSKPA 196
                                                                                                                                                                   Score 84; DB 1;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN VP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; Alternative initiation.

N 278 810 COAT PROTEIN VP.
N 323 810 COAT PROTEIN VP.
N 374 810 COAT PROTEIN VP.
                                                                                                                                                                                                                                                                   810 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003433; denso_VP4.
Pfam; PF02336; denso_VP4; 1.
                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Conservative
                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38,
15-JUL-1999 (Rel. 38,
20-AUG-2001 (Rel. 40,
COAT PROTEIN VP1 (STRU
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12524;
                                                                                                                                                                                                                                                              COAT_JCDNV
Q90053;
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rs-08-391 - 60e-1

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Chloroplast; Hypothetical protein.
SEQUENCE 1786 AA; 213727 MW; C
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Best Local Similarity 19.99
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                               181 TDSL 184
                                                                                                                                                                                                                         213 VASV 216
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P56785;
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                                                                                         132
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"Identification of the active site histidine in the corrinoid protein MtrA of the energy-conserving methyltransferase complex from Methanobacterium thermoautorrophicum.";
Eur. J. Biochem. 250:783-788(1997).
--- FUNCTION: THIS ENTYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN METHANOGENESIS, THE FORMATION OF METHYL-COBNZYME M AND TETRAHYDROMETHANOPTERIN FROM COBNZYME M AND TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING, SODIUM-ION
---LAKATKTTLNGKENLAWFIGGTLGGLR 113
                                                                                       -----ALSVPEIDVSGIGRGNLLKFWFAQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 TSTTEKAATN-----AMKYK---YCVWQWLVGKHSQVPWINGQKKPLYLYGAFLMN 85
                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-SUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last Annotation update)
17-JUL-1999 (Rel. 38, Last Annotation update)
186)
187-JUL-1999 (Rel. 38, Last Sequence update)
186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSLOCATING STEP.

CATALYTIC ACTIVITY: 5-METHYL-5,6,7,8-TETRAHYDROMETHANOPTERIN +
2-MERCAPTOETHANESULFONATE = 5,6,7,8-TETRAHYDROMETHANOPTERIN +
2-(METHYLTHO)ETHANESULFONATE
SUBUNIT: COMPOSED OF 8 DIFFERENT SUBUNITS (BY SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                        206 EKMPWYKG---PTLLEALDMLEPPVRPSDKPLRLPLOTCTKIGGIGTVP--VGRVETGVM
                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methyltransferase; Transmembrane; Methanogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 80; DB 1; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6FA9546897670D36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euryarchaeota; Methanopyrales; Methanopyrus
                                                                                                                                                                                                                                                                                                                                        225 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
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SQVPWINGQKKPLYLYGAFLMNP-----
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MEDLINE-98121200; Pubmed-9461302;
Harms U., Thauer R.K.;
                                                                                                                                                                                                                                                                                                                                                                              38, Created)
38, Last sequ
38, Last anno
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181 PC
224 PC
22872 MW;
                                                                                     114 KAGD-----WSATVRYEYVE---
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Best Local Similarity 23.99
Matches 44; Conservative
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                                                                                                                                                                                                                         315 GNTKNDPPKEAADFT 329
                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                            153 AIAANYDPKEANSFT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanopyrus kandleri.
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999
15-JUL-1999
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                 MTRD_METKA
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SEQUENCE
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MTRD_METKA
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                                      161 MSAALAGILAMG----FFYANAVLASYNIGGTIEGYHDPK----FTRLPKAVVCSLVFGI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 HSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSATV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             892 ETELPFGSAORKPSF-----FEPISKELKKRIKKLKKKSFVV---LKIFKERAPIFLKV 942
--FIGGTLGGLRKAGDWSATVRYEYVEALS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               840 WLTDGIQIKILFPFYLK----PWHKSKFQASQKARLKKTKDKGEKNDFCFLTVW----GM 891
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                                                                                                                             VPEIDVSGIGRGNLLKFWFAQAIAANY - - - - - - DPKEANSFTNY - KGFSALYMYGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA,
MEDLINE-20039611; PubMed-10574454;
Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
"Complete structure of the chloroplast genome of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 213.7 KDA PROTEIN YCF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1786 AA.
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-!- FUNCTION: NOT YET KNOWN.
-!- SIMILARITY: BELONGS TO THE YCF1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 21; 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA
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19.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
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VACJ_HAEIN
ID VACJ_HABIN
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NCBI_TaxID=86665;
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                                                                                                                                                       PEDSINE CONTROL ARCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Suthon G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 VDWNTFV--PSETSTTEKAATNAM----KYKYCVWQWLVGKHSQVPWINGQKKPLYLYGAF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATB_BACHD STANDARD; PRT; 476 AA.
09Z9X0; 09JPV7;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT B (EC 6.3.5.-) (GLU-ADT
                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VACJ LIPOPROTEIN HOMOLOG.
N-ACYL DIGLYCERIDE (POTENTIAL).
7DDEC4FC587091BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 77.5; DB 1; Length 250; 29.6%; Pred. No. 4.3; ive 10; Mismatches 35; Indels 3
                                                                                                                                                                                                                                                                                            Venter J.C.; "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 LMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGDWSATVRYEYVEAL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AVDARAK----NLNNAEL------LRQAQDPYITFREAYYQNL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGN: ALVILO; PROKAR_LIPOPROTEIN; 1.
OUTET membrane; Lipoprotein; Signal; Complete proteome.
SIGNAL 1
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                        01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VACJ LIPOPROTEIN HOMOLOG PRECURSOR.
         (Rel. 32, Created)
(Rel. 32, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 N
28110 MW;
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                                                                                                                                                                                                                                                                                                                                                          ANCHOR (BY SIMILARITY).
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                                                                            Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
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GATB OR BH0667.
                                                                                                                    NCBI_TaxID=727;
                                                                 VACJ OR HI0718
                                                                                                                                                                                                                                                                                                                      influenzae Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR; HI0718;
PROSITE; PS00
                                                                                                          Haemophilus
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28 44317-4331(2000).

-!- FÜNGTION: FÜRNISHES A MEANS FOR FÖRMATION OF CORRECTLY CHARGED GLN-TRNA(GLN) THROUGH THE TRANSAMIDATION OF MISACYLATED GLU-TRNA(GLN) IN ORGANISMS WHICH LACK GULTAMINYL-TRNA SYNTHETASE. THE REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE = ADP + PHOSPHATE + L-GLUTAMINYL-TRNA(GLN) + L-GLUTAMINE = ADP -: SUBUNIT: HETERROTRIMES FAND C SUBUNITS (BY SIMILARITY).
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                                                                                                                      Takami.H., Nakasone K., Ogasawara N., Hirama C., Nakamura Y., Masui N., Fuji F., Takaki Y., Inoue A., Horikoshi K.; "Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                  SEJUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
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C212B522413C579B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 IDVSGIGRGNLLKFWFAQAIAANYDPKEANSF 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 YDAMVLTLTKEMSDFFEETIAKGADPKLASNW 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP001509; BAB04386.1; -.
InterPro; IPR001773; Gln_amidotransf_B.
SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=99184646; PubMed=10086842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB011836; BAA75312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein biosynthesis; Ligase; SEQUENCE 476 AA; 53414 MW;
                                                                                                                                                                                                                                        Bacillus sp. strain C-125.";
Extremophiles 3:29-34(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 6.6'
Best Local Similarity 27.2'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01162; PET112; 1
PROSITE; PS01234; GATB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fuji F., Hira
Horikoshi K.;
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3

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REPEATS_REGION; 1
                   ransport;
                                                                                                                                                                                                                                         429117
                                                                                                                                                                                                                                                                                                        41; Conservative
                                        2452
1626
3422
3602
3653
3653
3653
3744
1531
                                                                                                                                                                                     3801
                                                                                                                                                                                                                            3801
                                                                                                                                                                                                                         2002 38C
3801 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 41; Conserv
                   transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
     PROSITE, PS50294;
                                                                                3139
                                                                                                         3614
3656
3700
                                                                                                                                                           1515
                                                                                                                                                                                     1532
1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 KPAND 198
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                                                                                                                                                                                                                          VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                             VARSPLIC
                                                                                                                                                                                     VARSPLIC
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                   Protein
                            DOMAIN
                                           DOMAIN
                                                      REPEAT
                                                                  REPEAT
                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFECTS IN CHS1 ARE THE CAUSE OF CHEDIAK-HIGASHI SYNDROME (CHS). A RARE AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY TYPOPFOGMENTATION, SEVERE IMMUNOLOGIC DEFICIENCY, A BLEEDING TENDENCY, NEUROLOGIC ABNORMALITIES, ABNORMAL INTRACELLULAR TRANSPORT TO AND FROM THE LYSOSOME, AND GIANT INCLUSION BODIES IN A VARIETY OF CELL TYPES.
SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE-97051925; PubMed-8896560;

Maple D.L., Karim M.A., Woolf E.A., Holmgren L., Bork P., Misumi D.J., McGrail S.H., Dussault B.J., Perou C.M., Boissy R.E., Duyk G.M., Spritz R.A., Moore K.J.,

Spritz R.A., Moore K.J.,

"Identification analysis of the complete gene for
                                                                                                                                                                  Barbosa M.D.F.S., Nguyen Q.A., Tchernev V.T., Ashley J.A., Detter J.C., Blaydes S.M., Brandt S.J., Chotai D., Hodgman C., Solari R.C.E.S., Lovett M., Kingsmore S.F.; "Identification of the homologous beige and Chediak-Higashi syndrome
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97358584; PubMed-9215680; Barbosa M.D.F.S., Barrat F.J., Tchernev V.T., Nguyen Q.A., Barbosa M.D.F.S., Darrat F.J., Tchernev V.T., Nguyen Q.A., Mishra V.S., Colman S.D., Pastural E., Dufourcq-Lagelouse R., Fischer A., Holcombe R.F., Wallace M.R., Brandt S.J., Gelanit Basile G., Kingsmore S.F., "Identification of mutations in two major mRNA isoforms of the chediak Higashi syndrome gene in human and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS). SIMILARITY: CONTAINS 1 BEACH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02138; Beach; 1.
Pfam; PF02138; Beach; 1.
Probom; PP0070848; Beige_BEACH; 1.
SMART; SM00320; WD40; 4.
PROSITE; PS50197; BBACH; 1.
PROSITE; PS500678; WD_REPEARS_1; 1.
PROSITE; PS50082; WD_REPEARS_2; 1.
                                                                                                                                              TISSUE=Liver;
MEDLINE=96353977; PubMed=8717042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000409; Beige_BEACH.
InterPro; IPR001680; WD40.
                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                      t. Genet. 14:307-311(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U84744; AAB87737.1; -. EMBL; U67615; AAB41309.1; -. EMBL; U72192; AAB39697.1; -.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-1475 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U70064; AAB41533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U72192; AAB39697.1; -
                                                                                                                                                                                                                                     Nature 382:262-265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U70064
MIM; 214500;
                                                                                                                                                                                                                          qenes.";
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1585 NIFLPSK--------WQHLVLTYLQQPQGKRRIHGKISIWVSGQRKPDVT 1626
                                                         WD 1.
WD 2.
BEACH.
WD 3.
WD 4.
WD 5.
WD 5.
WD 6.
WD 7.
ESDRPEGAEXINPGERL -> GMMTGLSDLYTKIVFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1668 -----GNLLLFNGAKVGSQ------EAFYLYACGPNHTSVMPCKYG 1702
  WD repeat; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 YGAFLMNPLAKATKTTLNGKENLAW-FIGGTLGG----LRKAGDWSATVRYEYVEALSVP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 EIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFTNYKGFSALYMYGITDSLSFRAYGAYS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 NTFVPSETSTTEKAATNAMKYKYCVWQWLVGKHSQVP-------WINGQKKPLYL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UCRI_SCHPO STANDARD; PRT; 228 AA.
009154: 042942;
01-NOV-1997 (Rel. 35, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
UBIGUINDL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR (EC 1.10.2.2) (RIESKE IRON-SULFUR PROTEIN) (RISP).
RIPI OR SPBC16H5.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Churcher C.M.;
                                                                                                                                                                                                                                                   (IN ISOFORM 3).
MISSING (IN ISOFORM 3).
VCRSFVKIIAEVLG -> MARSFRRKGGOSCT (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M., Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: COMPONENT OF THE UBIGUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dirago J., Bruel C., Graham L.A., Slonimski P., Trumpower B.L., "Heterologous complementation of a Rieske iron-sulfur protein-deficient Saccharomyces cerevisiae by the Ripl gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 3801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1627 LD3ML-----PRKTSLSSDSNKTFCMIGHCLSSQEEFLOLAGKWDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                              ISOFORM 2).
MISSING (IN ISOFORM 2).
MY: 288B370AD4BDAF11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota: Schizosaccharomycetes:
Schizosaccharomycetales: Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 77.5; 22.2%; Pred. No. 82;
Repeat; W
POLY-GLU.
POLY-LEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe.";
J. Biol. Chem. 271:15341-15345(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96279043; PubMed-8663290;
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7

us-09-391-606-7.rsp

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Bacillus thuringiensis (subsp. finitimus).
Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=29337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN).
CRY28AA OR CRYXXVIIIA(A).
                                                                                                                                                                                                             STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEOUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSAA_BACTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 TKTTLNGKENLAWFIGGTLGGLRKAG------DWSATVRYEYVEALSVPEIDVSGI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIESKE PROTEINS FROM OTHER SOURCES (MITOCHONDRIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion; Electron transport; Respiratory chain; Iron-sulfur; Oxidoreductase; Inner membrane; Transmembrane; Transit peptide.
TRANSIT 1 728 MITOCHONDRION (POTENTIAL).
CHAIN 7 228 UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBGUILT.
METAL 172 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
METAL 194 194 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
METAL 194 194 IRON-SULFUR (2FE-2S) (BY SIMILARITY).
                                                                  SUBUNIT: FUNCI BC1 COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY
                                                                                     SUBUNITS, 2 CORE PROTEINS AND 5 LOW MOLECULAR WEIGHT PROTEINS. SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE. MISCELLANEOUS: THE RIESKE PROTEIN IS A HIGH POTENTIAL 2FE-2S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ALPHA-L-ARABINOFURANOSIDASE 1 (EC 3.2.1.55) (ARABINOSIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.6%; Score 77; DB 1; Length 228; 30.0%; Pred. No. 4.3;
                         CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME C = 0 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A -> R (IN REF. 1).
C50CC8BA159E31B2 CRC64;
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Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 GRG-NLLKFWFAQAIAANY----DPKEANS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 PEGKNLVVKWQGKPVFIRHRTPEEIQEANS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL022104; CAA17904.1; -. SEMBL; SP; P1372; IRE. InterPro; IPR001709; RIA_pol_A_bac. InterPro; IPR001281; Rieske.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prodom; PD001179; RNA_pol_A_bac; PROSITE; PS00199; RIESKE_1; 1. PROSITE; PS00200; RIESKE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=168;
MEDLINE=97124191; Pubmed=8969504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABFA_BACSU STANDARD; P P94511; 005096; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last seque 20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
174
191
194
193
183
A 24740 MW;
TO ATP SYNTHESIS
                                                                                                                                                                                                      BACTERIAL, CHLOROPLAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00355; Rieske; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U40480; AAC49359.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Conservative
                                                FERROCYTOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00162; RIESKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
228 AA;
                                                                                                                                                                                 J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis,
                                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1423
                                                                                                                                                          PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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ABFA_BACSU
AD PAFFA_B
AC P94531
BAC P94531
DT 01-NOV
DT 20-NOV
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                               Sa-Nogueira I., Nogueira T.V., Soares S., de Lencastre H.;
"The Bacillus subtilis L-arabinose (ara) operon: nucleotide sequence,
genetic organization and expression.";
Microbiology 143:957-969(1997).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING ALPHA-L--
RABBINOFURANGSIDE RESIDUES IN ALPHA-L-ARABINOSIDES.
-!- SIMILARITY: BELONGS TO FAMILY 51 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 VPWINGQK--KPLY----LYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLRKAGD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 -WSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPK-EANSFTNYKGFSAL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PESTICIDIAL CRYSTAL PROTEIN CRYSBAA (INSECTICIDAL DELTA-ENDOTOXIN
CRYXVIIIA(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (126 KDA CRYSTAL
Wipat A., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J., Emmerson P.T., Harwood C.R.; "The dnaB-pheA (256 degrees-240 degrees) region of the Bacillus subtilis chromosome containing genes responsible for stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 NRLPKQFFVKCSVVDWNTFVPSETSTTE--KAATNAMK-YKYCVWQWLVGKHSQ---
                                                                                                                        responses, the utilization of plant cell walls and primary metabolism.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 77; DB 1; Length 500; 33.1%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P -> A (IN REF. 2).
7397FD52A4987686 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|: | |: :: | | |: 410 vvxSebeetLtifav----NKAEDQMETEISLRGFE 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SubtiList; BG11900; abfA.
Hydrolase; Glycosidase; Complete proteome.
CONFLICT 114 114 P -> A (IN RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 YMYG-ITDSLSFRAYGAYSKPANDKLGSDFTFRKFD
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97237725; PubMed=9084180;
                                                                                                                                                                                                                  Microbiology 142:3067-3078(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z75208; CAA99595.1; -. EMBL; X89810; CAA61937.1; -. EMBL; Z99118; CAB14832.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 AA;
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                               "Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 SIFALGWIHNSVNSQN--LISESVSTQIPLVKAYEVTNNSVIRGPGFTGGDLIELRDKCS 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 NEYQKNFNVN-----NQNEPQETTNYPNDYGGSNSQKFKHNLSHFPLIIHKLEFAEYFH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S--QVPW----INGQKKPLYLYGAFLMNPLAKATKTTLNGKENLAWFIGGTLGGLR---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 ---KAGD---WSATVRYEYVEALSVPEIDVSGIGRGNLLKFWFAQAIAANYDPKEANSFT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499 IKCKASSLKKYAISLFYAANNAIAV-SIDVGDSGAGVLLQPTFSR------KGNNNFT 549
                                                                        thuringiensis ssp. finitimus.";
FEBS Lett. 453:46-48(1999).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRLPKOFFVKCSVVDWNTFVPSETST--TEKAATNAMKYKYCV--WQWLVGK-----H 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86093646; PubMed-3909103; Barker D.C., White J.H.M., Johnston L.H.; mucleotide sequence of the DNa ligase gene (CDC9) from Saccharomyces cerevisiae: a gene which is cell-cycle regulated and
                                                                                                                                                                    MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                               EPITHELIAL CELLS OF INSECTS.
DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS I
                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                              'Match 6.6%; Score 77; DB 1; Length 1109; Local Similarity 27.0%; Pred. No. 24; les 51; Conservative 23; Mismatches 67; Indels
SEQUENCE FROM N.A.
STAIN-WKPW B-1161;
MEDLINE-99330166; PubMed-10403372;
Wojćiechowska J.A., Lewitin E., Revina L.P., Zalunin I.A., Chestukhina G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Indels
                                                                                                                                                                                                                                                                                                                                                                          1109 AA; 125712 MW; 10C80705508F5CDA CRC64;
                                                                                                                                                                                           SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last annotation update)
DNA LIGASE I, MITOCHONDRIAL PRECURSOR (EC 6'5.1.1)
(POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                              send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001178; Endotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNII_YEAST STANDARD; FP04819; 012736; B13-M02-1987 (Rel. 05, Created) 01-NOV-1997 (Rel. 35, Last sequi 30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                        EMBL; AF132928; AAD24189.1; -.
                                                                                                                                                                                                                                                                                                                                              Pfam; PF00555; endotoxin; 1.
Toxin; Sporulation.
                                                                                                                                                        OF THE SPORE COAT.
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PROSITE; PSO1010; DNA_LIGASE_A3; 1.
BNOSITE; PSO1010; DNA_LIGASE_A3; 1.
BNA repair; DNA replication; DNA recombination; Cell division; Ligase; ATP-binding; Nuclear protein; Mitochondrion; Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CULT: BIOL. 9:1085-1094(1999).
-I-FUNCTION: THIS PROTEIN SAALS NICKS IN DOUBLE-STRANDED DNA DURING DNA REPLICATION. DNA RECOMBINATION AND DNA REPLICATION. BAR ABLINE THE MITOCHOUNDELAL FORM IS REQUIRED FOR MITOCHOUNDELAL DNA MAINTENANCE BUT IS NON-ESSENTIAL WHILE THE NUCLEAR FORM IS ESSENTIAL FOR CELL
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20003237; Pubmed=10531002;
Willer M., Rainey M., Pullen T., Stirling C.J.;
"The yeast CDC9 gene encodes both a nuclear and a mitochondrial form
of DNA ligase T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRION (POTENTIAL).

DNA LIGASE I, MITOCHONDRIAL ISOFORM.

DNA LIGASE I, NUCLEAR ISOFORM.

FOR NUCLEAR ISOFORM.

AMP (BY SIMILARITY).

L -> V (IN REF. 1).

L -> E (IN REF. 1).

G -> E (IN REF. 3).

R -> I (IN REF. 3).
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                                                                                                                                                                                                                                                                                                        responsible for resistance to formaldehyde in Saccharomyces cerevisiae, and characterization of its protein product."; Mol. Gen. Genet. 237:351-358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE)(N) +
                                                                                                                                       Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            Wehner E.P., Rao E., Brendel M.; "Molecular structure and genetic regulation of SFA, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
induced in response to DNA damage.";
Nucleic Acids Res. 13:8323-8337(1985).
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97; DNA_LIGASE_Al; 1.
                                                                                                                                                                                                                                     PubMed-8483449;
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Pfam; PF01068; DNA_lidase: 1
                                                                                                                                                                                 SEQUENCE OF 610-755 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE INITIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
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PIR; S31138; S31138.
SGD; S0002323; CDC9.
                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                MEDLINE-93247548;
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                                                                                        STRAIN-S288C;
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                                                                                                                 Pohl T.M.;
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EMBL;
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                                                                                                             7;
                                                                                                                                                                                                                                                                               434 TMRIYSRNGENMTERYPEINITDFIQDLDTTKNLILDCEAVAWDKDQGKILPFQVLSTRK 493
                                                                                                                                                                                                                                                        44 ---AATNAMKYKYCVWQWLVGKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKEN 100
                                                                                                                                                                                                                                                                                                                                             101 LAWFIGGTLGGLRKAGDWSATVRYE--YVEALSVPEIDVSGIGRGNLLKFWFAQAIAANY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COAT_GMDNV STANDARD; PRT; 811 AA.
090125; 090128; Q90126; Q90127;
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 40, Last annotation update)
COAT PROTEIN VP1 (STRUCTURAL PROTEIN VP1) [CONTAINS: COAT PROTEIN VP2);
(STRUCTURAL PROTEIN VP2); COAT PROTEIN VP3);
                                                                                                                Gaps
                                                                                                                                                           2 TKKHYAWVVEGILNRLP------KOFFVKCSVVDWN----TFVPSETSTTEK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simpson A.A., Chipman P.R., Baker T.S., Tijssen P., Rossmann M.G.;
"The structure of an insect parvovirus (Galleria mellonella densovirus) at 3.7 A resolution.";
Structure 6:1355-1367(1998).

-! SUBUNIT: THE VIRUS CAPEID IS COMPOSED OF 60 ICOSAHEDRAL UNITS, OF A COMBINATION OF VP4, VP3, VP2 AND VP1.

-! ALTERNATIVE PRODUCTS: THE FOUR DIFFERENT COAT PROTEINS ARE PRODUCED BY ALTERNATIVE INITIATION.
                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galleria mellonella densovirus (GmDNV).
Viruses; ssDNA viruses; Parvoviridae; Densovirus.
                                                                Length 755;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tijssen P., "Organization and expression of the ambisense genome of "Organizations virus of Galleria mellonella (GmDNV)."; Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
84828 MW; B7C2ECAF5C61CAE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02336; denso VP4; I.
Coat protein; Alternative initiation; 3D-structure.
CHAIN 1 811 COAT PROTEIN VP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (3.6 ANGSTROMS) OF 396-811.
MEDLINE=99036856; Pubmed=9817847;
                                                                                                             90;
                                                                  DB 1;
                                                  6.6%; Score
21.0%; Pred. No. 10,
"''n 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           547 ATQITTNNLDELQKFLDESVNHSCEGLMVKMLEGPE---
                                                                                                                                                                                                                                                                                                                                                                                                                                        159 DPKEANSFINYKGFSALYMYGITDSLSFRAYGAY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COAT PROTEIN VP4 (STRUCTURAL PROTEIN VP4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L32896; AAA66964.1; -.
EMBL; L32896; AAA66965.1; -.
EMBL; L32896; AAA66967.1; -.
PDB; IDNY, 16-FEB-99.
InterPro; IPR003433; denso_VP4.
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                                                                                                                45; Conservative
  AA;
                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=37138;
755
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
COAT_GMDNV
                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: |: |: | || || 553 QISNVQ-----TAIGLNKLG-WGINRAFTAFQSDQPMIPTATTAPKYEPVTGDTGYRGMI 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 GKENLAWFIGGTLGGLRKAGDWSATVRYEYVE-----ALSVPEID-VSG-IG-RGNL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LKFWFAQAI-----AANYDPKEANSFTNYKGFSALYMY-----GITDSLSFRAYGAYS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20150255, PubMed-10684935,
MEDLINE-20150255, PubMed-10684935,
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Rickey E.K., Peterson J., Utterback T., Berry K., Hass S.,
Linher K., Weidman J., Rhouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                           414 TKSH-KFMIFGLAN------LTT 445
                                                                                                                                                                                                                                                                                                                                                                                                                  62 KHSQVPWINGQKKPLYLYGA------FTLMNPLAKAT-----KTTLN 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NORF_CHLPN STANDARD; PRT; 431 AA.

092723: 0940595;
20-40G-2001 (Rel. 40, Created)
20-40G-2001 (Rel. 40, Last sequence update)
20-40G-2001 (Rel. 40, Last sequence update)
20-40G-2001 (Rel. 40, Last annotation update)
PROBABLE NA(+)-TRANSLOCATING NADH-QUINONE REDUCTASE SUBUNIT F
(EC 1.6.5.-) (NA(+)-TRANSLOCATING NOR SUBUNIT F) (NAR COMPLEX SUBUNIT F) (NOR-1 SUBUNIT F) (NAR COMPLEX SUBUNIT F)
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                2 TKKHYAWVVEGILNRLPKQFFVKCSVVDWNTFVPSETSTTEKAATNAMKYKYCVWQWLVG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kubara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                            DB 1; Length 811;
                                                                                                                                                                                                                                         Indels
COAT PROTEIN VP2.
COAT PROTEIN VP3.
COAT PROTEIN VP4.
0A61B09172DF99B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
                                                                                                                                                                                                                                      82;
                                                                                                                                                                            6.5%; Score 76; DB 22.4%; Pred. No. 21; iive 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99206606; Pubmed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 KPANDKLGSDFTFRKFDLGIISA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88542 MW;
                                                                                                                                                                                                                                         59; Conservative
277
324
875
811 AA;
                                                                                                                                                                                                             Similarity
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HYDROLASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
       FUNCTION: NOR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONE-1 TO UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLEASM. THE FIRST STEP IS CAPALYZED BY NORF, WHICH ACCEPTS ELECTRONS FROM NADH AND PATHWAY (EN SIMILARITY).

CATALYZED CATIVITY: NAHICH HUBIQUINONE BY A ONE-ELECTRON TRANSFER CATALYZIC ACTIVITY: NAH + UBIQUINONE + NA(+)(IN) = NAD(+) + UBIQUINONE + NA(+)(IN) = NAD(+) + COPPCTOR FAD AND A 2FE-2S CLUSTER (BY SIMILARITY).

SUBUNIT: COMPOSED OF SIX SUBUNITS; NQRA, NQRB, NQRC, NQRD, NQRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 LAK-----ATKTTLNGKEN--LAWFIGGTLGGLRKAGDWSATVRYEYVEAL----SVPEI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 VPS-ETSTTEKAATNAMKYKYCVWQWL----VGKHSQVPWINGQKK-PLYLYGAFLMNP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (BY SIMILARITY).
L -> P (IN REF. 3).
DGD9A7A474C62708 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DV-----SGIGRGNLL-------KFWF-AQAIAAN-YDPKEANSFTNYKGFSALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 FLIGGAGSSFGRSHILDLLLNKHSKREIDLWYGARSLKENIYQEEYENLERQFPNFH--Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001433; Oxidored_FAD.
Pfam; PF00115; F6F2; 1.
Pfam; PF00175; NAD_binding; 1.
PROSITE; PS00197; ZFEZS_FERREDOXIN; FALSE_NEG.
Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport; Flavoprotein; FAD; Iron-sulfur; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.5%; Score 75.5; DB 1; Length 431; 26.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                     SUBCELLULAR LOCATION: INNER MEMBRANE (POTENTIAL).
SIMILARITY: BELONGS TO THE NORF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 MYGITDSLSFRAYGAYSKPANDKLGSDFTFRKFDLGIIS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 HLVLSEPLPEDIAAGWDK--DDPTKTNFLFRAFNLGQLS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542
                                                                                                                                                                                                                                                                                                                                                                                                                                     FERREDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001041; Ferredoxin.
InterPro; IPR001433; Oxidored_FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                   EMBL; AE001669; AAD19021.1; -. EMBL; AE002256; AAF38762.1; -. EMBL; AP002548; BAA99091.1; -. HSSP; P00235; IFRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESTS_DROVI STANDARD; 005487; 01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48500 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        29
123
413
76
82
82
85
                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
TRANSMEM 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                   CP0983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
Matches 5
Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                  TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
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                                                                                                                      Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE-89392127; PubMed-2783177;
MEDILINE-89392127; PubMed-2783177;
SETGEV P.V. Castillo J.E., Peunova N.I., Yenikolopov G.N.;
Primary structure of the esterase s gene from Drosophila virilis.";
Bioorg: Kilin. 15:839-843(1989).
-i- FUNCTION: TRANSFERRED FROM THE EJACULATORY BULBS OF MALES TO
THE FEMALED GENITALS UPON COPULATION, PLAYS AN IMPORTANT ROLE
IN THE REPRODUCTIVE BIOLOGY.
-i- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O = AN ALCOHOL
+ A CARBOXXLIC ANION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKHSQVPWINGQKKPLYLYGAFLMNPLAKATKTTLNGKE-----NLAW-----FIG--G 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                       Sergeev P.V., Yenikolopov G.N., Peunova N.I., Kuzin B.A., Khechumian R.A., Korochkin L.I., Georgiev G.P., "Regulation of tissue-specific expression of the esterase S gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: IN THE MALE, IT APPEARS 3 DAYS AFTER EMERGENCE IN THE IMAGO STAGE AND REACHES MAXIMUM LEVELS BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: MONOMER.
-1- TISSUB SPECIFICITY: SPECIFICALLY EXPRESSED IN THE EJACULATORY BULBS OF MALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . .) (POTENTIAL)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
ESTERASE S PRECURSOR (EC 3.1.1.1) (EST-S) (CARBOXYLIC-ESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 75; DB 1; Length 542; 26.0%; Pred. No. 17; ive 23; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINKED (GLCNAC. . .) (PO 9134648A7B573F84 CRC64;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
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PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1.
Hydrolase; Serine esterase; Glycoprotein; S
SIGNAL 1 22 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase, FBgn0013077; Dvir\EstS.
InterPro; IPR002018; Carboxylesterase_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 21:3545-3551(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
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                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93347990; PubMed=8346032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X70351; CAA49809.1; -.
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PIR, S32019, S32019.
PIR, S34853, S34853.
HSSP, P21836, 1MAH.
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Search completed: February 7, 2002, 21:42:39 Job time: 593 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2002, 21:34:34 February Run on:

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US-09-391-606-8 2412 1 WVNPIGFGPIDETERTPPAD......QKLISEEDLNSAVDHHHHHH 490 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

522463 seqs, 74073290 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

/SIDS2/gcgdata/geneseq/geneseqp/AA1980. /SIDS2/gcgdata/geneseq/geneseqp/AA1981. A_Geneseq_1101:*

.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1982.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1985.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1987.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1989.DAT: . DAT: /SIDS2/gcgdata/geneseq/geneseqp/AA1990 /gcgdata/geneseq/geneseqp/AA1991 /SIDS2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	C. pneumoniae 76 k	Chlamydia pneumoni	3'-truncated Chlam	Chlamydia pneumoni	5'-truncated Chlam	Chlamydia trachoma	Chlamydia sp. prot	Protein encoded by	Extracellular fact	Chlamydia trachoma	Streptococcus pneu
	ID	AAY71957	AAY71954	AAY71956	AAY35358	AAY71955	AAY37571	AAB13695	AAG83263	AAR27745	AAY37572	AAY81609
	DB	21	21	21	20	21	20	21	22	13	20	21
	Query e Match Length DB I	490	. 651	452	478	583	350	361	361	1822	331	1237
ф	Query Match	99.2	90.7	90.5	9.68	76.7	11.7	9.6	9.6	7.5	6.8	6.4
	Score	2392	2188	2184	2162	1850	281.5	231.5	231.5	182	164.5	153.5
	Result No.	1	7	m	4	S	9	7	80	6	10	11

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7.	12	153	6.3	009	22	AAG91443	C glutamicum prote
	13	152		1561	17	AAW02098	S. mutans antiqen
	14	150.5	6.2	643	16	AAR84568	Trypanosoma cruzi
٠٠.	15	148		571	21	AAG29572	Arabidopsis thalia
	16	148		729	22	AAB19849 .	Mycobacterium tube
	17	4	6.1	881	22	AAG70752	S cerevisiae apopt
1.2	18	147.5		1095	22	AAG83030	S. epidermidis ope
	19	4		1566	16	AAR79643	Immunodominant ant
	20	144	٠	5024	22	AAG82935	S. epidermidis ope
7	21	142.5		1279	22	AAG83047	
44	22	142	-	1607	19	AAW50897	
es.	23		5.9	605	20	AAY21870	Amino acid sequenc
•	24	141.5		654	20	AAY21859	Amino acid sequenc
•	25			. 564	16	AAR84565	Trypanosoma cruzi
. ,,	56	140	٠.	876	22	AAG91035	C glutamicum prote
	27	138	5.7	999	20	AAY21871	Amino acid sequenc
٥	28	138	5.7	715	50	AAY21860	Amino acid sequenc
• •	53	138	5.7	1576		AAB19802	Human laminin 2 ma
	30	138	٠.	1576		AAB48453	Human laminin 8 po
. :	31	138	5.7	1584		AAB19804	Human laminin 2 ga
	32	138	5.7	1609		AAW50898	Human laminin Gl c
·	33	138	•	1609		AAB19801	Human laminin 2 ga
اعد	34	138	5.7	1609		AAB48452.	Human laminin 8 po
L.,	35	138		1617		AAB19803	Human laminin 2 ga
2.	36	138		2742		AAB23012	Human APC protein
	37	138		2842		AAR63508	Adenomatous polypo
	38	138		2843		AAR26052	APC gene product 1
٠,	36	138		2843	15	AAR58634	Adenomatous polypo
ď	40	138	5.7	2843	16	AAW11922	Adenomatous polypo
•	41	138	5.7	2843	18	AAW35392	Human adenomatous
	42	138		2843	19	AAW76140	
	43	138		84	19	AAW76144	Human APC protein
	44	138	5.7	4	19	AAW38370	
	45	138	5.7	2843	21	AAB23011	Human APC protein

ALIGNMENTS

pheumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; fusion protein; truncation mutant; C. pneumoniae 76 kDa protein truncation mutant fusion protein. 76 kDa protein; bactericidal; diagnosis; prevention; AAY71957 standard; Protein; 490 AA (first entry) 26-MAR-2001 AAY71957; mutein RESULT. AAY71957

pneumoniae. Chlamydia p Synthetic. Location/Qualifiers 453..490 "This part of the sequence is unrelated to the C. pneumoniae 76 kDa protein" 03-MAY-2000; 2000WO-CA00511 WO200066739-A2 09-NOV-2000 Key Region

(AVET) AVENTIS PASTEUR LTD.

99US-0132270.

03-MAY-1999; 30-JUN-1999;

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DDAENETASILMSGFROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK 420
         Chlamydia pneumoniae 76 kDa full-length protein.
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                                                          pneumoniae,
                                                                                                        The present sequence is a fusion protein comprising a truncated Chlamydia pneumoniae 76 kDa protein and vector-encoded residues. C. pneumoniae 76 kDa protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal cheat sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
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                                                                                                                                                                                                                                                 ; Score 2392; DB 21; Length 490;
; Pred. No. 5.8e-153;
.1; Mismatches 3; Indels 0
                                                         Nucleic acids encoding a 76 kDa protein from Chlamydia useful for vaccinating against Chlamydia infections -
         Dunn P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY71954 standard; Protein; 651 AA
                                                                                      Claim 33; Fig 3; 112pp; English.
          Wang J,
                                                                                                                                                                                                                                                 99.2%;
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         Oomen RP,
                            WPI; 2000-687542/67.
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                                                                                                                                                                                                                      490 AA;
                                      N-PSDB; AAD02066
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         Murdin AD,
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76 kDa protein; bactericidal; diagnosis; prevention; treatment; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a 76 kDa protein from Chlamydia pneumoniae, useful for vaccinating against Chlamydia infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is Chlamydia pneumoniae full-length 76 kba protein. C. pneumoniae 76 kba protein of under diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, harseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
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Pred. No. 4.3e-139;
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                                                                      vaccine; immunisation
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30-JUN-1999;
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AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinualitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584435879) can be used in immunogenic compositions as vaccines. Vectors containing C pneumoniae nucleotides sequences can also be used as immunogenic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                             QTDATATOIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQ
                                                                                                                                               KKPPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL
                                                                                                                                                           ASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD
  IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKY
                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae surface exposed polypeptide.
                                                                                                                                                                                                                                                         Genome sequence of Chlamydia pneumoniae
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97FR-0014673
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21-NOV-1997;
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                                                                                                                                                                                                                   76 kDa protein; bactericidal; diagnosis; prevention; phoeumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; truncation mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein from Chlamydia pneumoniae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is 3'-truncated Chlamydia pneumoniae 76 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acids encoding a 76 kDa protein from Chlamydor vaccinating against Chlamydia infections
                                                                                                                                                                                            3'-truncated Chlamydia pneumoniae 76 kDa protein.
                                                421 ALEAALGKAGQQQGILNALGQIASAAVVSAGVLP
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                                                                                                                     AAY71956 standard; Protein; 452
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99US-0141276.
                                                                                                                                                                                                                                                                                                                                                                    2000WO-CA00511
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                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                               Chlamydia pneumoniae.
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N-PSDB; AAD02065.
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30-JUN-1999;
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es 448;
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pneumoniae 76

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a 76 kDa protein from Chlamydia pneumoniae, against Chlamydia infections -
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                                                                                                                                                                   The present sequence is 5'-truncated Chlamydia pneumoniae 76 kDa protein. C.
                                                                                                                             Claim 16b; Page 100-102; 112pp; English
                                                                                                                                                                                                                                                                                                                                           C. pneumoniae.
                                                                       acids encoding
for vaccinating
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               2000-687542/67
                                                                                                                                                                                                                                                                                                                                                                                 583 AA;
                                   N-PSDB; AAD02064
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les 381;
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                                                                     Gaps
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                               478;
                                 Length
                                                                   Indels
                             Score 2162; DB 20;
Pred. No. 1.6e-137;
1; Mismatches 3;
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Misc-difference 497
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                             89.6%;
99.1%;
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99US-0141276.
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                                                                   443; Conservative
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Synthetic.
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Best Local Similarity
Matches 443; Conserv
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30-JUN-1999;
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                                                                                                                                                                                                                248
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                                                                                                                                                                                       DIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAIL 188
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                                                 ;
Similarity 98.7%; Score 1850; DB 21; Length 583; Similarity 98.7%; Pred. No. 2e-116; Conservative 1; Mismatches 4; Indels 0
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(first entry)

us-09-391 ÷606-8

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AAG83263 standard; Protein; 361
                                                                 Chlamydia sp. protein # 6.
                        02-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                               AAY36754-Y37949 are encoded by open reading frames (ORFS) of the genome of Chlamydia trachomatis (see AAX01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genttal diseases such as perihepatitis, bartholinitis; penimpatitis, sentendial paratrachoma, and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 ksglenaktlaeyetkmadlmaalgdmeansdpsndhteelnnikkaleagkdti---- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 RSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTI 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 MQDNPVVPGKTPAIAQSLVDQTDATATQIEKD....--GNAIGDAYFAGQNASGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---isnykavltdvekvikefseagiklggalgsivdagdgsgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 VENAKSNNSISNIDSAKAAIATAKTQIAEAQ---KKFPDSPILQEAEQMVIQAEKDLKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 281.5; DB 20;
Pred. No. 2.6e-11;
1; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..6e-11;
122;
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 1226-1227; 1755pp; English
                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB13695 standard; Protein; 361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Scilarity 24.9%; Pr
Conservative 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tps-gldipivgpsgsgxpqe 345
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                                                                                                                          98US-0107077.
97FR-0015041.
97FR-0016034.
                                                                                   98WO-IB01939
                                                                                                                                                                                                                                                                                           WPI; 1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 AA;
                                                                                                                                                                                                             (GEST ) GENSET
W09928475-A2
                                                                                   27-NOV-1998;
                                                                                                                                                                   17-DEC-1997;
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                                                                                                                          04-NOV-1998;
28-NOV-1997;
                                         10-JUN-1999
                                                                                                                                                                                                                                                      Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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AAB13695
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The present invention relates to new nücleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can bead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is also thought to play a role in the pathogenesis of atherosclerosis and concernary heart disease. The present sequence is a protein isolated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fling SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pages 251-253; 256pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                            98US-0208277.
99US-0288594.
99US-0410568.
99US-0426571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhatia A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
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                                                                                                                                                                                                                 WO200034483-A2
                                                                                                                                                         Chlamydia sp..
                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1998;
08-APR-1999;
01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                    08-DEC-1999;
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y Match 7.5%; Score 182; DB 13; Length 1822; Local Similarity 23.2%; Pred. No. 0.0011; ndels 146; Gaps nes 123; Conservative 81; Mismatches 181; Indels 146; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from Streptococcus suis type II (non-pathogenic) which allows the detection and the prevention of infections by S. suis in a more effective manner than was previously possible. It facilitates screening of e.g. pigs and elimination of infected and carrier pigs can then be carried out. The new diagnostic tests can distinguish between avirulent and virulent strains. It may be used in the prodn. of a vaccine. See also AAR27744 and AAR27746.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deoxyribonucleic acid encoding virulence characteristic of
Streptococcus suis – useful for antibody and polypeptide for
diagnosing and preventing infections in pigs and humans
                                                                                                                                                                                                               "repetitive Asn-Pro-Asn-Leu sequence"
                                                                                                                                                                                                                                               "repetitive Asn-Pro-Asn-Leu sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "repetitive Asn-Pro-Asn-Leu sequence"
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1666..1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "repetitive Asn-Pro-Asn-Leu sequence"
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1741..1744
                                                                                                                                                                                                                                                                                                                                       1264..1267
/note= "repetitive Asn-Pro-Asn-Leu
1362..1365
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1075..1078
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                                                                                                                                                                                                                                                                                                                                                                                              /note= "repetitive Asn-Pro-Asn-Leu
                                                                                                                                                                                                                                                                                                                                                                                                               1438..1441
/note= "repetitive Asn-Pro-Asn-Leu
                               screening; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus suis type II (non-pathogenic).
                                                                                                                                                     ...1822
ofe= "mature peptide"
                                                                                                                                      "signal peptide"
Extracellular factor related protein.
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DIER-) CENT DIERGENEESKUNDIG INST.
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                                 prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92WO-NL00054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1992;
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                                                                                                                                                           Peptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease
                                                                                                                       Chlamydia; vaccine; infection; fusion protein; antigen; pelvic inflammatory disease; trachoma; atherosclerosis; heart disease; acute respiratory tract infection; Capl; CT529; OMCB; polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scholler J;
                                                                                        Protein encoded by Chlamydia trachomatis clone CT622.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fling SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 66; Page 257-259; 295pp; English
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19-APR-2000; 2000US-0556877.
20-JUN-2000; 2000US-0598419.
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Best Local Similarity 35.49
Watches 57; Conservative
                                                    (first entry)
                                                                                                                                                                                                                 Chlamydia trachomatis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
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                  AAG83263;
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AAR27745
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of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vecines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases. e.g. e.g. e.g. blaseases such as conventional trachoma, nonendemic trachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, partholialis, penimpeathy in breast feeding infants; and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be useful as immunogens and/or antigens. The proteins and nucleotides can be useful for the diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcal protein, useful as a vaccine, for diagnosis of pneumococcal diseases and for screening agents capable of antagonizing or inhibiting expression of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 GTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 AQARAAK---AAGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis; pneumococcal disease.
                                                                                                                                                                                                                                                                                                                                                                           Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae type 4 protein sequence #109.
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.8%; Score 164.5; DB 20; Best Local Similarity 38.5%; Pred. No. 0.0018; Matches 45; Conservative 12; Mismatches 53;
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                                                                                                                                                                                                                                                                                         331 AA;
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                                                   ALMSLADKLGIASSNSSSSTSRSAD------VDSTTATAPTPPPPTSDDYKTQAQTAY 118
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1488 vldaakqda------
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17-DEC-1997;
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AAY3757 10
AAY3757 20
AAX3757 20
AAX377 20
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interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the exemplification of the present invention.
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                                                                                                                                                48;
                                                                                                                 Length 1237;
                                                                                                                                                Indels
                                                                                                                    DB 21;
                                                                                                                  ; Score 153.5; DB 21;
; Pred. No. 0.054;
84; Mismatches 205;
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                     6.48;
19.98;
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                                                                                                                     Query Match
Best Local Similarity 19.9%
Matches 84; Conservative
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03-AUG-2000;
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Yokoi H;

Ochiai K,

Hayashi M,

Nakagawa S, Mizoguchi H, Ando S,

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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALV 135
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                                                                                                                                                                                                                                   present invention provides a number of nucleotide and protein
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                                                                                                                                                                                            Listing; English.
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21.6%; Pred. No. 0.023;
tive 66; Mismatches 187; Indels
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Ozaki A;
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Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -aqalreqaltaa--siaaaaliaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
  Senoh A,
                                                                                                                                                                                                Claim 17; SEQ ID NO:
                                    WPI; 2001-376931/40.
N-PSDB; AAH66662.
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600 AA
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rateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW02098
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Matches
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AAR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi
The proteins are all fusion products with glutathione-Stransferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
a 95 amino acid (aa) N.terminal region; 69 repeats of a highly
conserved 14 as sequence and a 68 as C.terminal region. This sequence
encodes the GST sequence, the Ag44 polypeptide contg. 16 of the 69
repeat units and also contains the amino and carboxy terminal
contentiagnosis of Chagas disease (American Trypansonalisals), they
are capable of detecting anti-T.cruzi antibodies; or for blood
screening. The TCR27 protein has epitopes to which most T.cruzi
infected individuals have antibodies. The TCR27 polypeptides will not
react with serum from patients with leishmaniasis, schistosomiasis,
or autoimmune disease and are hence less likely to cause false
-- KQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTE 385
                      New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a immunoassay reagent for specific diagnosis of Chagas disease, also felated nucleic acid and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
329..552
/label= repeat_region
/note= "16 of 69 repeat units of 14 amino acids"
                                                                                                                                                                                                                                                                                                                                                                          TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 150.5; DB 16; Length 643; Pred. No. 0.037;
                                                                                                   NFDSQAAQQELAAQARAAKAA--GDDSAAAAL-ADAQKALEAALGK
                                                                                                                                                                                                                                                                                                                                     Trypanosoma cruzi TCR27 polypeptide, Ag15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 40-41; 68pp; English.
                                                                                                                                                                                                                   ΑĄ
                                                                                                                                                                                                                   AAR84568 standard; Protein; 643
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21.5%;
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                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-344618/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma cruzi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (irchhoff LV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09525797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0-MAR-1995;
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343 GS-
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                                                                                                           409
                                                                                                                                                                                              AAR84568
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                                                                            Óγ
                                                                                                             Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus mutans antigen I/II (AAW02098) is a 185 kDa cell surface protein at least partly responsible for 5. mutans adhesion to teeth. The I/II antigen includes a series of overlapping T-cell, B-cell and adhesion epitopes. Fragments (see also AAT36111-21) of the I/II antigen gene (see also AAT3612) can be used to produce recombinant polypeptides (AAW02087-97) carrying such epitopes for use in vaccines for immunisation against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 KESKIDSVERWSILRSAVNALMSLADKLGIASSN-SSSSTSRSADVDSTTATAPTPPPPT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 -----SDDYKTQAQTAYDTIFTST-----SLADIQAALVS-LQDAVTNIKDT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 AATDEETAIAAEWE-----TKNADAIK-----VGAQITELAKYASDNQAILDSLGK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 vktaee-avgketeikedytkgaedikkttdgyksdvaaheaevakikakngatkegygk 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----dmvahkaeverinaanaasktayeaklaqyqadlaavqktnaanqasy-qkalaay 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GSDVPNPGTTVG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caries; antigen I/II; epitope; tooth decay; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding polypeptide for prevention or treatment of dental caries - which stimulates T or B cell response, and/or adheres to tooth in competition with Streptococcus mutans antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 LTSFDLL-QTALLQSVANNNKAAEL-----LKEMQDNPVVPGKTPAIAQSLVDQTDATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIE----KDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK----TQIAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
                                                                                                         Key Location/Qualifiers
Misc-difference 618..650
/note= "maino acids 618-650 differ from the residues deduced from the nucleic acid sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1561;
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Best Local Similarity 22.3%; Pred. No. 0.093;
Matches 104; Conservative 82; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q---KKFPDSPILQEAE-QMVIQA-EKDLKNIKPAD----
                                                                                                                                                                                                                                                                                                                                                                                           (UNME-) UNITED MEDICAL & DENTAL SCHOOLS GUYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 45-46; 63pp; English.
                                                                                                                                                                                                                                                                                                                96WO-GB00207
                                                                                                                                                                                                                                                                                                                                                   95GB-0001826
S. mutans antigen I/II.
                                                                          Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-371434/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Lehner T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1561 AA;
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99US-0142055.
99US-0142390.
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99US-0144814.
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990S-0138540.
990S-0138547.
990S-0139119.
990S-0139452.
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990S-0134320
990S-0134370
990S-0134768
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                                                      99US-0132863
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                   05-MAY-1999;
06-MAY-1999;
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07-MAY-1999;
11-MAY-1999;
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14-MAY-1999;
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 17;
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                                                                                                                                                                                                                 127 LADIQAALVSLQDAVTN----IKDTAATDE-----ETAIAAEWETKNADAIKVGAQI 174
                                                                                                                           A----QSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSN-----NSISNID 283
                                                                                                                                                                                                                                               SAKAALATAKTQIAEAQK-KFPDSPILQEAEQM-----VIQAEKDLKNIKPADGSDVP 335
                                                                                                                                                                                                                                                             336 NPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQE 395
                                                                                                                                                                                                                                                                                                                 e----aekgkaaeatkva----eaekgkaaeatk-----vaeaekgkaaeat 533
                                                                  ALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT1FTSTS 126
                                                                                                                                                        175 TELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAI 234
                                                                                                                                                                               ------aekrkaaeaakavetekqraaeatkv 381
58; Mismatches 169; Indels 135; Gaps
                       PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVN 66
                                                                                        274 qaykaahk---aeeekaktfqrlitfeseninlkkrp--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 35209.
                                                                                                                                                                                                                                                                                                                                                    |:| ||| || || 534 kvaeaekgkaaeaakamesgkgrfl 572
                                                                                                                                                                                                                                                                                                                                       396 LAAQARAAKAAGDDSAAALADAQKALEAALGKAGQQQGIL 436
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
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  Conservative
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tkvae-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 termination sequence
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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06-APR-1999;
08-APR-1999;
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                                                                                                                                                                                                                       Indels 108;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Issued_Patents_AA:*

Database

SUMMARIES

		de			COLEGUITES	
Result No.	Score	Query Match	Length	DB	ID	Description
	152	6.3	1561	- 6	US-08-894-017-23	Segmence 23. Appl
2	150.5	2	643	C	-08-216-894-	i a
m	150.5	6.5	643	4	-09-115-746-	
4	147	6.1	1566	7	-08-687-956A	
2	146.5	6.1	1565	9		Patent No. 5352450
9	138.5	5.7	564	7	US-08-216-894-2	
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19	138	5.7	2973	7	US-08-821-355A-7	Sequence 7, Appli
20	138	5.7	2973	7	US-09-003-687A-7	7
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56	135.5	5.6	639	Н	08-467-78	7
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Gaps

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Length 1561; Indels

Ouery Match
6.3%; Score 152; DB 3; L
Best Local Similarity 22.3%; Pred. No. 0.004;
Matches 104; Conservative 82; Mismatches 182;

, MOLECULE TYPE: protein US-08-894-017-23

linear

TOPOLOGY:

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                        ---KQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTE
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TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 NPDSQAAQQELAAQARAAKAA--GDDSAAAAL-ADAQKALEAALGK 428
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
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3000 K Street, N.W., Suite 500
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APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-216-894-8; Sequence 8, Application US/08216894; Sequence 8, Application US/08216894; Patent No. 5876734; GENERAL INFORMATION:
                                                                                        SDDYKTQAQTAYDTIFTST
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202)672-5300 (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 643 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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                                                                                     7 PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEARPKESKTDSVERWSILRSAVN 66
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  Length 643;
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APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                              Indels
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  DB 2;
6.2%; Score 150.5; DB:
21.5%; Pred. No. 0.0015;
Ive 58; Mismatches 16
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09115746
Patent No. 6228601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 85.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                       21.5%;
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APPLICATION NUMBER: US
                                                Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                      351 TKVAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLIATE USA COUNTRY: USA TER 20007-5109
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                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-115-746-8
      Query Match
                                Local
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                                                Matches
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210 NNWKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGA 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 QMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 KESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSSTS--RSADVDSTTATAPTPPPP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 TSDDYKTQAQTAY-----DTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AANK-AEVERITNEN-----AQRKADY-EAKLAQYQKDLAAVQQANNDSQAAYAA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 VENAKSNNSISNIDSAKAAIATAKTQIAEA-----QKKFPDSPILQ-----EAE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              374 GFROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQ 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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TITLE OF INVENTION: METHOD FOR PREPARING VACCINE FOR DENTAL; CARIES OF VACCINAL COMPOSITIONS FOR DENTAL CARIES USED AS NASAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 AYEQALAANTAKN--AQITAENEAIQQRNAQAKA--NYEAKLAQYQKDLAAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.1%; Score 147; DB 2; Length 15
22.6%; Pred. No. 0.0097;
ive 75; Mismatches 209; Indels
                                                                                                                                      16,773
4R: 50885/222892
                                              APPLICATION NUMBER: GB 9401689.6
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus sobrinus
                                                                                                                                    REGISTRATION NUMBER: 16,777
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                             1566 amino acids
                                                                                                                                                                                                          202/861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.64
Matches 106; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                               KOKULIS, PAUL N
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unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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ORIGINAL SOURCE:
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;Patent No. 5352450
                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                    67 ALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------AEKRKAAEAAKAVETEKQRAAEATKV 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AEAEKOKAAEAAKAVETEKORAAEATKVAEAEKORAAEAMKVAEAEKOKAAEATKVAEAE 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 NPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 LADIQAALVSLQDAVTN----IKDTAATDE-----ETAIAAEWETKNADAIKVGAQI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 TELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAI 234
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                                                                                                                                                                                                                                                                                                              7 PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVN 66
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APPLICANT: MATTHEWS, RUTH C
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCI AND ENTEROCOCCI
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      Indels 135;
                                                                                                                                                                                                                               Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PILLSBURY, MADISON & SUTRO, LLP
STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9TH
STREET: FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                             QAYKAAHK---AEEEKAKTFQRLITFESENINLKKRP------
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,956A
FILING DATE: 29-UUL-1996
                                                                                                                                                                                                                          Score 150.5; DB 4;
Pred. No. 0.0015;
3; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 23, Application US/08687956A Patent No. 5861157 GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                        Query Match 6.2%;
Best Local Similarity 21.5%;
Matches 99; Conservative 5
                           œ
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acids
                                                                                                                                  , MOLECULE TYPE: protein US-09-115-746-8
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                                                                                                               TOPOLOGY:
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Query Match
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                                                                                                                                                                                                                                                                                                                                                          193 KLTSFDLLQTALLQSVANNNKAA--ELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIE 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----KDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK----TQIAEAQ-- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 IKERNENAKATYEAALKQYEADLAAVKKANAANEADYQAK---LTAYQTELARVQKANAD 412
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              180 KDMAAHKAEVERINAANAASKTAYEAKLAQYQADLAAVQKTNAANQAAY-QKALAAYQAE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 LKRVQEANAAAKAAY---DTAVAANNAKNTEIAAANEEIRKRNATAKAEYETKLAQYQAE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 T-----SDDYKTQAQTAYDTIFTST-----SLADIQAALVS-LQDAVTNIKD 146
                                                                                                                                                                                                                                                                                                                                      ---VGAQITELAKYASDNQAILDSLG 192
                                                                                                                                                                                           48 KESKTDSVERWSILRSAVNALMSLADKLGIASSN--SSSSTSRSADVDSTTATAPTPPPP 105
                                                                                                                                                                                                                        2 KVKKIYGFRKSKISKILCGAVLGTVAAVSVAGQKVFADETTTITSDVDTKVVGTQTGNPA 61
                                                                                                                                                         91;
                                                                                                                        Length 1565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08216894
Patent No. 5876734
GENERAL INFORMATION:
APPLICANT: Kirchhoff, Louis V.
APPLICANT: Kirchhoff, Louis V.
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQAAQQELAAQARAAKAA--GDDSAAAAL-ADAQKALEAALGK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                      Ouery Match 6.1%; Score 146.5; DB 6; Best Local Similarity 21.8%; Pred. No. 0.011; Matches 101; Conservative 81; Mismatches. 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 85326/102/DRLO
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
APPLICATION NUMBER: US/07/529,602
FILING DATE: 29-MAY-1990
                                                                                                                                                                                                                                                                                                                                         147 TAATDEETAIAAEWE-----TKNADAIK-
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MEDIUM TYPE: Floppy disk
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20007-5109
                                 ;SEQ ID NO:2:
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5352450-2
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US-08-216-894-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VIQAEKDLKNIKPADGSDVPNPGTTVG 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 AEKOKAAEATKVA-----EAEKOKAAEATK-----VAEAEKOKAAEATKVAEAEK 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 PPKSDLVPRGSPSQL--QQAENNITNSKKEMTKLREKVKKAEKEKLDAINRATKLEBERN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 LADIQAALVSLQDAVTN----IKDTAATDE-----ETAIAAEWETKNADAIKVGAQI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTS 126
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     7 PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKIDSVERWSILRSAVN 66
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                                                                                                                                                                                                                                                                                                                                                                                   Indels 137;
                                                                                                                                                                                                                                                                                                                                   Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE FOLGY & Landner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                              ; Score 138.5; DB 2;
; Pred. No. 0.01;
54; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 QAYKAAHK---AEEEKAKTFQRLITFESENINLKKRP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 TAKTQIAEAQK-KFPDSPILQEAEQM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kirchhoff, Louis V. APPLICANT: Otsu, Keiko
; TELEFAX: (202)672-5300
TELERAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino
                                                                                                                                                                                                                                                                                                                                                           21.4%;
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Matches 97; Conservative
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APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-216-894-2
                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 TKVAE---
                                                                                                                                                                                                            TOPOLOGY:
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1838 AFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAEL----RKAKENK---ESE 1890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKP 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1658 DLIIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKA 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1778 IPONTEYRTRVRKNADSKNNLNAERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSF 1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TNIKDT--AATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKLTSFDLLQTALLQSVANNNKAAELLKEM----QDNPVVPGKTPAIAQSLVDQTDATAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAARAAGDDSAAAAL 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 PPTSDDYKTQAQTAYDT----IFT-----STSLADIQAALVSLQDAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 138; DB 1; Length 2842;
20.0%; Pred. No. 0.11;
ive 82; Mismatches 194; Indels 144;
       GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 DETERTPPADLSA-QGLEASAANKSAEAQRIAGAEAKPKE----SKTDSV
                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 ILOEAEOMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1946 TDEKLON-----FAIENTPVCFSHNSSLSSLSDID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1107.035574
                                                                                                                                                                                                                                                                                                                                              US/07/741,940
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                           32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 11 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                       Birch,
                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2842 amino acids
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                                                                         3: Banner, Bir
1001 G Street,
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US
FILING DATE: 19920109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kagan, Sarah A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
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                                                                                                   STATE: P
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Best Local Similarity
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                                                                                                                                                               N: USA
20001-4598
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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CLONE: APC
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                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308 -----NDAVSNRDKKKNSETAKTDEVEKQRAAEAAKAVETEKQRA-----AEA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 GSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARA 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 PPKSDLVPRGSPSQL--QQAENNITNSKKEMTKLREKVKKAEKEKLDAINRATKLEEERN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 LADIQAALVSLQDAVTN----IKDTAATDE-----ETAIAAEWETKNADAIKVGAQI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 A----QSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 ---TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQ----KAAEATKVAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 TELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 AEAEKOKAAEAAKAVETEKORAAEATKVAEAEKORAAEAMK-----VAEAEKOKAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 QAYKAAHK---AEEEKAKTFQRLITFESENINLKKRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.01;
                                                                                                             29,768
3R: 85326/102/DRLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 138.5; 21.4%; Pred. No. 0.0
                APPLICATION NUMBER: 08/216,894
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/07741940 Patent No. 5352775
                                                                                     NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                             TELERAX: (204)
TELERAX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 amino acids
"YPE: amino acids
"YPE: amino acids
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GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALBERTSEN, HANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21.49
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-115-746-2
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ALBERT
APPLICANT: ANAND,
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US-07-741-940-7
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2031 I-----DSEDDLLQECISS-----AMPKKKKPSRLKGDNEKHSPRNMGGILGED-LTLDL 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%; Score 138; DB 1; Length 2842;
20.0%; Pred. No. 0.11;
ve 82; Mismatches 194; Indels 144;
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 DETERTPPADLSA-QGLEASAANKSAEAQRIAGAEAKPKE----SKTDSV-
                                                           416 ADAOKA-LEAALG------KAGOQ--QGILNALGQIASAAVVS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,548A
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERNCE/DOCKET NUMBER: 1107.46943
TELECOMMUNICATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Banner & Allegretti, LTD 1001 G Street, NW
                                                                                                                                                                 Sequence 7, Application US/08289548A Patent No. 5648212
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KINZLER, KENNETH
MARKHAM, ALEXANDER F.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                        CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
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SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 20.0
Matches 105; Conservative
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IMMEDIATE SOURCE:
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APPLICANT: ALBERT
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                                                                                                                                  RESULT 9
US-08-289-548A-7
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                    248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
                                                                                            -TNIKDT---AATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSL 191
                                                                                                                                                                                                                                                                                                                                                                                      ----QGSSIGSIR 355
--STSLADIQAALVSLQDAV---- 141
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GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2080 KDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLS 2124
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                                                                                                                                                                                                                                                                                                                       1946 TDEKLQN-----FAIENTPVCFSHNSSLSSLSDID----
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILLING DATE: 25-MAY-1995
CLASSIFICATION: 536
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
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CORRESPONDENCE ADDRESS
     104 PPTSDDYKTQAQTAYDT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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1659 DLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKA 1718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
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                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19920109
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,141
REFERENCE/POCKET UNMBER: 1107.035574
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.7%; Score 138; DB 1; L. Best Local Similarity 20.0%; Pred. No. 0.11; Matches 105; Conservative 82; Mismatches 194;
                                                           3: Banner, Birch, McKie & Beckett
1001 G Street, NW
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                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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                                                                                                                              Washington
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                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1838 AFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAEL----RKAKENK---ESE 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1976 -- OENNN---KENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLS 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | :|| :|| :| :| :| | : | | DLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKA 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | || || :| : || || :| || || EBGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKP 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : :|:|: | : :| |: |: |: |: |: |- |: |- |: |- |: |- |: |- |: |- |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |- |: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 138; DB 1; Length 2842;
Pred. No. 0.11;
2; Mismatches 194; Indels 144;
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TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DETERTPPADLSA-QGLEASAANKSAEAQRIAGAEAKPKE----SKTDSV-
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MARKHAM, ALEXANDER F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
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   INFORMATION FOR SEQ 12.
SEQUENCE CHARACTERISTICS:
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GRODEN, JOANNA
                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens; IMMEDIATE SOURCE: CLONE: APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 20.0°
Matches 105; Conservative
202-508-9299
                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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APPLICANT: ALBERT
TELEFAX:
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US-07-741-940-2
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Gaps

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1892 AKVTS----HTELTSNQQSANKTQAIAKQPINKGQPKPILQ-KQSTFPQSSKDIPDRGAA 1946
                                                                                                                                             2032 I-----DSEDDLLQECISS-----AMPKKKRPSRLKGDNEKHSPRNMGGILGED-LTLDL 2080
                                     248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
                                                                                                                      ----QGSSIGSIR 355
                                                                                                                                                                                                   356 VSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF A
                                                                                                                                                                                                                                                                                                       2081 KDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLS 2125
                                                                                                                                                                                                                                                                              416 ADAQKA-LEAALG------KAGQQ--QGILNALGQIASAAVVS 449
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                      308 ILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQ----
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                                                                                 1947 TDEKLON----FAIENTPVCFSHNSSLSSLSDID
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APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08452654
Patent No. 5691454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MARKHAM, ALEXANDER
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REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALBERTSEN, HANS
ANAND, RAKESH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOSLYN, GEOFF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAKAMURA,
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                                                                                                                                                                                                                                                                                                                           AND SOMATIC MUTATIONS OF APC
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF PTITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
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PatentIn Release #1.0, Version #1.25
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12-AUG-1994
                                                                  Sequence 2, Application US/08289548A Patent No. 5648212
                                                                                                                                                                                                                                              KINZLER, KENNETH
AARKHAM, ALEXANDER F.
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TELEPHONE: 202-508-9100
                                                                                                                                                                  CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
                                                                                                                                                                                                                                                                                      NAKAMURA, YUSUKE
THLIVERIS, ANDRE
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kagan, Sarah A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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Matches 105; Conserv
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                                                                                                              GENERAL INFORMATION
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US-08-289-548A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                   US-08-289-548A-2
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1892 AKVTS----HTELTSNQQSANKTQAIAKQPINRGQPKPILQ-KQSTFPQSSKDIPDRGAA 1946
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llarity 20.0%; Pred. No. 0.11;
Conservative 82; Mismatches 194;
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                                                                                                                                                                                                                  1107.49964
            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
                                                                                                              APPLICATION NUMBER: US 07/741,940 FILING DATE: 08-AUG-1991 ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
                                                                                                                                                                                             32,141
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMÁUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFÁX: 202-508-9299
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GRODEN, JOANNA
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                                                                                                                                                                            NAME: Kagan, Sarah A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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TELEFAX: 20
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TOPOLOGY:
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Best Local S
Matches 105
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                                                                                                                1659 DLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKA 1718
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                                                                                                                                                     ERWSILRSAVNALM ....-SLADKLGIASSNSSSSTSRSADVDSTTATAPTPP 103
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                                   Gaps
                                                                                                                                                                                                                                     104 PPTSDDYKTQAQTAYDT-----IFT----STSLADIQAALVSLQDAV---
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                                   194; Indels 144;
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TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                          DETERTPPADLSA-QGLEASAANKSAEAQRIAGAEAKPKE----SKTDSV
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                Pred. No. 0.11; Mismatches
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25-MAY-1995
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APPLICATION DATA:
APPLICATION NUMBER: US/08/467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: Banner & Witcoff, Ltd.
T: 1001 G Street, NW
Washington
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OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
20.0%; Pie-
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THLIVERIS, ANDREW
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CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
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APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
              Best Local Similarity 20.09
Matches 105; Conservative
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COMPUTER READABLE FORM:
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US-08-452-655B-2
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APPLICANT:
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12	Qy 248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
MARKHAM, NAKAMURA,	Db 1947 TDEKLQNFAIENTPVCFSHNSSLSSLSDID1976
: THLIVERIS, INVENTION: I	QY 308 ILQEAEQMYIQAEKDLKNIKPADGSDVPNFGTTVGGSKQGGSSIGSIR 355
6	2.5. UGUT TINA ENIEMACHT MCCHENIEMENINI ENIEMACAN ACANA MANAKANANA
CORRESTORMENT ADDRESS. SADDRESSE: Banner & Mitcoff, Ltd. STREET: 1001 G Street, NW	OY 500 VSMILDUDARENETAS.LMSGFROMIHMFNTERFUSQAAQQELAAQQARAAAAUDDSAAAAL 415 - - - - - - - - - - - - - - - - - -
- N	A16 ADARKA: IDANICVARON. COTINATORIA SANTOR A40
COUNTRY: USA	410 ADAQNA-DEAALGAGAQQQGILNALGQIASAAVVS
; ZIP: 20001-4598 ; COMPUTER READABLE FORM:	Db 2081 KDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLS 2125
; MEDIUM TYPE: Floppy disk : COMPUTER: THW PC Compa+ihle	
OPERATING SYSTEM: POPENSY OF THE STATE OF TH	Search completed: February 7, 2002, 21:36:19
ATA:	100 CIEC. 20400 SCC
; APPLICATION NUMBER: US/US/452,655B ; FILING DATE: 25-MAY-1995	
; CLASSIFICATION: 530 ; PRIOR APPLICATION DATA:	
: APPLICATION NUMBER: US 08/289,548 : FILING DAME: 12-AUG-1994	
À	
.; APPLICATION NUMBER: US 07/741,940 ; FILING DATE: 08-AUG-1991	
П	
; REFERENCE/DOCKET NUMBER: 1107.49964 ; TELECOMMUNICATION INFORMATION:	
; TELEPHONE: 202-508-9100 ; TELEPHONE: 202-508-9299	
<u>ب</u> ب	
: LENGTH: 2843 amino acids : TVPE: amino acids	
8 6	
⊣ …	
; HYPOTHETICAL: YES ; ANTI ESENSE: NO US-08-452-655B-7	
atch 5.7%; cal Similarity 20.0%;	
)5; Conserva	
11	
DD 1659 DLILESPPNELAAGEGVRGGAQSGEFERRDTIPTEGRSTDEAQGGRTSSVTIPELDDNKA 1718	
56 ERWSILRSAVNALMSLADKLGIASSNSSSTSRSADVDSTTATAPPP	
Db 1719 EEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKFTSPVKP 1778	
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GTPYCFSRNDSLSSLD	
QY 192 GKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATAT 247	

us-09-391 606-8.rpr

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; Search time 96.2 Seconds (without alignments) 387.999 Million cell updates/sec
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2412
1 WVNPIGPGPIDETERTPPAD......QKLISEEDLNSAVDHHHHH 490
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                           February 7, 2002, 21:38:03
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                 Title:
Perfect score:
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Run on:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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intermediate filam transducer protein Htrl transducer [i halobacterial tran Htr5 transducer [i hypothetical 76K p conserved hypothet CHLPN 76 kDa homol hypothetical prote probable membrane probable tail fibe extracellular matr EF protein - Strep Htr7 transducer [i transducer protein probable secreted related to transcr hypothetical prote Htr2 transducer [i transducer protein hypothetical prote hypothetical prote ransducer protein halobacterial tran Htr14 transducer {R27-2 protein - Tr Description SUMMARIES 140729 D72042 D72042 G714591 G714591 C85683 T73141 E84194 T744934 T744934 T744934 T744934 T74892 T74892 T74892 T74892 T74892 T74892 T74892 T74892 T74892 T74892 T74892 T74892 T7508 T75082 T750 Query Match Length DB 11122 20055 20055 10055 11128 11128 11158 11158 11158 11158 11158 11169 11169 11169 11169 11169 11169 11169 11169 11 188 178 174.5 174.5 171 170 166.5 160.5 160.5 158 158 158 156.5 156.5 155.5 155.5 155.5 155.1 154.5 154.5 2214 2188 2188 2188 451.5 201 190 Score Result Š

tail fiber protein	phage lambda-relat	surface antigen A	surface antigen sp	hypothetical prote	probable exonuclea	Htr8 transducer (i	cell surface antig	hypothetical prote	hypothetical prote	probable membrane	saliva-interacting	surface-located me	transducer protein	microtubule-associ	hypothetical prote
T14650	T14968	A60338	806839	T34418	T03465	H84305	A43607	D86164	E70803	S56032	A60988	JC6009	T48897	T13564	н83098
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6.3	6.3	6.3	6.3	6.3	6.3	6.2	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1
152.5	152.5	152.5	1.52	152	151.5	150.5	1.49	1.48	1.48	1.48	1.48	147.5	1.47	1.47	146.5
30	31	۳ ش	33	34	35	36	37	38	39	40	4.1	42	43	44	45
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ALIGNMENTS

RESULT	1
140729 hypotheti C;Species C;Date: 1	140729 Nypothetical 76K protein - Chlamydophila pneumoniae (strain AR39) C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C.Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000
C; Accessi R; Perez-N Infect. I	C;Accession: 140/29 R;Perez-Melgosa, M.; Kuo, C. Infect. Immun. 62, 880-886, 1994
A; Title: A; Referer A: Accessi	A:Title: Isolation and characterization of a gene encoding a Chlamydia pneumoniae 76 A:Reference number: 140729; MUID:94156481 A:Anchesion: 140720
A; Status:	Status: Iranslated from GB/EMBL/DDBJ
A: Residue	A;Residues: 1-715 <res> A;Cross-references: (Re:12392): NTD:a435961: DIDN:AAA23117 1: DID:a435962</res>
A; Experin	A:Experimental source: strain AR-39 C:Comment: This is the hypothetical translation of a sequence that was reported as t
- - -	
	91.8%; Score 2214; DB 2; Length 715; Similarity 98.9%; Pred. No. 1.6e-110;
Matches	454; Conservative
0y 1	1 MVNPIGPGPIDETERTPPADLSAGGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI 60
Ďb 257	7 LVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI 316
0γ 61	
Db 317	7 LRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTFDDYKTQAQTAYDT 376
Qy 121	
225 qa	7 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAVKVGAQITELAKY 436
Qy 181	ASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD 240
Db ,437	
Qy 241	
DD 497	7 OTDATATOIEKDGNAIRDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATATATOIAEAQ 556
Qy 301	
ob 1557	7 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL 616
Qy 361	1 DDÄENETASILMSGFROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK 420
pb 617	
oy 421	l albaalgkagqqqtinalgqiasaavvsagvlplqqvl 459

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K.; Shiba,

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Gaps

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J138)

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hypothetical protein CT622 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
N.Alternate names: chlpn 76kda homolog CT622
C.Species: Chlamydia trachomatis
C.Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C.Accession: G71490
R.Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitch Science 282, 754-759, 1998
A.;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia A;Reference number: A71570; MUID:99000809
A.Accession: G71490
A.;Accession: G71490
A.;Molecule type: DNA
A.;Molecule type: DNA
A.;Molecule type: DNA
A.;Molecule type: DNA
A.;Cross-references: GB:AE001333; GB:AE001273; NID:93329068; PIDN:AAC68226.1; PID:933
                                                  CHLPN 76 kDa homolog_1 (CT622) [imported] - Chlamydophila pneumoniae (strain J138) C. Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae, C. Species: C. Anar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C. Ancession: E86581
R: Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000
A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID:20330349
A; Reference number: A86491; MUID:20330349
A; Residues: 1-651 <ATO>
A; Residues: 1-651 <ATO>
A; Residues: 1-651 <ATO>
A; Residues: CSPIDN; BAA98935.1; GSPDB:GN00142
A; Residues: CSPIDN28
A; Residues: CSPIDN28
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                                                                                                                                          conserved hypothetical protein CP0018 [imported] - Chlamydophila pneumoniae (strains CWI N; Alternate names: Chlpn 76 Kda homolog_1 (Ct622); hypothetical protein CP00728

C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C; Accession: D72042; D81623

R; Kalman, S; Mitchell, W; Marathe, R; Lammel, C; Fan, J; Olinger, L; Grimwood, J;
R; Kalman, S; Mitchell, W; Marathe, R; Lammel, C; Fan, J; Olinger, L; Grimwood, J;
R; Kalman, S; Mitchell, W; Marathe, R; Lammel, C; Fan, J; Olinger, L; Grimwood, J;
R; Kalman, S; Mitchell, W; Marathe, R; Lammel, C; Fan, J; Olinger, L; Grimwood, J;
R; Keference number: A72000; MUID:99206606

A; Accession: D72042
A; Molecule type: DNA
A; Residues: 1-651 ARNA
A; Residues: 1-651 ARNA
A; Cross-references: GB:AE001654; GB:AE001363; NID:94377031; PIDN:AAD18867.1; PID:9437703
A; Cross-references: Strain CWID29
A; Experimental source: strain CWID29
A; R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J; McClarty, G; Salzberg, C; Dodson, R; Gwinn, M; Nelson, W; DeBoy, R; Kolonay, J; McClarty, G; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AE002165; GB: AE002161; NID: 97188948; PIDN: AAF37914.1; PID: 9718895 A; Experimental source: strain AR39, HL cells C; Comment: This sequence was originally identified as homologous to part of a sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
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larity 98.9%; Pred. No. 3.5e-109;
Conservative 1; Mismatches 4;
ALEAALGKAGQQQGILNALGQIASAAVVSAGVLP 454
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Matches 449; Conserv
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A;Gene: CPn0728; CP0018
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probable tail fiber protein GP37 - Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 **sequence_revision 17-Sep-1997 **text_change 21-Jul-2000
C;Accession: G64887; T09189
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1455-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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A;Reference number: A64720; MUID:97426617

A;Accession: G64887

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1122 <BLAT>
A;Cess references: GB:AED000234; GB:U00096; NID:91787633; PIDN:AAC74454.1; PID:91787
A;Cess references: GB:AED000234; GB:U00096; NID:91787633; PIDN:AAC74454.1; PID:91787
A;Experimental source: strain K-12, substrain MG1655
B;Aiba, H; Baba, T; Fujita, K; Hayashi, K; Inada, T; Isono, K; Itoh, T; Kasai
A; Motourta, K; Nakade, S; Nakamura, Y; Nashimoto, H; Nishlo, Y; Oshima, T; Sa
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A;Molacoule type: DNA
Residues: 3-1122 <ALB>
A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74454.1; PID:g1787
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DNA Res. 3, 363-377, 1996
Arithe: A 570-Kb DNA sequence of the Escherichia coli K-12 genome corresponding A; Reference number: 216603; MUID:97251357
A; Accession: T09189
        TSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT1FTSTSLADIQAALVSLQDAVTNIK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NIDSAKAAIATAKTQIAE-----AQKKFPDSPILQEAEQMVIQAEKDLK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVALEDAS-----TTKKGIVQLSSATNSTSESLAATPKAVKAAYELANGKYTAQDATTA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 QKGIVQLSNATNSTSEM----LAATPKSVKAAYDLANGKYTAQDATTAQKGIVQLSSATN 566
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                                                                  ---ETNAKSSETAAEQSASAAAGSKTAAALSASAASTSAGQASASATAAGKSAESAASSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASKDEATROASAAKSSATTASTKATEAAGSATAAAQSKSTAESAATRAETAAKRAEDIAS
                                                                                                                                                                       DTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALL
                                                                                                                                                                                                                                                                                                                                          QSVANNNKAAELLKEMQDNPVVPGKTPA----IAQSLVDQTDATATQIEKD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GNAIGDAYFAGQNASGA---VENAKSNNSIS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||: || ||::|| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: |
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Matches 110; Conserv
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A;Cross-references: GB:AE005174; NID:912514847; PIDN:AAG56007.1; GSPDB:GN00145; UWGP:219
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.J.; Mayhew
K.; Apodaca,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDY---KTQAQTAY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 SSAKHALISLRD--AILNKNSSPTDSLS-QLEASTSTS-TVTRVAARDYNEAKSNFDTAK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGLENATTLAEYETKMADLMAALQDMERLAKQKAEVTRIKEALQEKQEVID----KLNQLV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQKK---FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSI- 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 VDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAE
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                                                                                                                                                                                                                                                                                                                                                                              51;
ital source: serotype D, strain UW-3/Cx This sequence was originally identified as homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 130;
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                                                                                                                                                                                                                                                                                     18.7%; Score 451.5; DB 2; 29.6%; Pred. No. 7.3e-17; ive 85; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.3%; Score 201; DB 2; L
22.9%; Pred. No. 0.0026;
tive 64; Mismatches 210;
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20; Conservative
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 29.6
Matches 138; Conservative
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                                   C;Comment: Thi
PIR:E72042).
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                                                                                                                  C;Genetics:
A;Gene: CT622
                                                                                                                                                                                                                                                                                          Query Match
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Matches 12
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T.; N. T.; S

Db 1	150 AADSARAASTSAGQAAS-SAQSASSSAGTASTKATEASKSAAAAESSKSAAATSAGAAKT 208	ON SAIDSAKAAITAHAKTOIAEAOKK
Qy 1	124 STSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASD 183	1851 AOKDAGKDAINAVPOTPTAKTDAKNAVDQAATD
Dp 5	209 SETNASASLQSAATSASTATTKASEAATSARDAAASKEAAKSSETNASSSA 259	326
	NQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTD	1911
DD 7	260 SSAASSATAAGNSAKAAKTSETNARSSETAAGOSASAAAGSKTAAASSASAASTS 314	Qy 384 TENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK
Qy 2 Db 3	244 ATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKF 303 	1971
Qy 3	304 PDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDA 363	Oy 442 IASAAVVSAGVLPLQQVLMIRARYQAYVEQKLISEEI
Dp 3	350ASAARSASAAKTSETNAKASETSAESSKTAAASSASSASSASSASSASKDEA 402	2020 IFIANIDANNAVD
0y 3	364 ENETASILMSGFRQMIHMFNTENPDSQAAQOELAAQARAAKAAGDDSAAAALAD 417 : ::	RESULT 8 \$33441 FF protein - Streptococcus suis
		C: Pate: Strengtococcus suis C:Date: 06-Jan-1995 #sequence revision 06-Jan-1
	ASTTKAUKGIVQLSSAINSTSETLAATPKAVKSAYDNAEKRLQK	C; Accession: S33441 R; Smith, H.B.; Reck, F.H.; Vecht, U.; Gielkens,
Qy 4	478 DLNSA 482	Submitted to the EMBL Data Library, May 1993 A; Description: Repeats in an extracellular prot
Dp 2	505 DQNGA 509	on: S33441
RESULT	7	Asserves pre-imminary Associate type: DNA Asserves 11822 < STILL S
Extrace	llular matrix binding protein - Abiotrophia defectiva (fragment)	A;CIOSS-IETETETICES: EMBL:A/IOOU; NID:YZ90U31;
C; Speci C; Date:	es: Abiotrophia defectiva 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000	90
C; Acces R; Mange	nelli, R.; van de Rijn, I.	Best Local Similarity 22.9%; Pred No. 0.0 Matches 122; Conservative 80; Mismatchee
Intect A; Title A; Refer	Infinding and characterization of emb, a gene encoding the major adhesin of Strep ence number: 220988; MUID:99081722	
A; Acces A; Statu	sion: T31110 s: preliminary; translated from GB/EMBL/DDBJ	1201
A; Molec A; Resic A; Cross	A; Molecule type: DNA A; Residues: 1-2055 CMAN> A; Cross-references: EMBL:AF067776; NID:93249002; PID:93249003; PIDN:AAD03320.1	QY 71 LADKKGIASNNSSSSTSKRAD-VUSTATAPTPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
C; General A; General	ics: emb	QY 130 IQAALVSLQDAVTNIKDTAATDEETAIAAEWETK
Quer}	7.88;	1310 LEKAKETOKIADKAAIDRLTILVKDGE
Best Matc)	Similarity' 23.9%; Pred. No. 0.034; 4; Conservative 68; Mismatches 197;	QY 188 LDSLGKLTSFDLLQTALLQSVANNNKAAEI
Qy Db 16	19 ADLSAQGLEASAANKSAEAQRIAGAEAFPKESKTDSVERWSILRSAVNALMSIAD 73	241
		DD 1415 AAKQDAKNKIAKDAAAAKEAIGSNPNLTDAEKKŢFŢ QY 290 ATAKTQIAEAQKKFPDSPILQEAEQWVIQAEKDLKN
oy Lo		1466 AATSPADVQKE-EDAGVAAIAE
DP 16	1699 QNEGTKAINDVPQTPTAKTDAKNAVDQAATDKKSAIENDPALTREEKDAAKAKVDAEATK 1758	QY 341VGGSKQGGSSIC Db 1522 KESAKKAVDADAKAATDAIDASTSPVEAQSAEDKGV
Oy 1	177 LAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAI 234	
ζ	235AQSLVDQTDATATQIEKD-GNAIGDAYFACQNASGAVENAKSNNSI- 279	1582
Db 17		QY 433 QCILNALGLASAAVVSAGVLFLQQVLWIRAKKQAI
		,

otein of wek-pathogenic strains are abse 23; DDSAAAALADAQKALEAALGKAGQQ 432 | | | : : | | | : : :D--ASTSPVEAQSAEDKGVGSI--R 1637 IGSIRVSML---LDDAENETASILM 372 |||| || || || || || VGSIAQDVLDAAKQDAKNKIAKEVA 1581 OKALEAALGKAGQQQG--ILNALGQ 441
| | : | : |
| ------TAKQNEGTKAINIVPQ 2019 :| :|: | :|11 DNADKRTQEAEKA-----QALAD 1309 | ||:|::|| TDAVDAEVAKANDAIS----- 1465 -1995 #text_change 15-Oct-1999 || : || : 1364 TKQDAKNKIAKDAAAKEAIASNPN 1364 ||:| | RTDAKNAVDQAATDKKNAIENDPA 1970 NIKPADGSDV-----340 LLDDAENETASILMSGFROMIHMFN 383 PIDN:CAA50714.1; PID:g298032 PTSDDYKTQAQTAYDTIFTSTSLAD 129 KNADAIKVGAQITELAKYASDNQAI 187 ----VENAKSNNSISNIDSAKAAI 289 KES-KTDSVERWSIL-RSAVNALMS 70 DB 2; Length 1822; 1.098; les 201; Indels 130; AVEQKLISEED-LNSAVD 484 s, A.L.J.; Smits, M.A. NDAN 2047 EDLN 480

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17;

Gaps

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C; Species: Halobacterium sp. NRC-1
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C; Accession: F84194
R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lask; J. Lathauser: B.; Kellar, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; J. Jung, K.H.; Alam, M.; Frettas, T. 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M. A;Tille: Genome sequence of Halobacterium species NRC-1.
                                                              A; Cross-references: EMBL: X95589; NID:g1435130; PIDN: CAA64842.1; PID:g1435132 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 TPAIAQSLVDQTDAT-----ATQIEKDGNAIGD--AYFAGQNASGAVENAKSNNS 278
                                                                                                                                                                                                                                                                                                                                                                        72 ADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPT-SDDYKTQAQTAYDTI-----FTST 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLADIQAALVSLQDAVTNIKDT----AATDEE----TAIAAEWETKNADAIKVGAQITE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAKYASDNQAILDSLGKLT-----SFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 EEERA-----EAERAREKAEOKQAEAER----OTAEAESAKQDARERSAEIEOLAADLESQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISN-IDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 QETTDGVQE-----USQAMDEQAQRSERVVSS------VDDIATISQATA 483
                                                                                                                                                                                                                                                                                      ETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 171; DB 2; Length 627;
23.4%; Pred. No. 0.057;
tive 87; Mismatches 184; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE004437; NID: 910579976; PIDN: AAG18922.1;
                                                                                                                        A;Gene: htpV
C;Superfamily: Halobacterium salinarum transducer protein htrI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halobacterium salinarum transducer protein htrI
                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                       7.2%; Score 174.5; DB 2;
21.7%; Pred. No. 0.031;
Live 79; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Htr14 transducer [imported] - Halobacterium sp. NRC-1
                     preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
Matches 120; Conserv
                 A Status: preliminary; 1
A Molecule type: DNA
A Residues: 1-545 <RUD>
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-627 <STO>
                                                                                                                                                                                                                                                  100;
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Best Local
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Matches
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                                             C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C; Accession: E84327
R; 94, W.V; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li, A; Reference number: A84160; MuID:20504483
A; Status: preliminary
A; Molecule tvop. NAT
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T46811
halobacterial transducer protein V [imported] - Halobacterium salinarum
C;Speciaes: Halobacterium salinarum
C;Speciaes: Halobacterium salinarum
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 15-Sep-2000
C;Accession: T46811
R;Rudolph, J; Nordmann, B.; Storch, K.F.; Gruenberg, H.; Rodewald, K.; Oesterhelt, RFEMS Microbiol. Lett. 139, 161-168, 1996
A;Title: A family of halobacterial transducer proteins.
A;Reference number: 224094; MUID:96275896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GB:AE004437; NID:g10581214; PIDN:AAG19985.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLADIQAALVSLQDAVTNIKDT ---- AATDEE --- TAIAAEWETKNADAIKVGAQITE 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPT-SDDYKTQAQTAYDTI-----FTST 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISN-IDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :68
  --KNKIAKESDAAKSAID 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 174.5; DB 2;
21.7%; Pred. No. 0.031;
iive 79; Mismatches 192;
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Best Local Similarity 21.7%
Matches 100; Conservative
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Residues: 1-545 <STO>
1638 QDVLDAAKQDA-
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27;

Gaps

GSPDB:GN00138

Qy 17 PPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKIDSVERWS-ILRSAVNALMSL 71	Db 783 AEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVA 839
Db 145 PALDESVPGAFGESITEMADSLEAYTABLEDKTAELEHQQAELERQSEQLRALVDALSEA 204	OY 232 PAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDS 284
Qy 72 ADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTS 124 Ob 208 mbanabachtanabachtanabachtanabachtanabachtanabachtanabachtanabacht	EAEKQKAAEATKVAEAEKQKAAEATKVAEAEKOKAAEATKVAEAEK XXXXXTXIIIXVIIIXXIIXXXXXXXXXXXXXXXXXXXX
125 TSLADIQAALVSLQDAVTNIKDTAATDEETALAABAA	CY ZOO ARAALATAKUULARAUN-KEPOSTLUGABUMVIQHAKUUNANTAKAUGSUYPN 330
	QY 337 PGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQEL 396
QY 168 IKVGAQITELAKYASDNQAILDSLGKL-TSFDLLQTALLQSVANNNKAAELLKEMQ 222 :: ::	Db 953AEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATK 991 Qy 397 AAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAGV 452
QY 223 DNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKS 275 :	D 992 VAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAAKA 1048 OV 453 LPLOOVLWIRARYOAVVEOKLISEEDLNSAV 483
NNSISNIDSAKAAIÄTÄKTQIAEAQKKFPDSP-ILQEAEQMVIQAEKDLKNIKP 328 	pb 1049MESQKQRFLERFAVLEEEKKAAL 1071
SIRVSMLLDD 362 : : : : TDEVADQMDE 535	RESULT 13 T34434 Typothetical protein K06A9.1a - Caenorhabditis elegans C;Species: Caenorhabditis elegans
OY 363 AENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADA 418 1	C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000 C;Accession: 134434 R;Geisel, C:; Gattung, S. submitted to the EMBL Data Library, December 1996
OY 419 OKALEAALGKAGQOOGILNALGQIASAAVVSAG 451 DD 588 QPASDAEDEGVPPSGGESVAVSDGG 613	A;Description: The sequence of C. elegans cosmid K06A9. A;Reference number: 221525 A;Accession: 734434 A;Status: preliminary: translated from GB/EMBL/DDBJ
	A; Molecule type: DNA A; Residues: 1-2232 <gel> A; Cross-references: EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9.1a A; Experimental source: strain Bristol N2; clone K06A9</gel>
999 #text_change 17-Mar-2000	C;Genetics: A;Gene: CESP:K06A9.la A;Map position: X
C.Accession, 190230, J.E.; Kirchhoff, L.V. Mol. Biochem. Parasitol. 57, 317-330, 1993 A.Title: Interruption of a Trypanosoma cruzi gene encoding a protein containing 14-amind A.Beferonce number. 720813. MITD: 03185082	A; Incrons: 50/1; /5/5; 105/5; 152/2; 158/2; 242/1; 108/1; 130//1; 2039/1; 2049/1; 2 Query Match
A; Accession: T30296 A; Status: preliminary; translated from GB/EMBL/DDBJ	Matches 79; Conservative 70; Mismatches 174; Indels 79; Ga
A:Molecule type: DNA A;Residues: 1-1128 <ots> A;Cross-references: EMBL:L04603; NID:g385171; PID:g1256742; PIDN:AAA96494.1 C;Superfamily: neurofilament triplet H protein</ots>	QY 4 PIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWS 59 by 598 pssospapntgsttpsqtssqspspsmnpssstptgssqsttppegstassptgstgstf 657
Query Match 7.0%; Score 170; DB 2; Length 1128;	QY 60 ILRSAVNALMSLADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTSDDYKTOAGTA 117 : : : : : :
BEST LOCAL SIMILATILY 22.7%; Pred. NO. 0.14; Matches 117; Conservative 82; Mismatches 222; Indels 90; Gaps 20; Qy 10 IDETERTPPADLSAQGLEASAANKSAEAQRIAGAEA-KPKESKTDSVERWSILRSA 64	OY 118 YDTIFT-STSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITE 176 D
Db 614 VAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEA 673 Qy 65 VNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDXKTQAQTAXDTIFTS 124	OY 177 LAKYASDNQAILDSLGKLTTSFDLLQTALLQSVANNNKAABLLKEMQDNPVVPGKTPAIAQ 236 Db 760 -SSQGSTSPAASTTSGEMTSQGSTQT
	237 SLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK
OY LEST TEMBLIQUEAUTHOUSE TRANSPORTE TRANSPORTE TO THE TOTAL TO THE TOTAL TRANSPORTED TO THE TOTAL TRANSPORTED TO THE TOTAL THE TOTAL TRANSPORTED TO THE TOTAL TRANSPORTED THE TOTAL TRANSPORTED THE TOTAL TRANSPORTE TRANSPORTE TRANSPORTE TRANSPORTE TRANSPORTED TO THE TOTAL TRANSPORTE TRA	DD /94 ALLISTQQSVSTNSPGSTVTRFSTVSGSTSSGSTVTVGSTEASTSGSSVASSSPAPSTSQ 853 QY 294 TQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQ 347
QY 178 AKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKT 231	854 NPNPSTSSGSSMITQSPYPSQSTSPVESSTTPSPGSPGTTLTSTSPSPG

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Rioliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M submitted to the EMBL Data Library, February 1999
A; Reference number: 221559
A; Accession: T34652
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: DNA
A; Residues: 1-1156 < OLL)
A; Residues: 1-1156 < OLL)
A; Cross-references: EMBL:AL035478; PIDN:CAB36606.1; GSPDB:GN00070; SCOEDB:SC2G5.19
A; Experimental source: strain A3(2)
A; Gometics:
A; Gometics:
A; Gometics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVAAQASGAAQSEAAVARAAAAEADAQAARA----TKAANRAQSLANTAASAAAARKAA 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 ILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRALPDKAALDDRATILTILNTAGPYTAAAAQVA----LEGTSWMRRDFITTVQHSAAQL 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMS-
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 1156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                 6.7%; Score 160.5; DB 2;
21.0%; Pred. No. 0.46;
ive 79; Mismatches 240;
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Best Local Similarity 21.0%
Matches 102; Conservative
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Job time: 7096 sec
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                                                                                                                                                                                                                                     Transducer protein htpv [similarity] - Halobacterium salinarum
N'Alternate names: methyl-accepting taxis protein ht]; transducer protein ht]; transduce;
Species: Halobacterium salinarum
C;Becies: Halobacterium salinarum
C;Becies: Halobacterium salinarum
C;Baccession: T44938
R;Zhang, W; Brooun, A; McCandless, J; Banda, P; Alam, M.
R;Zhang, W; Brooun, A; McCandless, J; Banda, P; Alam, M.
R;Zhang, W; Brooun, A; McCandless, J; Banda, P; Alam, M.
R;Zhang, W; Brooun, A; McCandless, J; Banda, P; Alam, M.
R;Reference number: 222804; MUID:96209786
A;Tille: Signal transduction in the archaeon Halobacterium salinarium is processed throu A;Reference number: 222804; MUID:96209786
A;Reference number: 22804; MUID:96209786
A;Refous: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-544 < CHA
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C;Superfamily: Halobacterium salinarum transducer protein htrI
C;Keywords: methylated amino acid; signal transduction; transmembrane protein
F;246-502/Region: MCP signalling domain similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable secreted protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T34852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 TS-----LADIQAALVSLQDAVTNIKDTAATDEE----TAIAAEWETKNADAIKVGAQI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 ----IAELISDIAEQTNMLALNANIEAARAGSGGGTNGDGFAVVADEVKELATESQRSA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 KDIAELIEEVOSOTATTVEEIRVAEORVNDGAAAVEETVDAFGAVTENIQETTDGVQEIS 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKTPAIAQSLVDQTDAT------ATQIEKDGNAIGD--AYFAGQNASGAVENAKSN
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                                                                        348 GSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDS
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US-09-391-606-8 2412 1 MVNPIGPGPIDETERTPPAD......QKLISEEDLNSAVDHHHHH 490 Title: Perfect score: Sequence:

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SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query					
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7	174.5		545	Н	HTR5_HALN1	. 048318	
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13	147		778	Н	HTR6_HALSA	048319	halobacteri
14	146.5		774	~	STF_LAMBD	P03764	bacteriopha
15	146		1714	٦	SYEP_DROME	P28668	
16	145		705	Н	CWBA_BACSU	002113	
17	145	0.9	1565	Н	PAC_STRMU	P11657	
18	144		1637	Н	MRSP_STAAU	P80544	
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20	142.5		778	Н	HTR6_HALN1	Q9hr92	
21	140		436	Н	Y868_CHLMU	09pjg1	_
22	139.5	٠	2492	Н	TALA_DICDI	P54633	_
23	139		797	Н	VGLX_HSVEB	P28968	_
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56	137.5		2453		NCR1_MOUSE	060974	mus n
27	137		200	Н	FLJB_SALAE	P52615	salmonella
28	137		535	-	HTR1_HALSA	P33955	halobacteri
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                                                                                                                                                                   AVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFT 123
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SPECIES=H.salinarium; STRAIN=S9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 QETTDGVQE------USQAMDEQAQRSERVVSS------VDDIATISQATA 483
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                                                                                                                                                                                    MICTODIOL LELL. 139:161-168(1996).
FUNCTION: POTENTIALLY INVOLVED IN CHEMO- OR PHOTOTACTIC SIGNAL
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Rodewald K.,
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Nordmann B., Storch K.F., Gruenberg H.,
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21.7%; Pred. No. 0.028;
ive 79; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 AQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGILN 437
                                                                                                                               proteins.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transducer; Transmembrane; Complete proteome.
TRANSMEM 10 30 POTENTIAL.
TRANSMEM 44 64 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X95589; CAA64842.1;
InterPro; IPR000122; Chemotaxis_transducer.
InterPro; IPR003660; HAMP.
Pfam, PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
                                                                                                                        halobacterial transducer pol. Lett. 139:161-168(1996)
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64 PC
100 PC
57070 MW;
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SRSADVDST---TATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTN 143

87

221

59

--SADIEASAGDTVEAVSKIESQANDQRTELDSAAD------DVQQVSASAEEIAAT

EAAATGDLTQRVDVDTDHEAMETVGTAFNQMMDDLQATVRTVTTVADEIEAKTERMSET- 220

86

-----SILRSAVNALMSLADKLGIASSNSSSST

8 GPIDETERTPPADLSAQGLEASAANKSAE--AQRIAGAEAKPKE---SKTDSVERW----

. Q άġ ō IKDTAATDEETAIAAE-------WETKNADAIKVGAQITELAKYASDNQAIL 188 270 IDDLASRSEDVATASDAARDSSKSALDEMSSIETEVDDAVGQVEQLRDQVAEITDIVDVI 329

144

qq ... X ... qq ... X

189

: : | : | : | : | : : | 330 TDIGEQTNMLALNASIEAARAGGNADGDGFSVVADEVKDLAEETQDR----ANEIAAVVEK 386

DSLGKLTSFDLLQTALLQSVANNN------KAAELLKEMQDNPVVPGKTPAIAQS

387

P ò q δy g

238

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435

298

LVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIA

EIDRITSEQAETVOSTATSVERVAGLSDDTTALASDAE---SAVIGORESAEEIAA---- 487

358 MLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAG 407

A

STANDARD;

HTR4_HALN1

HTR4_HALN1

EAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVS

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rsp.
ns-00-391+60e-8
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                                                                                                                                                                                                                                                                                                                                                                                                 NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Wellti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Genome sequence of Halobacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methyl-accepting protein associated with sensory rhodopsin I.";
Proc. Natl. Acad. Sci. U.S.A. 89:11915-11919(1992).
-!- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR SENSORY RHODOPSIN I (SR-I) TO THE FLAGELLAR MOTOR. RESPONDS TO LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
-!- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
20-AUG-2001 (Rel. 40, Last annotation update)
SENSORY RHODOPSIN I TRANSDUCER (HTR-1) (METHYL-ACCEPTING PHOTOTAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-10; 350-377 AND 457-476.
                                                                                                                      Halobacterium sp. (strain NRC-1), and
Halobacterium halobium.
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-H.halobium; STRAIN-FLX5R;
MEDINE-93101637; PubMed-1465418;
Yao V.J., Spudich J.L.;
"Primary structure of an archaebacterial transducer, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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InterPro; IPR000658; DUF5.
InterPro; IPR003660; HAMP.
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METHYLATION.
METHYLATION.
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                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20504483; PubMed=11016950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L05603; AAA72315.1;
PIR; A47190; A47190.
                                                           PROTEIN I) (MPP-I).
HTRI OR HTRI OR VNG1659G.
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SM00283; MA; 1.
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                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                      Halobacterium
                                                                                                                                                                                                                                                                                                                                                STRAIN=NRC-1
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                              MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
My W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSDUCTION (BY SIMILARITY).
                                                                                                                             Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                      20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HIRS OR HIPIV OR VNG1760G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE005080; AAG19986.1; -.
InterPro; IPR000122; Chemotaxis_transducer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seq
                                                                                                                                                                                            NCBI_TaxID=64091;
                                                                                                                                                                          Halobacterium
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15;

Gaps

Indels 110;

6.6%; Score 158; DB 1; Length 535; 18.7%; Pred. No. 0.19; tive 83; Mismatches 189; Indels 1

Conservative

Query Match Best Local Similarity Matches 88; Conserv

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FUNCTION: POTENTIALLY INVOLVED IN CHEMO- OR PHOTOTACTIC SIGNAL TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                          Length 810;
                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
37B0F6046A39D9BA CRC64;
                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                          6.6%; Score 158; DB 1; L
21.8%; Pred. No. 0.31;
iive 75; Mismatches 169;
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Last annotation update)
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InterPro; IPR000122; Chemotaxis_transducer
InterPro; IPR000658; DUF5.
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(Rel. 32, Last sequ
(Rel. 32, Last anno
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Pfam; PF00672; DUF5; 1.
Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
                                                                                                                                                                                                                                                           Transducer; Transmembrane.
DOMAIN 1 38
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345
810 AA;
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01-NOV-1995 (
01-NOV-1995 (
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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                        6.6%; Score 158; DB 1; Length 810; 22.0%; Pred. No. 0.31;
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                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                           CYTOPLASMIC (POTENTIAL).
4BF36E4B7D22BD80 CRC64;
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                                                                                           CYTOPLASMIC (POTENTIAL).
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Rudolph J., Nordmann B., Storch K.F., Gruenberg H.,
Oesterhelt D.;
"A family of halobacterial transducer proteins.";
"A family of halobacterial transducer proteins.";
FEMS Microbiol. Lett. 139:161-168(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HALOBACTERIAL TRANSDUCER PROTEIN IV.
                                                                                Transducer; Transmembrane; Complete proteome.
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                                                                                                                                   POTENTIAL.
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                                                                                                                                                        85219 MW;
                            Pfam; PF00672; DUF5; 1.
Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
                                                                                                                                                                                                                       Matches 102; Conservative
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    IPR000658;
IPR003660;
                                                                                                                                                                                                            Best Local Similarity
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SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
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552 -SAAIEEVA-------ASADSVAEHSHQTA-EIARDGE-----
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MA W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Ashartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Acham M., Lower T.M., Liang P., Riley M., Hood L., DasSarma S.;

Ronome, sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

RRODOPSIN II (SR-II) TO THE FLAGELIAR MOTOR. RESPONDS TO LIGHT

CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION (BY
                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SENSORY RHODOPSIN II TRANSDUCER (HTR-II) (METHYL-ACCEPTING PHOTOTAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GPIDETERTPPADLSAQGLEASAANKSAE----AQRIAGAEAKPKE---SKTDSVERW 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY
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                                                                                                                                                                                                                                                                                                                                                            Halobacterium sp. (strain NRC-1).
Archaea: Euryarchaeota; Halobacteriales; Halobacteriaceae;
Halobacterium.
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CF7A8FF04DFF309A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000658; DUFS.
                                                                                                                                                                                  763
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Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
SMART; SM00283; MA; 1.
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                                                    472 OTDLATADKAVDKHN 486
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                               PROTEIN II) (MPP-II).
HTR2 OR VNG1765G.
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763 AA;
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INIT_MET 0
DOMAIN 1
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Q9HP81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leu S., Hutcheson S.W.; Nucleotide sequence and properties of the hrmA locus associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 DSVERWSILRSAVNALMSLADKLGIASSNSSSSTSRSADVDS-----TTATAPTPPPPT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 KNADAIKVGAQITELAKYASDNQAILDSL -----GKLTSFDLLQTALLQSVANNN 212
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                                                                                                                                                                                                                                                   Xiao Y., Heu S., Yi J., Lu Y., Hutcheson S.W.;
"Identification of a putative alternate sigma factor and
characterization of a multicomponent regulatory cascade controlling
the expression of Pseudomonas syringae pv. syringae Pss61 hrp and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 ADKDVAKYMEDNPGADPQSLEMVRSAAVMRANMPLATAADPHHAVGAADKTDV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 AEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAE-NETASI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 LMSGFROMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAALGKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 154.5; DB 1; Length 641;
Pred. No. 0.35;
9; Mismatches 204; Indels 121;
                                               Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Pseudomonas syringae pv. syringae 61 hrp gene cluster.";
Mol. Plant Microbe Interact. 6:553-564(1993).
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SEQUENCE 641 AA; 67678 MW; EC098941E5B46C8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 176:1025-1036(1994)
                                                                                                                                                                                                                         MEDLINE-94148760; PubMed-8106313;
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PATHOGENICITY LOCUS PROTEIN HRPK
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SEQUENCE FROM N.A.
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                                                                                                                                                     [1]
SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=321;
                                                                                                                                                                                                    STRAIN-PSS61
                                                                                                 Pseudomonas
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Photoreceptor;
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                                                                                                                                               Similarity
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37
278
299
764 AA;
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NCBI_TaxID=1317;
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P21979;
01-AUG-1991 (
01-FEB-1996 (
01-FEB-1996 (
 Transducer;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SENSORY RHODOPSIN II TRANSDUCER (HTR-II) (METHYL-ACCEPTING PHOTOTAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              salinarium blue
                                                                                                                                                                                     616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 93:8230-8235(1996).
-!- FUNCTION: TRANSDUCES SIGNALS FROM THE PHOTOTAXIS RECEPTOR
SENSORY RHODOPSIN II (SR-II) TO THE FLAGELLAR MOTOR. RESPONDS TO
LIGHT CHANGES THROUGH THE VARIATION OF THE LEVEL OF METHYLATION.
-!- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
                                                                                                                                                                                                                274 -KSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGS 332
                                                                                                                                                                                                                                                                   DVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAA 392
                          396 RALESAAADYEEALTAVAD--GDLTRRVDASRDHDAMARIGHALNDMLDDIETSVAAATA 453
                                                                                                        162 TKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEM 221
 -DVDSTTATAPT 101
                                                   102 PPPPTSDDYKTQAQTAYDTIFTSTADIQAALVSLQDAVTNIKDTAATDEETAIAAEWE
                                                                                                                                                                                                                                454 FSDHVSDAAQRVEADAGDAIDAGT---DVSTAVDEISDGATE-----QTDRLHEVAGEVD
                                                                                                                      QDNPVVP-GKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENA-----
                                                                                                                                                                                    563 LDSEMADIGEIVDVIADIADQTNMLAL-----NASIEAARTGADGDGFAVVADEVKTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang W., Brooun A., Mueller M.M., Alam M.;
"The primary structures of the Archaeon Halobacterium salinarium
light receptor sensory rhodopsin II and its transducer, a methyl
                                                                                                                                                                                                                                                                                              -----VSFVADTDTAAGEIRAA---TDRQAHAASRVASAVDEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                        393 QQELAAQARA-AKAAGD-----DSAAAALADAQKALEAALGK 428
                                                                                                                                                                                                                                                                                                                                                 707 SQETAAQATAVADSAATQTDTLSSVDDAAADLADRAAALDDLLAE 751
                                                                                                                                                                                                                                                                                                                                                                                                                    ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000122; Chemotaxis_transducer.
InterPro; IPR000668; DUF5.
InterPro; IPR000560; HAMP.
Pfam; PF00672; DUF5; 1.
Pfam; PF0015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
 SILRSAV - - - - NALMSLADKLGIASSNSSSSTSRSA
                                                                                                                                                                                                                                                                                                                                                                                                                   764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96323203; PubMed=8710852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium salinarium.
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MPP-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accepting protein."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2242;
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HTR2 OR HTRII
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P71410;
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-----DVDSTTATAPT 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSDHVSDAAQRVEADAGDAIDAGT----DVSTAVDEISDGATE-----QTDRLHEVAGEVD 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          507 DLSASAEEVAETVASLADTAGQAASAVDD-GRQATEDAVET--MDDVADDAEAAADAMDA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 LDSEMADIGEIVDVIADIADQTNMLAL-----NASIEAARTGADGDGFAVVADEVKTLA 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNIKPADGS 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 DVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 GTLAESFRSMRDSLSESLTDAERATARAEDAREDAEQORADAEAAREDAEAARKDAQETA 396
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                              8 GPIDETERTPPADLSAQGLEASAANKSAE-----AQRIAGAEAKPKE---SKTDSVERW 58
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SEQUENCE FROM N.A.
MEDIANE=91310320; Pubmed=1855987;
Lapolla R.J., Haron J.A., Kelly C.G., Taylor W.R., Bohart C.,
Hendricks M., Pyati J., Graff R.T., Ma J.K.C., Lehner T.;
Sequence and Structural analysis of surface protein antigen I/II
(SpaA) of Streptococcus sobrinus.";
Infect. Immun. 59:2677-2685(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 PPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| :| :| | | : EESRDAAEDIESRLLALQGQVSDVADEMRATSDT--VSDGRATVGDAATALDDV-----
                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                                                                                                                   DB 1; Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODNPVVP-GKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENA-
                                                                                                                                                                                                                                                                                                                                      71; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQETAAQATAVADSAATQTDTLSSVDDAAADLADRAAALDDELAE 752
                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 QQELAAQARA-AKAAGD-----DSAAAALADAQKALEAALGK 428
                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
1E0D7B4E460FC588 CRC64;
Transmembrane; Methylation.
                             BY SIMILARITY.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 423-817 FROM N.A.
MEDLINE-90299827; PubMed-1694526;
Goldschmidt R.M., Thoren-Gordon M., Curtiss R. III;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus downel (Streptococcus sobrinus).
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.SILRSAV----NALMSLADKLGIASSNSSSSTSRSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                   Score 154.5; Di
Pred. No. 0.44;
                                                                                                                                        POTENTIAL.
                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                   MM;
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79187 M
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Conservative
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                                                                                                                                                                                                                                           Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 104;
                                                                                                SPAP_STRMU
P23504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                 SPAP_STRMU
                                                                RESULT
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                      CELL SURFACE ANTIGEN II.
CONSERVED IN GRAM-POSITIVE COCCI SURFACE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 TATAPTPPPPTSDDYKTQAQTAY-----DTİFTSTSLADIQAALVSLQDAVTNIKDTA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 TGNPATNLPDKQDNPSSQAETSQAQARQKTGAMSVDVSTSELDEAAKSPQEAGVTVSQDA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 ATDEETAIAAEWETKNADAIK--VGAQITELAKYASD-----NQAILDSLGKLTSFDL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 LQTALLQSVANNNKAAE--LLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 DAYFAGON-------ASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 -AYAAAKEAYDKEWARVQAANAAAKKAYEEALAANTAKN-DQIKAEIEAIQQRSAKA--- 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DYEAKLAQYEKDLAAAQAGNAANEADYQAKKAAYEQELARV------Q 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 AANAAAK---QAYEQALAANSAKNAQITAENEAIQQN--AQAKA------DYEAKLAQY 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 QKALEAA-LGKAGQQQGILNALG-----QIASAAVVSAGVLPLQQVLWIRARYQAY 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 KRLLGA-AKVKSGRTLS---GALLGTAI--LASGAGOKALAEETSTTSTSGGDTAVVGTE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 QRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSSTS--RSADVDST 95
                                            -i- SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-i- MISCELLANEOUS: IMMUNODOMINANT DETERMINANTS ARE LOCATED IN THE C-TERMINAL TWO-THIRDS OF THE SPAP PROTEIN.
-i- SIMILARITY: BELONGS TO THE SPAP/SSPS/SPAA FAMILY.
-i- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AENETASILMSGFRQMIHMFNTEN----PDSQAAQQELAAQARAAKAAGDDSAAAALADA
   Streptococcus sobrinus spaA gene encoding major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1528;
                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> E (IN REF. 2).
Q -> K (IN REF. 2).
Q -> K (IN REF. 2).
A -> S (IN REF. 2).
A -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                    Antigen; Signal; Transmembrane; Repeat; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                 CELL SURFACE ANTIGEN CELL SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.3%; Score 152.5; 23.3%; Pred. No. 1.3
                                                                                                                                                                                                                                                                                 EMBL; X57841; CAA40973.1; --
EMBL; M38210; AAA26977.1; --
InterPro; IPR001899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; 1.
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                     J. Bacteriol. 172:3988-4001(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116; Conservative
"Regions of the Streptocodeterminants of antigen I
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1508
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531
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434 43.
531 53
600 60
1528 AA;
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CONFLICT
SEQUENCE
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Best Local S
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STRAIN-NGS SERCTYPE C;
MEDLINE=91207143; Pubmed=1982405;
MEDLINE=91207143; Pubmed=1982405;
MEBLINC C., Evans P., Ma J.K.C., Bergmeier L.A., Taylor W., Brady L.J.,
Lee S.F., Bleiweis A.S., Lehner T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90076473; PubMed-2687020;
Kelly C., Evans P., Bergmeier L., Lee S.F., Progulske-Fox A.,
Harris A.C., Aitken A., Bleiweis A.S., Lehner T.;
"Sequence analysis of the cloned streptococcal cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus mutans.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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HELICAL (POTENTIAL).
TANDEM REPERTS, ALA-RICH.
X TANDEM REPEATS, PRO-RICH.
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W; 540D92768FC8AB4B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL SURFACE ANTIGEN I.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CELL SURFACE ANTIGEN I/II PRECURSOR.
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                                                                                                                                                                                                                                                                                     1561 AA
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STANDARD;
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Pred. No. 0.56;
59; Mismatches 168;
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21.0%; Pred. No. 0
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EMBL; V01370; CAAZ4655.1; -...
EMBL; D26168; BAA05156.1; -...
StyGene; SG10564; fijs.
InterPro; IPR001029; Flagellin_C.
InterPro; IPR001029; Flagellin_C.
Pfam; PF00700; Flagellin_C; I...
Pfam; PF00700; Flagellin_N; I...
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ProDom; PD000316; Flagellin_C; 1.
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Submitted (JAN-1994) to the ENBL/GenBank/DDBJ databases.
-!- FUNCTION: FLAGELLIN IS THE SUGUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
-!- MISCELLANEOUS: INDIVIDUAL SALMONBLLA SEROTYPES USUALLY ALTERNATE BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED PHASE-1 AND PHASE-2. BACH SPECIFIED BY SEPARATE STROUTUAL GENES.
-!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIE----KDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK----TQIAEA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 QAELKRVQEANAANEADYQAKLTAYQTELARVQKANADAKAAYEAAVAANNAKNAALTAE 351
                                                                                                                                                  121 VKTAEE-AVOKETEIKEDYTKOAEDIKKTTDOYKSDVAAHEAEVAKIKAKNOATKEOYGK 179
                                                                                                                                                                                                                                                                                                                                                        194 LTSFDLL-QTALLQSVANNNKAAEL-----LKEMQDNPVVPGKTPAIAQSLVDQTDATAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KESKIDSVERWSILRSAVNALMSLADKLGIASSN-SSSSISRSADVDSTIATAPIPPPPT 106
                                                                                                                -----SDDYKTQAQTAYDTIFTST-----SLADIQAALVS-LQDAVTNIKDT 147
                                                                                                                                                                                                                                    AATDEETAIAAEWE-----TKNADAIK------VGAQITELAKYASDNQAILDSLGK 193
                                                                                                                                                                                                                                                                                                                                                                                                           ----DMVAHKAEVERINAANAASKTAYEAKLAQYQADLAAVQKTNAANQASY-QKALAAY 234
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                                                   KVKKTYGFRKSKISKTLCGAVLGTVAAVSVAGQKVFADETTTTSDVDTKVVGTQTGNPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Silverman M., Zieg J., Mandel G., Simon M.;
"Analysis of the functional components of the phase variation
system.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 NPDSQAAQQELAAQARAAKAA--GDDSAAAAL-ADAQKALEAALGK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 NADAKAAYEAAVAANNAANAALTAENTAIKKRNADAKADYEAKLAK 454
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Last annotation update)
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P52616; P97159;
Ol-oCT-1996 (Rel. 34, Created)
Ol-oCT-1996 (Rel. 34, Last sequ
30-MAY-2000 (Rel. 39, Last ann
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SEQUENCE OF 482-505 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLJB OR H2.
Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 GS----
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Pfam; P=00672; DUF5; 1
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778 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2242;
                                                                                                                                                                                                                                                                                          HTR4 OR HTPVI.
                                                                                                                                                                                                                                                                                                                                                                Halobacterium
                                                                                               RESULT 13
HTR6_HALSA
ID HTR6_HALSA
AC Q48319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
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                                                                                                                                                  <u>Б</u>.
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DVDSTTATAPTPPPTSDDYKTQAQTAYDTIFT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 -SDNQAILDSLGKLTSFDLLQTALLQSVANN----NKAAELLKEMQDNPVVPGKTPAIA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISTSCSTLNGASTOTSELTTSPMKT ----NTVVPASSFPSTTTTCLENDDTAFSSIYTE 743
                                                                                                                                                                                                            Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)2-Cys6 binuclear cluster domain and a putative alpha 2-ScB-alpha 2 binding site. "; Yeast 11:681-689(1955).
-:- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 SAQGLEASAA--NKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIAS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: | |: | |: || ETAQAS-----SSTEKNISNSAATSSSI-----YSNSASVS-GHGVTYAAEYAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 AVTIDPTLDPTDNSASPTDNAKHTSTYGSSSTGASLDSLRTTTSISVSSNTTQLVST---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      521 SEQSSALATSVPATNCSSIVKTTTLENSSTTTITAITKSTTTLATTANN-----STRAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                   Miosga T., Schaaff-Gerstenschlaeger I., Chalwatzis N., Baur A. Boles E., Fournier C., Schmitt S., Velten C., Wilhelm N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Score 148; DB 1; Length 881;
21.8%; Pred. No. 1.1;
                                                                                                                                                                                          "Sequence analysis of a 33.1 kb fragment from the left arm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 199; Indels
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37DBAC660CA9D12A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00198; SCP, 1.
PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
                                                                                          MEDLINE=96093911; PubMed=7483841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
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881 AA; 89152 MW;
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EMBL; X83502; CAA58492.1; -.
EMBL; CAA61314.1; -.
HSSP; P04284; ICFE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGD; S0003614; YJL078C.
InterPro; IPR001283; SCP.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
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                                                                                                                                                                      Zimmermann F.K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALGDDGQAAAQDAV - - AQLEEIEDETQAAATAVDDLEAKMSEIETIVAAITDIAEQTNM 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ADKLGIASSN-SSSSTSRSADVDSTTATAPPPPFTSDDYKTQAQTAYDTIFTSTSL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE CHEMOTAXIS SENSORY TRANSDUCERS FAMILY.
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                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSL-
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EXTRACELLULAR (POTENTIAL)
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134C7D7F0A3334CD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-96275896; PubMed-8674984;
Rudolph J., Nordmann B., Storch K.F., Gruenberg H.,
Oesterhelt D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A family of halobacterial transducer proteins.";
744 VNAATIINPGETSSLASDFATSEKPNEPTSVKSTSNEG 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HALOBACTERIAL TRANSDUCER PROTEIN VI.
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InterPro; IPR000658; DUF5.
InterPro; IPR003660; HAMP.
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317
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82077 A
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Best Local Similarity 22.98
Matches 97; Conservative
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                                                                                                                                                                                                                                                                                              Halobacterium salinarium.
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SMART; SM00283; MA; 1.
                                                                                                                                   STANDARD;
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CDD1DF85E919123B CRC64;

77527 MW;

774 AA;

Fiber protein.

S W DR

Chemotaxis_transducer. POA_allergen.

InterPro; IPR000122; InterPro; IPR001778;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web yn on-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;
Hendrix R.W., Duda R.L.;

Science 258:1145-1148(1992).
-!- MISCELLANEDGE THE COMMON LABORATORY STRAIN OF BACTERIOPHAGE
LAMBDA, THE COMMON LABORATORY STRAIN OF BACTERIOPHAGE
LAMBDA, THE CONGINAL ISOLATE. THE UR-LAMBDA VIRIONS HAYE THIN
JOINTED TAIL FIBERS (SIDE TAIL FIBERS) THAT ARE ABSENT FROM LAMBDA
WILD TYPE. RELATIVE TO LAMBDA PAPA, UR-LAMBDA HAS EXPANDED
RECEPTOR SPECIFICITY AND ADSORBS TO E.COLI CELLS MORE RAPIDLY.
-!- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
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                                                             603 LALNANIEAARADQDGDGFAVVADEVKDLADESKASAAEIEALVAEVRAQTETSVAAMDR 662
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Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
--NAKSNNSISNIDS
                                                                                                                                     AKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAE---KDLKNIKPADGSDVPNPGTTV
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"Nucleotide sequence of bacteriophage lambda DNA.";
J. Mol. Biol. 162:729-773(1982).
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(Rel. 40, Last sequence update)
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   LVDQTDATATQIEKDGN---AIGDAY--FAGONASGAVE
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EMBL; J02459; AAA96557.1; ALT_FRAME.
PIR; A0438; QXBP1L.
PIR; A04370; QXBP2L.
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MEDLINE=92165720; Publ
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Lambda phage group.
NCBI_TaxID=10710;
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P03764; P03745;
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                                                                           Gaps
                                                                                                                                 LEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSS
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                                                                        65;
            Length 774;
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         ; Score 146.5; I; Pred. No. 1.1; 66; Mismatches
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RADAMS M.D. Celnikree S.E., Holf R.A., Gocayne J.D., RADAMS M.D., Celnikree S.E., Holf C. STRAIN FURKILERY;

RADAMS M.D., Celnikree S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Is Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Panalla M.D., Zhang O., Chen L.X.,

RADILON G.G., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayari A., An H.-J., Andrews-Frankoch C., Baldwin D., Radelew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Benckova D.A., Bultar H., Cadleu E., Center A., Chanjakov S., Borkova D.A., Bultar H., Cadleu E., Center A., Chanjakov S., Andrews D.A., Bulhle C., Davenport L.B., Davies P., Andrews D.A., Durbin R.J., Evaley S., Dalhke C., Davenport L.B., Davies P., Burtar B.R., Ballew R.A., Gabliel B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Durbin R.J., Evalegisis C.C., Ferraz C., Ferriera S., Fleischman W., R.A., Gabliel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., Gabriel B., McIntosh T.C., Mellow D., Houck J., Martiel B.E., Kodira C.D., Kraft C., Kratt C., Kratt C., Kratt C., Kratt C., Kratt C., Kratt C., Kratt C., Kratt C., Mortis J., Morberson D.L., Merkulov G. Milshina N.V., Mobbarry C., Mortis J., Workhorson D.L., Merkulov G., Milshina N.V., Mobbarry C., Mortis J., Worker M., Plankon K.A., Nixon K., Nussen D.K., Parlor K., Sanders R., Spier E., Spadling A.C., Stapleton M., Stupski M.P., Smith T., Sylene B.C., Siden-Klamos I., Simpson M., Stupski M.P., Smith T., Sylene B.C., Siden-Klamos I., Simpson M., Stupski M.P., Smith H.O., Sheng S., Well P.C., Shapson M., Stupski M.P., Smith T., Ribbs R.A., Woodeg T., Worsele B.C., Shapson M., Stupski M.P., Smith H.O., Sheng S., Pheng S., Pollack C., Wassarman D.A., Welter B., Speller E., Spadling R.V., Shon B.C., Sheng S.W., Woodege T., Welser B.C., Shon S., Pollack C., S Intron/exon structure of the gene, control of expression of the two mRNAs, selective advantage of the multienzyme complex."; Eur. J. Biochem. 244:176-185(1997). PROTEINS, P18, P48 AND P43.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CLASS-I SAMINOACYL-TRNA SYNTHETASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
SIMILARITY: CONTAINS 6 "WHEP-TRS" DOMAINS. COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH IS -i- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP + PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).

-i- CATALYTIC ACTIVITY: ATP + L-PROLINE + TRNA(PRO) = AMP + PYROPHOSPHATE + L-PROLINE. SEQUENCE FROM N.A. SUBUNIT:

COMPRISED OF A BIFUNCTIONAL GLUTAMYL-PROLYL-TRNA SYNTHETASE, THE MONOSPECIFIC ISOLEUCYL, LEUCYL, GLUTAMINYL, METHIONYL, LYSYL, ARGINYL, AND ASPARTYL-TRNA SYNTHETASES AS WELL AS THREE AUXILIARY

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EMBL, U59923; AAC47469.1; -. EMBL, AE003745; AAF56211.1; -. PIR; S18644; S18644 HSSP; P00962; 10RU.

R INCEPTO'S IFROUDO'S SG, WERE-TAS.

R INCEPTO'S IFROUDO'S SG, WERE-TAS.

R INCEPTO'S IPROUG134; TRNA-Synt_1C.

R INCEPTO'S IPROUG131; TRNA-Synt_1C.

R INCEPTO'S IPROUG131; TRNA-Synt_1.

R PÉAM: PFOUTO\$9; TRNA-Synt_1C.

R PÉAM: PFOUTO\$9; TRNASYNTHORO.

R PRINTS: PROUG97; TRNASYNTHORO.

R PRINTS: PROUG97; TRNASYNTHORO.

R PROSITE: PSOUTO\$1; AA_TRNA_LIGASE_II.1; FALSE_NEG.

R PROSITE: PSOUTO\$1; AA_TRNA_LIGASE_II.1; FALSE_NEG.

R PROSITE: PSOUTO\$2; WHEP_TRS; 6.

R PROSITE: PSOUTO\$2; WHEP_TRS; 6.

M MALIGUELOUS SYNTHERASE.

T DOMAIN 170 754 GLUTAMYL-TRNA SYNTHETASE. 808 AASSS-----SANDAV----SVNASIVKQGDLVRDLKGKKASKPEIDAAVKTLL 852 --- AEWETKNADAIKVGAQITELAKYASDNQAI---LDSLGKLTSFDLLQTALLQSVANNN 212 KAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVEN 272 904 KVRELKSAKADKATVDAAVKTLLSLKADYKAATGSD-WKPGTT-----APAPAAAPVKV 956 273 AKSNN----SISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAEQMVIQAEKDLKNI-- 326 44 EAKPKESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTAT-APTP 102 853 ELKAQYKTLTGQDWKPGTVPPTAAPSASAAPSVGGNDSVAQILS------QITAQGD 903 7 PGFI------DETERTPPADLSAQGLEASAANKSAEAQRIAG------A 43 103 PPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEEFAIA----1 6.1%; Score 146; DB 1; Length 1714; Similarity 19.8%; Pred. No. 3.2; 31; Conservative 74; Mismatches 192; Indels 142; TSPLP -> DKSIA (IN REF. 3). VC -> AF (IN REF. 3). NTACA -> KYCVR (IN REF. 3). -> V (IN REF. 3). 6FE8C58045E48A8C CRC64; PROLYL-TRNA SYNTHETASE. "HIGH" REGION. "KMSKS" REGION. (BY SIMILARITY) -> R (IN REF. 3).
-> A (IN REF. 3).
-> S (IN REF. 3).
-> S (IN REF. 3).
-> T (IN REF. 3).
-> Y (IN REF. 3).
-> S (IN REF. 3).
-> H (IN REF. 3). WHEP-TRS 1.
WHEP-TRS 2.
WHEP-TRS 3.
WHEP-TRS 4. 'lyBase; FBgn0005674; Aats-glupro. InterPro; IPR002106; AA_tRNA_ligase_II. InterPro; IPR000738; WHEP-TRS. POLY-GLY 189197 Matches 101; Conservative AA; CONFLICT CONFLICT CONFLICT ; Query Match CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT CONFLICT Local BINDING DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN a ٠ ٥ Q oy Ob oy Oy g ò

	Search completed: February 7, 2002, 21:42:42	rch co	Sea
	1128 AQGEKVRAAKGNKAAKEVIDAEVAKLLAL 1156	1128	QQ
	398 AQARAAKAAGDDSAAAALADAQKALEAAL 426 : : : :	398	QY
1127	1073 DPEVKTLLALKGEYKTLSGKDWTPDAKSEPAVVKKEASPVSMASPAKDELTQEIN 1127	1073	qq
397	355RVSMLL	355	QY
1072	1017 QEWKPGTVAPAPTTVNVIDLTGGDSGSDVGSVLSKIQAQGDKIRKLKSEKAAKNVI 1072	1017	qq
354	327KPADGSDVPNPGTT VGGSKQQGSSIGSI	327	δŽ

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 7, 2002, 21:41:09 ; Search time 172 Seconds
(without alignments)
416.706 Million cell updates/sec

1 MVNPIGPGPIDETERTPPAD.....QKLISEEDLNSAVDHHHHH 490 US-09-391-606-8 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 473505 segs, 146272329 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_17:* Database :

sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* _vertebrate: sp_mhc:*
sp_organelle:* sp_archea:* sp_bacteria:* _rodent:* sp_mammal:* sp_plant:* sp_virus:* sp_phage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Q46166 chlamydia p	0927h7 chlamydia p	084627 chlamydia t			Q91ch2 staphylococ	_					Q07290 streptococc		Q9bit0 plectreurys		0999z5 staphylococ		O9as09 orvza sativ	P91365 caenorhabdi
CTIVUMOC	110		046166	Ф927Н7	084627	Q9X7M2	Q9RL69	о91сн2	085472	Q99QR6	Q9RDQ1	05GN60	Q99QY4	007290	Q9LCJ9	Q9BIT0	Q9HS86	0990Z5	026947	09AS09	P91365
	DB	1	7	7	7	7	7	~	7	7	7	Ŋ	7	7	~	2	Н	7	S	10	2
	Length DB		715	651	647	1327	2478	2478	2055	2481	1545	697	2271	1822	1795	2016	627	993	1128	1038	2232
ďP	Query		91.8	90.7	18.7	8.1	8.1	8.0	7.8	7.6	7.5	7.5	7.5	7.4	7.2	7.2	7.1	7.1	7.0	7.0	6.9
	Score		2214	2188	451.5	195.5	195.5	193.5	188	182.5	182	181	180	178	174.5	173	171	171	170	168.5	166.5
	Result No.		1	7	m	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

	Q99u54 staphylococ	Q910n7 streptomyce				Q9z5a4 streptomyce	Q9kwr3 streptococc	Q99mpl mus musculu	Q9wtq5 mus musculu	Q49525 mycoplasma	Q99tb0 staphylococ	Q9ldbl oryza sativ	Q49545 mycoplasma	Q9n435 caenorhabd1	Q9ks57 vibrio chol	Q9y1p8 plasmodium	Q91803 xenopus lae	09asl3 oryza sativ	Q16967 aplysta cal	Q9asa4.oryza sativ	Q9u141 leishmania	Q9p3p5 neurospora	Q9ndi9 plasmodium	.087848 streptomyce	Q54183 streptococc	Q20684 caenorhabdi	
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	099054	Q9L0N7	Q9A0K5	Q9KX33	P71409	Q925A4	Q9KWR3	Q99MP1	Q9WTQ5	049525	Q99TB0	Q9LDB1	049545	Q9N435	Q9KS57	09Y1P8	091803	Q9ASL3	016967	Q9ASA4	Q9U141	Q9P3P5	61QN60	087848	054183	020684	
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	6.9	9.8	6.8	6.7	6.7	6.7	6.7	9.9	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	
	166.5	163.5	163.5	161.5	160.5	160.5	160.5	159	159	. 158	158	157.5	157	157	156.5	156	156	156	155,5	155.5	155.5	155	155	155	155	154.5	
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ALIGNMENTS

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61 LRSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI 60
                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-94156481; Pubwed-7509320;
Perez-Melgosa M., Kuo C.C., Campbell L.;
"Isolation and characterization of a gene encoding a Chlamydia pneumoniae 76-kilodalton protein containing a species-specific
                                                                                                                                                                                                                                                                                                                                         Length 715;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                             Infect. Immun. 62:880-886(1994).
EMBL; L23921; AAA23117.1; -.
SEQUENCE 715 AA; 76626 MW; 3F01C9A59DE964C5 CRC64;
                        046166 PRELIMINARY; PRT; 715 AA.
046166;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
76 KDA PROTEIN.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TAXID-83558;
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Pred. No. 1.8e-114;
2; Mismatches 3;
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98.9%;
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Best Local Similarity 98.9
Matches 454; Conservative
                                                                                                                                                                                                                                                    epitope."
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            QTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQ 300
                        KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL 360
                                                                       DDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                              Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey B.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J. McClarty G., Salzberg S.L., Eisen J., Fraser C.M., "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.";
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1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47AE6C3FF2FF0123 CRC64;
                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CHLDN 2001 (TrEMBLrel. 17, Last annotation update)
CHLDN 76 KDA HOMOLOG_1 (CT622).
CPN0728 OR CPU0728 OR CP0018
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria, Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2188; DB 2;
                                                                                                                                                                     ALEAALGKAGQQQGILNALGQIASAAVVSAGVLPLQQVL 459
                                                                                                                                                                                                                                           651 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20330349; PubMed=10871362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001654; AAD18867.1; -. EMBL; AP002547; BAA98935.1; -. EMBL; AE002165; AAF37914.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 90.7%; al Similarity 98.9%; 449; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                651 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEGUENCE 651 AA;
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SEOUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CWL029;
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MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGLENATTLAEYETKMADLMAALQDMERLAKQKAEVTRIKEALQEKQEVID---KLNQLV 165
                                                                                                                                                                                                       301 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLL 360
                                                                                                                                                                                                                                                                                                                                                     QTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQ 300
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MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VNPIGPGPIDETERTPPADLSAGGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSIL
                                                                                                                                                                                                                                                                                 LRSAVNALMSLADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT
                                                          121 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKY
                                                                                                                                                                                     ASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD
                                                                                                                                                                                                                                                                                                                                                                                                            361 DDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
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Last annotation update)
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29.6%; Pred. No. 2.3e-17;
live 85; Mismatches 192
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MEDLINE=99000809; Pubmed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 282:754-759(1998).
EMBL; AE001333; AAC68226.1;
Complete proteome.
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13,
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084627;
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01.NOV-1998 (TYEMBLEEL. 01
01.NOV-1998 (TYEMBLEEL. 01
01.NAY 2000 (TYEMBLEEL. 1:
CHLAN 76 KDA HOMOLOG.
CT622.
CHlamydia trachomatis.
Bacteria; Chlamydiales; Cl
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Best Local Similarity 29.6
Matches 138; Conservative
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SEQUENCE FROM N.A.
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1145 NAVTQAN---SNIEAANSQNDVDQAKTTGENSIDOVTPTVNKKAT-----ARNEITAILN 1196
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                                                                                                              1086 VEAAK-KAAIAKIEAIQPATTTKDNAKEAIATKANERKTAIAQTQDITAEEIAAANADVD 1144
                                                                                                                                                                                                                                                                                        NKLQEIQATPDATDEEKQAADAE--ANTENGKANQAISAATTNAQVDEAKANAEAAINAV 1254
                                                                                                                                                                                                                                              SGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAA-----ALADAQKALEAA 425
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                                                                                                                                                                                                                                                                                                                                                               ---LADKLG-----IASSNSSSTS 87
                                                                                                                                                                                                                                                                                                                                 426 LGKAGQQQGILNALGQIASAAVVSAGVLPLQQVLWIRARYQAYVEQKLISEEDLNSAV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PICPGPIDE----TERTPPADLSAQGLEASAANKSA-EAQRIAGAEAKPKESKTDS---
                                                                       --DSAKAAIAT----AKTQIAEAQKKFPDSPILQEA--E
                                                                                                                                                            QMVIQAEKDLKNIKPADG-SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263029 MW; 6B9859A02D023C74 CRC64;
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Last annotation update)
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23.6%; Pred. No. 0.016;
tive 91; Mismatches 211;
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Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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"Mrp-a new auxiliary gene essential for optimal methicillin resistance in Staphylococcus aureus. Microb. Drug Resist. 5:9-18(1999).
EMBL: Y09927; CAB55329.1;
EMBLERE 2478 AA. 263029 MW, 6B9859A02D023C7.
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Microb. Drug Resist. 2:277-286(1996)
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MEDLINE=99265121; PubMed=10332717;
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J. Bacteriol. 179:5321-5325(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIGPGPIDE----TERTPPADLSAQGLEASAANKSA-EAQRIAGAEAKPKESKTDS--- 54
                                                KYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSL
                                                                                                           VDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAE
                                                                                                                                                                                                AQKK---FPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LADKLG----IASSNSSSSTS
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Pred. No. 0.0072;
.; Mismatches 211; Indels 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mrp-a new auxiliary gene essential for optimal expression of methicillin resistance in Staphylococcus aureus."; Microb. Drug Res. 5:9-18(1999).
EMBL; Y09928; CAA71062.1;
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a	838 KMDAYNEVKGAATARKAONATVSNATNEEVAEADAAVDAAQKQGLHDIQVVKSKQEVADT 897	, Db	868	: KSKVLDK
δ D		QY	138 955	-QDAVTN : KQEARTN
Qy Db		QQ Op	191	LGKLT: : MNDSTTE
δy Dp	191 LGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKT	QV	232	232PAIA 1 1067 NVKPAAR
Oy Dp	232PAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGA 269 : :	. og da	270	VENAKSP VEAAK-F
Qy	270 VENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSPILQEAE 313 	Qy	314	OMVIQAI
Qy Db	314 OMVIQAEKDIKNIKPADG-SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILM 372 372 1184 NAVTQANSNIEAANSQNDVDQAKTTGENSIDQVTPTVNKKATARNEITAILN 1235	QY Db	373	SGFRQM:
Qy Dp	373 SGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAA 425 : ::	Qy Ub	-	426 LGKAGQ(: 1294 TPKVVKI
QY	426 LGKAGQQQGILNALGQIASAAVVSAGVLPLQQVLWIRARYQAYVBQKLISBEDLNSAV 483 :: :: :: 	RES O85	SU]	7
RESULT Q9LCH2 ID Q9	T 6 2 2 QUCH2 PRELIMINARY; PRT; 2478 AA.	AC DT DT		085472; 01-NOV-1998 01-NOV-1998 01-MAY-2000 EXTRACELLUL
	01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2000 (TrEMBLrel. 15, Last annotation update) FMTB.	000		EMB. Abiotrophia Bacteria; F Abiotrophia
00000 800 800 800 800 800 800 800 800 8	FWTB. Stabhylococcus aureus. Bacteria; Firmicutes; Bacillus/Clostridium group; Bacteria; Firmicutes; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=1280;	OX RN RC RA		NCBI_TaxID= [1] SEQUENCE FR STRAIN=NVS- Manganelli "Cloning an
R R R R R R R R R R R R R R R R R R R	SEQUENCE FROM N.A. STRAIN-COL; Konatsuzawa H.; "Staphylococcus aureus gene for affecting the methicillin resistance.";	RI DR		Adhesin of Submitted (EMBL; AF067 NON_TER SEQUENCE
RL SQ	Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AB025716, BAA93438.1; - SEQUENCE 2478 AA; 262993 MW; 1C118EBE0DB03B34 CRC64;		Query M Best Lo	Query Match Best Local Sim
Query Best Match	Query Match Best Local Similarity 23.6%; Pred. No. 0.02; Matches 141; Conservative 90; Mismatches 212; Indels 155; Gaps 28;		1	2 – 1
Oy Db	4 PIGPGPIDETERTPPADLSAQGLEASAANKSA-EAQRIAGAEAKPKESKTDS 54 :	V Q	16	
Qy Db	55VERWSILRSAVNALMSLADKLGIASSNSSSTS 87 :: :	QY		133 1699 QNEGTK
QY	88 RSADVDSTTA-TAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALVSL 137			t

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EEQQAAKDKVDQAVVTANADIDNAA-----ANNDVDNAKTTNEATIAAITPDA 1066
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milarity 23.9%; Pred. No. 0.032;
Conservative 68; Mismatches 197; Indels 130; Gaps
                                                                                                                                                   NIKDTAATD-----EETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDS 190
KKQAAKDEIDQLQAT------QTNVINNDQNATTEEKEAAIQQLATAV 1340
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Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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and Characterization of emb, a Gene Encoding the Major
E Streptococcus defectivus ";
(MAY-1998) to the EMBL/GenBank/DDBJ databases.
57776, AAD03320.1; -
2055 2055
2055 AA; 215640 MW; 9699C11DDE93E2FD CRC64;
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88 (TrEMBLrel. 08, Last sequence update)
100 (TrEMBLrel. 13, Last annotation update)
JLAR MATRIX BINDING PROTEIN (FRAGMENT).
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--AELLKEMQDNPVVPGKT--PAI 234

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1115 EIAKIEAIQPATTTKDNAKQAIATKANERKTAIAQTQDITAEEIAAANADVDNAVTQAN- 1173
                                                                                                                                                                                                                                                                                                                                                           --SNIEAANSQNDVDQAKTTGETSIDQVTPTVNKKAT----ARNEITAILNNKLQEIQA 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                    DLKNIKPADG-SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIH 380
                                                                                                                                    235 AQSLVDQTDATATQIEKDGNA------IGDAYFAGQNASGAVENAKSNN 277
938 KQEARTNL-DAANTNSDVTTAKDNGIAAINQVQAATTKKSDAK-AEIAQKASERKTAIEA 995
                                                                                                                                                                                                                         381 MFNTENPDSQAAQQELAAQARAAKAAGDDSAAA-----ALADAQKALEAALGKAGQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seeger K.j., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                          191 LGKLT----SFDLLQTALLQSVANNNKA--
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, DUTATIVE SECRETED PROTEIN. SCAA7.11. Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 13,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                     1911 KKAKDAIDAATSNADVTAKQTEGTQAINAVPOTPTAKTDAKNAVDQAATDKKNAIENDPA 1970
                                                                                                                                                                          SNIDSAKAAI-----ATAKTQIAEA-----QKKFPDSPILQEAEQMVIQAEKDLKN 325
                                                                                                                                                                                                                                                                 IKPADGSDVPNPGTTVGGSKQQGS-SIGSI-RVSMLLDDAENETASILMSGFRQMIHMFN 383
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LAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPV--VPGKTPAI 234
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Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

"Whole genome sequencing of meticillin-resistant Staphylococcus
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                                                                                     ---AQSLVDQ-----TDATATQIEKD-GNAIGDAYFAGQNASGAVENAKSNNSI-
                                                                                                                                                                                                                                                                                                                                                         384 TENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQG--ILNALGQ
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Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=158879;
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Pred. No. 0.081;
5; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                442 IASAAVVSAGVLPLQQVLWIRARYQAYVEQKLISEEDLN 480
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23.1%; Pred
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EMBL; AP003136; BAB43253.1;
Complete proteome.
SEQUENCE 2481 AA; 263767
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Matches 136; Conservative
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                                        1759 -AKNAID----
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24; Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of condered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MMOI. Microbiol. 21:77-96(1996).
EMBL; AL133423; CAB62715.1; Gaps Indels 126; DETERTPPADLSA--QGLEASAANKSAEAQRIAGAEAKPK----ESKTDSVERWS--Length 1545; InterPro; IPR000772; Ricin_B_lectin.
Pfam; PF00652; RICin_B_lectin; 1.
SMART; SM00458; RICIN, 1.
SEQUENCE 1545 AA: 161519 MW; 81EF325143593AEA CRC64; Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. ; Score 182; DB 2; Lk; Pred. No. 0.048; 67; Mismatches 205; 7.5%; Score 182; 24.6%; Pred. No. 0

DD 173 ELQKLKDEVDKAARKAKOLQLKAI QY 98TAPTPPPPTSDDYKTQA QY 98TAPTPPPPTSDDYKTQA QY 143 KSENVTKALDMAKKEEEETKNQA QY 143 NIKDTAATDEETALAAEWETKNA QY 143 NIKDTAATDEETALAAEWETKNA QY 197 KDLLQTALLQSVANNKAAELLK QY 197 FDLLQTALLQSVANNNKAAELLK DD 350QTAEKIARTSKSTEKIT QY 257 GDAXFAGQNASGAVENAKSNNSI	Db 392 GDVSSEEGKGKVLLESIK-GKAE Qy 312AEGMYIQAEKDLKNIKP	RESULT 11 0990Y4 AC 0990X4; DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DT 01-JUN-2001 (TrEMBLrel.17, DE SAZ447 PROTEIN. CA SAZ447 PROTEIN. CA Bactllus/Staphylococcus ground active acti	Ouery Match Best Local Similarity Matches 79; Conservat 22 SAGGLEASAANKSAEA 1516 SASASESDSSSTSLSL 82 SSSTSRSADVDSTP 1571 TSVSTSESGSTSSTSTS
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II., Nagai Y., Lian J., Ito T., Kanamori M.,
Murakami H., Hosoyama A., Mizutani-Ui Y.,
to Dious K.I., Kaito C., Sekinizu K.,
oto S., Yabuzaki J., Kanehisa M.,
Furuya K., Yoshino C., Shiba T., Hattori M.,
Hiramatsu K.,
of meticillin-resistant Staphylococcus
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; Pred. No. 0.1;
96; Mismatches 187; Indels 56; Gaps
                                                                                                                                            ADAIKVGAQI-----TELAKYASDNQAILDSLGKLTS 196
                                                                                                                                                                         KEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAI 256
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AEIAEHAVKAQVAKTEAEKAQKDATTAKEVAIKETGTS 232
                                                             AQTAYDTIFTSTSLA------DIQAALVSLQDAVT 142
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llus/Clostridium group;
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                                                                                                                           KESAKKAVDADAKAATDAIDASTSPVEAQSAEDKGVGSIAQDVLDAAKQDAKNKIAKEVA 1581
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interProrp 1PR0000890; Acetate_Kin.
PROSITE; PR01075; ACETATE_KINNSE_1; UNKNOWN_1.
SEQUENCE 1795 AA; 191006 MW; 6CB77CCFCB33D350 CRC64;
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Bacteria: Firmicutes; Bacillus/Clostridium grc
Bacillus/Staphylococcus group; Staphylococcus.
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Matches 132; Conservative
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                                                                                       -TSMRTSTSDSQSMSLSTSTSTSMSDS-----TSLSDSVSDSTS--DSTSASTSGSMS 1678
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                                    141 UTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDL- 199
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Smith H.E., Reek F.H., Vecht U., Gielkens A.L.J., Smits M.A.;
"Repeats in an extracellular protein of weakly pathogenic strains
Streptococcus suis type 2 are absent in pathogenic strains.";
Infect. Immun. 61:3318-3326(1993).
EMBL; X71880; CAA50714.1: -
SEQUENCE 1822 AA; 192631 MW; 3838960C77641D7D CRCF4.
                                                                                                                                                LQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDA
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Matches 122; Conservative
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NCBI_TaxID=1307;
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                                                            1194 -SNIEAANSQNDVDQAKTTGETSIDQVTPTVNKKAT----ARNEITAILNNKLQEIQAT 1247
                                                                                                                                                                                         -----LAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQG-----ILNALGQI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 TSFDLLQTA-----LLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVD-QTDAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSNSSSSTSRSADVDSTTATAPTPPPFTSDDYKTQAQTAYDTIFTSTSLADIQAALVSLQ 138
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323 LKNIKPADG-SDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHM 381
                                                                                                                                            382 FNTENPDSQAAQQEL----AAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEAQKKFPDSPILQEA-----SQMVIQAEKDLKNIKPADG------SDVPNPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21179804; PubMed-11283372; MEDLINE-21179804; PubMed-11283372; Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.; "Extreme Diversity, Conservation, and Convergence of Spider Silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plectreurys tristis (Spider).
Eukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Araneomorphae; Haplogynae; Plectreuridae; Plectreurys.
NCBL_Tax1D-33319;
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                                                                                                                                                                                                                                                                                                                                             436 LNALGQIASAAVVSAGVLPLQQVLWIRARYQAYVEQKLISEEDLNSAV 483
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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MINUAL H.D., Lasky S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl Tr., Wellt R., Goo Y.A.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Poblischroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Genome sequence of Halboacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S. A. 97:1218(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 R---IDGIT-ALIEDIAEETNMLALNASIEAARTGSDGD--GFAVVADEVKDLAEETREQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 NNSISNIDSA-----KAAIATAKTQIAEAQKKFPDSP-ILQEAEQMVIQAEKDLKNIKP 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GSIRVSMLLDD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 IKVGAQITELAKYASDNQAIL----DSLGKL-TSFDLLQTALLQSVANNNKAAELLKEMQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 ADKLGIASSNSSSTSRSADVDSTTATAPTPPPPTSDDYKTQA-----QTAYDTIFTS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 PPADLSAQGLEASAANKSAEAQRIAGAEAKPK----ESKTDSVERWS-ILRSAVNALMSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1%; Score 171; DB 1; Length 627;
23.4%; Pred. No. 0.063;
tive 87; Mismatches 184; Indels 122;
                                                                                                                                              Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteriales; Halobacteriaceae;
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                                                                              Last sequence update)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	C. pneumoniae 76 k	Chlamydia pneumoni	3'-truncated Chlam	Chlamydia pneumoni	5'-truncated Chlam	Chlamydia trachoma	Chlamydia sp. prot	Protein encoded by	Extracellular fact	Chlamydia trachoma	Streptococcus pneu
	ID	AAY71957	AAY71954	AAY71956	AAY35358	AAY71955	AAY37571	AAB13695	AAG83263	AAR27745	AAY37572	AAY81609
	DB	21	21	21	20	21	20	21	22	13	20	21
	luery Match Length DB	490	651	452	478	583	350	361	361	1822	331	1237
æ	Query Match	99.1	8.96	96.6	92.6	81.8	12.5	10.2	10.2	8.0	7.3	6.8
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(AVET) AVENTIS PASTEUR LTD.

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                                                                                                                                                                                                                                                                                                                                                                                                                                        96.88;
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                      vaccine; immunisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumoniae,
                                                                                                                   The present sequence is a fusion protein comprising a truncated Chlamwdia pneumoniae 76 kDa protein and vector-encoded residues. C. pneumoniae 76 kDa protein is used in the diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases caused by C. pneumoniae.
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                                                              Nucleic acids encoding a 76 kDa protein from Chlamydia useful for vaccinating against Chlamydia infections -
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                                                                                                                     Chlamydia
                                                                                                                   Nucleic acids encoding a 76 kDa protein from Chlamyć
useful for vaccinating against Chlamydia infections
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Pred. No. 2.9e-139;
1; Mismatches 4;
Dunn P;
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QTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQ
                                                                                                                                                DDAENETAS I LMSGFROM I HMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQK
                                                                                                  KKFPDSP1LQEAEQMV1QAEKDLKN1KPADGSDVPNPGTTVGGSKQQGSS1GS1RVSMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.6%;
99.1%;
                                                                                                                                                                                                                                                                                                                                 13-SEP-1999. (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffais R;
                                                                                                                                                                                                                                                                                                          AAY35358;
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                                                   241
                                                                                                 301
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                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                    76 KDa protein; bactericidal; diagnosis; prevention; promonate is approached; sinusitis; backers respiratory disease; cough; sore throat; hoarseness; fever; vaccine; immunisation; treatment; truncation mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a 76 kDa protein from Chlamydia pneumoniae, useful for vaccinating against Chlamydia infections –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis, prevention and treatment of C. pneumoniae infections (e.g. pneumonia, upper respiratory tract disease, broohitis, sinustis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases caused by C. pneumoniae.
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Chlamydia pneumoniae 76 kDa protein. C. pneumoniae 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2184; DB 21;
Pred. No. 3.4e-139;
                                                                                                                                              3'-truncated Chlamydia pneumoniae 76 kDa protein.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 16c; Page 104-106; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                         Dunn
                                                                          Ā
                                                                      AAY71956 standard; Protein; 452
                                                                                                                                                                                                                                                                                                                                                                                                         Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.68;
99.18;
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Matches 448; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Oomen RP,
                                                                                                                                                                                                                                Chlamydia pneumoniae.
Synthetic.
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N-PSDB; AAD02065.
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30-JUN-1999;
                                                                                                                      26-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                       Murdin AD,
                                                                                              AAY71956;
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            421
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                                                            AAY71956
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AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory diseases such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY3484-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae included as esquences an also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Respiratory disease; pneumonia; bronchitis; heart disease; sarcc
sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia pneumoniae surface exposed polypeptide.
421 ALEAALGKAGQQQGILNALGQIASAAVVSAGV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia pneumoniae
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                                               AAY35358 standard; Protein; 478 AA
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97FR-0014673
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Length 478;

Score 2162; DB 20; Pred. No. 1.1e-137;

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Matches
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                                                                                                                                 121 IFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKY 180
                                                            Gaps
                                     1 MVNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 kDa protein; bactericidal; diagnosis; prevention; pneumonia; upper respiratory tract disease; bronchitis; sinusitis; acute respiratory disease; cough; sore throat; hoarseness; fever; vacchne; immunisation; treatment; truncation mutant; mutein.
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   Indels
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     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 aleaalgkagqqqqilnalgqiasaav 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 ALEAALGKAGQQQGILNALGQIASAAV 447
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99US-0141276.
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     Conservative
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30-JUN-1999;
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     443;
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Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAALADAQKALEAALGK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 MSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSISLA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 DIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAIL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from Chlamydia pneumoniae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQ
                                                                                                                                                                                            infections (e.g. pneumonia, upper respiratory tract disease, bronchitis, sinusitis and acute respiratory disease such as cough, sore throat, hoarseness, fever; and abnormal chest sounds on auscultation). C. pneumoniae sequence is also used as vaccines for immunising humans against diseases
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 583;
                                                                                                                                kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                pneumoniae 76
                                                                                                                                                                      diagnosis, prevention and treatment of C. pneumoniae
Nucleic acids encoding a 76 kDa protein from Chlamyvuseful for vaccinating against Chlamydia infections
                                                                                                                                                                                                                                                                                                                                                                                                        Score 1850; DB 21;
Pred. No. 1.4e-116;
1; Mismatches 4;
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                                                                                                                                ပ်
                                                                  Page 100-102; 112pp; English.
                                                                                                          The present sequence is 5'-truncated Chlamydia pneumoniae 76 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                            81.8%;
98.7%;
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                                                                                                                                                                                                                                                                                                        C. pneumoniae.
                                                                                                                                                      protein is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
381; Conser
                                                                                                                                                                                                                                                                                                                                                   583 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09928475-A2
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                                                                    Claim 16b;
                                                                                                                                                                                                                                                                                                        caused by
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                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369
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g-90-391 606-9

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The present invention relates to new nucleic acid sequences and the proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chiamydia antigen. The encoded proteins are useful for the sercidiagnosis and treatment of Chiamydia infection. Chiamydia are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is and infertility. Trachoma due to ocular infection with C. trachomatis is major cause of acute respiratory tract infections in humans and is also thought to play a role in the pathogenesis of atherosclerosis and correct infection is partially also connary heart disease. The present sequence is a protein isolated in the
                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 -RVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAK---AAGDDS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 KKPPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pelvic inflammatory disease; PID; tubal obstruction; infertility; trachoma; blindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                       Jen S,
                  Chlamydial infection; sexually transmitted disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.2%; Score 231.5; DB 335.4%; Pred. No. 5.8e-08; Live 30; Mismatches 61
                                                                                                                                                                                                                                                                                                                                     Skeiky YAW, Fling SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Pages 251-253; 256pp; English.
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ID AAG83263 standard; Protein; 361
                                                                                                                                                                                                                                       99US-0288594.
99US-0410568.
99US-0426571.
                                                                                                                                                                                           99WO-US29012
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                                                                                                                                                                                                                                                                                                                                       Probst P, Bhatia A,
                                                                                                                                                                                                                                                                                                       CORI-) CORIXA CORP
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tes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
                                                                                                                            WO200034483-A2
                                                                                             Chlamydia sp.
                                                                                                                                                                                          08-DEC-1999;
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                                                                                                                                                                                                                                                                      2-0CT-1999
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                                                                                                                                                                                                                                                 AAX36754-Y37949 are encoded by open reading frames (ORPS) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, barthollinitis; pummopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSAVNALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STSLADIQAALVSLQ------DAVTNIKDTAATDEETAIAAEW 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 VENAKSNNSISNIDSAKAAIATAKTQIAEAQ---KKFPDSPILQEAEQMVIQAEKDLKNI 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VNPIGPGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSIL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::| : | :::| :::| :::| :::| :::|
----dklnklvtlqnqnksltealkttdsadqipainsrleinknsahqiike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 ksglenaktlaeyetkmadlmaalqdmeansdpsndhteelnnikkaleagkdti----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETKNADAIKVGAQITELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 MQDNPVVPGKTPALAQSLVDQTDATATQIEKD------GNAIGDAYFAGQNASGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 lkeg-----isnykavltdvekvikefseagiklggalgsivdagdgsgaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%; Score 281.5; DB 20; 24.9%; Pred. No. 2.4e-11; ive 71; Mismatches 122;
                                                                                                                                                                                                                    Disclosure; Page 1226-1227; 1755pp; English.
                                                                                                                                                                                      Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327 KPADGSDVPNPGTTVGGSKQQ 347
                            98US-0107077.
97FR-0015041.
97FR-0016034.
98WO-IB01939
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Best Local Similarity 24.99
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia sp. protein # 6.
                                                                                                                                                        WPI; 1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                350 AA;
                                                                                         (GEST ) GENSET
27-NOV-1998;
                                                           17-DEC-1997;
                             04-NOV-1998;
                                            28-NOV-1997;
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                                                                                                                           Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAB13695
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Stromberg

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Gaps

WO200140474-A2

Chlamydia;

07-JUN-2001

03-DEC-1999; 20-JUN-2000;

Probst P,

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67 ALMSLADKLGIASSNSSSSTSRSAD------VDSTTATAPTPPPPTSDDYKTQAQTAY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Streptococcus suis type II (non-pathogenic) which allows the detection and the prevention of infections by S. suis in a more effective manner than was previously possible. It facilitates screening of e.g. pigs and elimination of infected and carrier pigs can then be carried out. The new diagnostic tests can distinguish between avirulent and varients. It may be used in the prodn of a vaccine. See also AAR27744 and AAR27746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is that of the extracellular factor related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deoxyribonucleic acid encoding virulence characteristic of
Streptococcus suis - useful for antibody and polypeptide for
diagnosing and preventing infections in pigs and humans
                                                                                                                                                                                                         /note= "repetitive Asn-Pro-Asn-Leu sequence"
1075..1078
/note= "repetitive Asn-Pro-Asn-Leu sequence"
1264..1267
                                                                                                                                                                                                                                                                                                                                                 /note= "repetitive Asn-Pro-Asn-Leu sequence"
1514..1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "repetitive Asn-Pro-Asn-Leu sequence"
                                                                                                                                       "repetitive Asn-Pro-Asn-Leu sequence"
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                                                                                                                                                                                                                                                                          /note= "repetitive Asn-Pro-Asn-Leu
1362_.1365
//note= "repetitive Asn-Pro-Asn-Leu
1438..1441
                                                                                                                                                                        "repetitive Asn-Pro-Asn-Leu
                                                                                                                                                                                                                                                                                                                                                                                "repetitive Asn-Pro-Asn-Leu
                                                                                                                                                                                                                                                                                                                                                                                                                   "repetitive Asn-Pro-Asn-Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 181.5; DB 23.9%; Pred. No. 0.0011; tive 78; Mismatches 17
Streptococcus suis type II (non-pathogenic).
                                                                                                      "mature peptide"
                                  Location/Qualifiers
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                                                                "signal
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1590..1593
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Matches 117; Conservative
                                                                                                                                         /note= "r
934..937
                                                                                    ..1822
                                                                                                                       858..861
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                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                      /note=
                                                                     /note=
                                                                                                                                                                            /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                  Peptide
                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia polypeptides and fusion proteins useful for preventing pelvic inflammatory disease, trachoma, acute respiratory tract infections,
                                                                pelvic inflammatory disease; trachoma; atherosclerosis; heart disease; acute respiratory tract infection; Capl; CT529; OMCB; polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 KKFPDSPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSI----- 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 -RVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAK---AAGDDS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is provided in a specification relating to compounds and methods for the treatment and diagnosis of chlamydial infection. The compounds provided include polypeptides and fusion proteins comprising immunogenic portions of chlamydia antigens and DNA sequences encoding such polypeptides. They are useful for vaccinating against chlamydial infection, which causes pelvic inflammatory disease, trachoma, acute respiratory tract infections, atherosclerosis and heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Indels
                                                     vaccine; infection; fusion protein; antigen;
                                                                                                                                                                                                                                                                                                                                                                                      Scholler
                  Protein encoded by Chlamydia trachomatis clone CT622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EF*; detection; prevention; screening; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.2%; Score 231.5; DB 2 35.4%; Pred. No. 5.8e-08;
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                                                                                                                                                                                                                                                                                                                                                                                      Fling SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 66; Page 257-259; 295pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extracellular factor related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR27745 standard; Protein; 1822 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atherosclerosis and heart disease -
                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW,
                                                                                                                                                                                                                                                                               03-DEC-1999; 99US-0454684.
19-APR-2000; 2000US-0556877.
20-JUN-2000; 2000US-0598419.
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                                                                                                                                           Chlamydia trachomatis.
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                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
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Best Local Similarity
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Sequence

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                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
1123 litakadakgviaakladeikkledkgaeaekaidastmt-----neekaiakkal 1173
                                                                                                                                                                      |||| | : ||| : : | :: | :: | :: | | :: || : : | | :: || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || | : : || : : || | : : || | : : || | : : || | : : || | : : || : : || | : : || | : : || | : :
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                                                                                              1174 qdv------vdkgkaeledaarvatneiheaittekakaaelageksltdtgkearda
                                                                                                                                          TELAKYASDNQAILDSLGK--LTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGK--
                                                                                                                                                                                                                                  -----TPAIAQSLV---DQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY37572 standard; Protein; 331 AA
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97FR-0016034.
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1488 vldaakqda 1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 GTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELA 397
diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneral lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antiinflammatory; meningitis; infection; diagnosis; pneumococcal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 AQARAAK---AAGDDSAAAALADAQKALEAALGKAGQQQGILNALGQIASAAVVSAG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                               Length 331;
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                                                                                                                                                                                                                                                                                                       Score 164.5; DB Zu;
Pred. No. 0.0017;
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pneumococcal diseases and f
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Best Local Similarity
Matches 45; Conserva
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                                                                                                                                          133 ALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSLG 192
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                                                                                   13 TERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVNALMSLA 72
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                                                               49;
                                        Length 1237;
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                                                               Indels
                                          DB 21;
                                                             Mismatches 205;
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Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C glutamicum protein fragment SEQ ID NO: 5197.
                                         Score 153.5; DE
Pred. No. 0.051;
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Ikeda M,
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                                                               84;
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2000JP-0159162.
2000JP-0280988.
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                                          6.8%;
19.9%;
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                                                                Conservative
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Senoh A,
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N-PSDB; AAH66662.
           AA;
                                                     Similarity
           1237
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03-AUG-2000;
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Tateishi N,
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                                                               84;
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mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene for identifying polynucleotides derived from Coryneform bacteria,

Claim 17; SEQ ID NO: 5197; 246pp + Sequence Listing; English

These The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium coryneform bacterium of a gene derived from coryneform bacterium. Coryneform bacterium of a gene derived from coryneform bacterium. Coryneform bacterium are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.

600 AA; Sequence

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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 IGDAYFAGONASGAVENAKSNNSISNIDSAKAAIATAKTOIAEAOKKFPDSPILQEAEOM 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 MSGFROMIHMFNTENPDSQAAQQE-----LAAQARAAKAAGDDSAAAALADAQKALEAA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----aetgaagaagagaeandraaaggraaeagagreadgageadagaandag 362
                                                                                                                                                                                                                 GIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTSLADIQAALV 135
                                                                                                                                                                                                                                                             --- qarqdalaakkdlddsqaqie 107
                                                                                                                                                                                                                                                                                                                 SLODAVINIKDIAAIDEETAIAAEWETKNADAIKVGAQITELAKYASDNOAILDSLGKLT 195
                                                                                                                                                                                                                                                                                                                                                                   aaqerldeisraayrqngtskglsgisgngnsedaldrqtylrtsaekqqaaveeldrlr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 VIQAEKD----LKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASIL 371
                                                       Gaps
                                                                                                        PADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVE-RWSILRSAVN-ALMSLADKL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pddaaiaqaeenvsagdgevarlags-lsstdaeinrvelemgalreevnkslvdlhdag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         t-----arivaegreaeavekgvgtea
                                                    96;
     Length 600;
6.8%; Score 153; DB 22; Length 6 21.6%; Pred. No. 0.022; tive 66; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -agalregaltaa--siaaaaliaa 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 LGKAGQQQGILNALGQIASAAVVSA
                              Similarity 21.6 96; Conservative
                                                                                                                                                                                                                                                                   83 alae----
     Query Match
                                   Best Local
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AA. AAW02098 standard; Protein; 1561

AAW02098;

(first entry) 27-0CT-1996

S. mutans antigen I/II

Caries; antigen I/II; epitope; tooth decay; vaccine; immunisation.

386 NFDSQAAQQELAAQARAAKAA--GDDSAAAAL-ADAQKALEAALGK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus mutans antigen I/II (AAW02098) is a 185 kDa cell surface protein at least partly responsible for 5. mutans adhesion to teeth. The I/II antigen includes a series of overlapping T-cell, B-cell and adhesion epitopes. Fragments (see also AAT3611-21) of the I/II antigen gene (see also AAT3612) can be used to produce recombinant polypeptides (AAW02087-97) carrying such epitopes for use in vaccines for Immunisation against dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 KESKTDSVERWSILRSAVNALMSLADKLGIASSN-SSSSTSRSADVDSTTATAPTPPPPT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 -----SDDYKTQAQTAYDTIFTST-----SLADIQAALVS-LQDAVTNIKDT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AATDEETAIAAEWE-----TKNADAIK------VGAQITELAKYASDNQAILDSLGK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 LTSFDLL-QTALLQSVANNNKAAEL----LKEMQDNPVVPGKTPAIAQSLVDQTDATAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 Q---KKFPDSPILQEAE-QMVIQA-EKDLKNIKPAD------GSDVPNPGTTVG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 gaelkrygeanaaneadygakltaygtelarygkanadakaayeaavaannaknaaltae 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 GS------KQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding polypeptide for prevention or treatment of dental caries - which stimulates T or B cell response, and/or adheres to tooth in competition with Streptococcus mutans antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 QIE----KDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK----TQIAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
                                                                                                 /note= "amino acids 618-650 differ from the residues deduced from the nucleic acid sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    match 6.7%; Score 152; DB 17; Length 1561; Local Similarity 22.3%; Pred. No. 0.087; es 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            (UNME-) UNITED MEDICAL & DENTAL SCHOOLS GUYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 45-46; 63pp; English.
                                            Location/Qualifiers 618..650
                                                                                                                                                                                                                                                                                                                  96WO-GB00207
                                                                                                                                                                                                                                                                                                                                                                       95GB-0001826
Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-371434/37.
N-PSDB; AAT36122.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Lehner T;
                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                  31-JAN-1996;
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Matches
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ARR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi
The proteins are all fusion products with glutathione-S-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and some contain a linker sequence. The TCR27 protein comprises
(GST) and some contain a linker sequence. The TCR27 protein region. This sequence concerved 14 as sequence and a 68 as C-terminal region. This sequence concerved the GST sequence. The Ag44 polypeptide contg. is of the 69 repeat units and also contains the amino and carboxy terminal peptides of TCR27. The TCR27 polypeptides of the invention are useful for the diagnosis of Chagas disease (American Trypanosomiasis), they screening. The TCR27 protein has epitopes to which most T cruzi infected individuals have antibodies. The TCR27 polypeptides will not react with serum from patients with less manalasis, schistosomiasis, care capaline of detection and are hence less likely to cause false
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - a immunoassay reagent for specific diagnosis of Chagas disease, also related nucleic acid and transformed cells
                                                                                                                                                                                                                                                                                                                                                                         amino acids"
                                                                                                                                                                                                                                TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-5-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 643;
                                                                                                                                                                                                                                                                                                                                   329..552
/label= repeat_region
/note= "16 of 69 repeat units of 14
6.7%; Score 150.5; DB 16;
21.5%; Pred. No. 0.035;
tive 58; Mismatches 169;
                                                                                                                                                                                                 Trypancsoma cruzi TCR27 polypeptide, Ag15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 40-41; 68pp; English.
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                              AAR84568 standard; Protein; 643
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Matches 99; Conserv
                                                                                                                                                                                                                                                                                     Trypancsoma cruzi.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 - MAR-11994;
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                                                                                                                                                                 09-MAY-1996
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                                                                                                                                AAR84568;
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                                                                                AAR84'568
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Job time:
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                                                                                                                                                                                                                                                                                                           284 SAKAAIATAKTQIAEAQK-KFPDSPILQEAEQM-----VIQAEKDLKNIKPADGSDVP 335
                                                                                                                                                                                                                                                                                                                               336 NPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQE 395
                                                                                                                                                                                                                                                                                                                                                                                                             e-----vaekgkaaeatkva----eaekgkaaeatk-----vaeaekgkaaeat 533
ppksdlvprgspsgl--ggaennitnskkemtklrekvkkaekekldainratkleeern 273
                                                                                                                                                                                                          ------aekrkaaeaakavetekgraaeatkv 381
                                                                                                                                                                                                                                                                           382 aeaekgkaaeaakavetekgraaeatkvaeaekgraaeamkvaeaekgkaaeatkvaeae 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of the Mycobacterium tuberculosis MTBNB protein. This is 1 of 8 proteins, 1.e. MTBN1-8 (see AAAB19842-49), encoded by 8 open reading frames (see AAA8035-42) identified as being present in the genome of M. tuberculosis but absent from the genome of the BGG strain of Mycobacterium bovis. MTBN1-8 represent reagents that are useful in discriminating between M. tuberculosis and BGG and, in particular, for diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptide encoded by open reading frames present in Mycobacterium tuberculosis genome and not by the BCG strain of M. bovis, useful as vaccine and for diagnosing tuberculosis infection
                                                                                                                                   -----ndavsnrdkknsetaktdevekqraaeaakavetekqra----aea
                                   ALMSLADKLG1ASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDT1FTSTS
                                                                                                      LADIQAALVSLQDAVTN----IKDTAATDE-----ETAIAAEWETKNADAIKVGAQI
                                                                                                                                                                        TELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAI
                                                                                                                                                                                                                                           A----QSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSN-----NSISNID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTBN8; tuberculosis; BCG; vaccine; infection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                396 LAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGIL 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
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                                                                                                                                                                                                          351 tkvae-----
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N-PSDB; AAA89042.
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completed: February ne: 20757 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347
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                                                                                                                                                                                                                                                                                                                    AVNALMSLADKLGIASSNSSSSTSRSADVDSTTA----TAPTTPPPFTSD--DYKTQAQTA 117
                                                                                                                                                                                                                                                                                                                                                                                        118 YDTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAAEWETKNADAIKVGAQITEL 177
                                                                                                                                                                                                                                                                                                                                                                                                                        ddg--tpvsmipvsaa------aardaataaasargrgrgdalrlarria-a 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAIAQS 237
                                                                                                                                                                                                                                                                                                                                                     svgtaaasgagshaatgrapvatsdkaaapstraasartapparppstdhidkpdrsesa 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVDQTDATATQIEKDG-----NAIGDAYFA-GQNASGAVENAKSNNSISNIDSAKAAIAT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----tavttdgsivvansyglayipdgmelpnkvylasadhaip-vdei-arcat 561
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                GPGPIDETER--TPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRS 63
which discriminate between exposure of a subject to M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKTQIAEAQKKFPD---SPILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQ-
                                                                                                                                                                                                            Mismatches 181; Indels 114;
                               polypeptides, functional fragments of them, DNA encoding them, vectors, transformed cells, and diagnostic, therapeutic, and prophylactic (vaccine) methods, including genetic vaccination
                  The invention features these MTBN
                                                                                                                                                                          Length 729;
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No. 0
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                                                                                                                                                                            6.5%;
                  and vaccination with BCG.
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                             Similarity
                                                                                                                         729 AA;
                                                                                                                                                                                                               103;
                                                                                                                           Sequence
                                                                                                                                                                            Query Match
                                                                                                                                                                                                 Local
                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                 351
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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length: 2000000000
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US-08-894-017-23
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; Patent No.
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 Query Match
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Matches 104;
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SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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APPLICANT: Kelly, Charles
TITLE OF INVENTION: POLYPEPTIDE FRAGMENTS CAPABLE
TITLE OF INVENTION: OF COMPETITION WITH STREPTOCOCCUS
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEPAX: 202-822-0168
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/GB96/00207
FILING DATE: 31-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01 FILING DATE: 31-JUL-1997 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                          TYPE:
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Score 152; DB 3; I
Pred. No. 0.004;
Pred. No. 1004;
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APPLICANT: Kirchh
                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SCETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
FILING DATE: 24-MAR-1994
                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Otsu, Keiko
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                                      TYPE: amino acid
TCPOLOGY: linear
                                                                                LENGTH:
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                                                                              643 amino acids
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                 protein
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RESULT 4
5352450-2
;Patent No. 5352450
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                                                                                                                                                                                                            5352450-2
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KOGA, TOSHIHIKO;OKAHASHI, NOBUO;TAKAHASHI, ICHIRO;SHIBUYA, KOJI;OHTA, HIROTAKA
TITLE OF INVENTION: METHOD FOR PREPARING VACCINE FOR DENTÂL
CARIES AND VACCINAL COMPOSITIONS FOR DENTAL CARIES USED AS NASAL
                                                                                                                                                                                                                                                SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 99
                                                                                                             Query Match
Best Local Similarity
Matches 101; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 29-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382
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106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 KQKAAEA---TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQ----KAAEATKVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 LAAQARAAKAAGDDSAAAALADAQKALEAALGKAGQQQGIL 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 QAYKAAHK---AEEEKAKTFQRLITFESENINLKKRP---
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                                 KVKKTYGFRKSKISKTLCGAVLGTVAAVSVAGQKVFADETTTTTSDVDTKVVGTQTGNPA
                                                                       KESKTDSVERWSILRSAVNALMSLADKLGIASSN--SSSSTSRSADVDSTTATAPTPPPP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NDAVSNRDKKKNSETAKTDEVEKQRAAEAAKAVETEKQRA----AEA
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SDDYKTQAQTAYDTIFTST--
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                                                                                                           6.5%; Score 146.5; DB 6; 21.8%; Pred. No. 0.011; tive 81; Mismatches 190;
                                                                                                                                                                                                                                                                                    US/07/529,602
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--SLADIQAALVS-LQDAVTNIKD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VAEAEKQKAAEAT 533
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                                                                                                                                              Length 1565;
                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW YORK AVENUE, N.W., EAST TOWER, 9T.
STREET: FLOOR
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPIRED: 10005
                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9401689.6

FILING DATE: 28-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 50885/222
                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BURNIE, JAMES P
APPLICANT: MATTHEWS, RUTH C
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: INFECTIONS DUE TO STREPTOCOCCCI AND ENTEROCOCCCI
NUMBER OF SEQUENCES: 23
                TOPOLOGY: u
MOLECULE TYPE:
                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1566 amino acids
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 ----KDGNATGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAK----TQIAEAQ-- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 KLTSFDLLQTALLQSVANNNKAA--ELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIE
                                                                                                                                                                                                                                                                                                                                               FILING DATE: 29-JUL-1996
CLASSIFICATION: 536
                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKERNENAKATYEAALKQYEADLAAVKKANAANEADYQAK----LTAYQTELARVQKANAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATDEETAIAAEWE-----TKNADAIK------VGAQITELAKYASDNQAILDSLG
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                                                                         amino acid
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                    unknown
peptide
NO
                                                      single
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                                                                                                                                                                                                                                                                                                                                                                                      US/08/687,956A
                                                                                                                                  23:
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FRAGMENT TYPE:

internal

ANTI-SENSE:

NO

SEQUENCE CHARACTERISTICS:

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US-08-216-894-2
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
OFGANISM: Streptococcus sobrinus
                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI NUMBER OF SEQUENCES: 10
                                                     NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                       NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 VENAKSNNSISNIDSAKAAIATAKTQIAEA------QKKFPDSPILQ------EAE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 DEANQKETEIKDDYSKQAADIQKTTEDYKAAVARNQAETD---RITQENAAKKAQYEQDL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 QMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQQGSSIGSIRVSMLLDDAENETASILMS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 NNNKAAELLKEMQDNPVVPGKTPAIAQSLVDQTDATATQIEKDGNAIGDAYFAGQNASGA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 TSDDYKTQAQTAY------DTIFTSTSLADIQAALVSLQDAVTNIKDTAATDEETAIAA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 94; Conserv
                    TELEFAX:
                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 KQDNPSSQAETSQAQAGQKTGAMSVDVSTSELDEAAKSAQEAGVTVSQDATVDKGTVETS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 RKSKISRTLCGALLGTAI -- LASVTGQKALAEETSTTSTSGVNTAVVGTETGNPATNLPD
                                                                                                                                                                                                                                                                                                                                                                        STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 KESKTDSVERWSILRSAVNALMSLADKLGIASSNSSSSTS--RSADVDSTTATAPTPPPP 105
                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWETKNADAIK--VGAQITELAKYASD-----NQAILDSLGKLTSFDLLQTALLQSVA
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Otsu, Keiko
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                                  (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                  Foley & Lardner
                                                                                                                                                                           JMBER: US/08/216,894
24-MAR-1994
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                                                                                                                                                                                                                                     Release #1.0,
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                                                                                                85326/102/DRLO
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Pred. No. 0.019;
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                                                                                                                                                                                                                                       Version
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                                                                                                                                                                                                                                       #1.25
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US-09-115-746-2
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Applic Patent No. 6228601
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                              PRIOR APPLICATION DATA:
                                                                                              CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             527 QKAAEATKVAEAEKQKAAEATKVAEAEKQKAGE 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
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                                                                                                            COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                ZIP:
             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                CITY:
                                                                                                                                                                                                                                              STREET:
                                                            FILING DATE:
                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKAAGDDSAAAA----LADAQKALEAALGKAGQ 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAYKAAHK---AEEEKAKTFQRLITFESENINLKKRP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKTQIAEAQK-KFPDSPILQEAEQM-----VIQAEKDLKNIKPADGSDVPNPGTTVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPPTSDDYKTQAQTAYDTIFTSTS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEAEKQKAAEAAKAVETEKQRAAEATKVAEAEKQRAAEAMK-----VAEAEKQKAAEA
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                                                                                                                                                                                                                           SSEE: Foley & Lardner T: 3000 K Street, N.W. Washington, D.C.
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                                                                                                                                                                                                20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09115746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 amino acids
                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                              Kirchhoff, Louis V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                               POLYPEPTIDES FOR DIAGNOSING WITH TRYPANOSOMA CRUZI
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21.4%; Pred. No. 0.01;
                              08/216,894
                                                                             US/09/115,746
                                                                                                                                                                                                                                              N.W.,
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                                                                                                               Version
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                                                                                                               #1.25
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1838 AFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAEL----RKAKENK---ESE 1890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SLADKLGIASSNSSSTSRSADVDSTTATAPTPP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TNIKDT---AATDEETALAAEWETKNADAIKVGAQITELAKYASDNQAILDSL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 GKLJSFDLLQTALLQSVANNNKAAELLKEM----QDNPVVPGKTPAIAQSLVDQTDATAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------QGSSIGSIR 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 PPTSDDYKTQAQTAYDT-----IFT----STSLADIQAALVSLQDAV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---KAGQQ--QGILNALGQIASAAVVS 449
                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.1%; Score 138; DB 1; Le 20.0%; Pred. No. 0.11; iive 82; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 ILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQ---
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                                                                                                                                                                                                                                                                US/07/741,940
                                                                                                                                            : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                        NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION: TELEPHIONE: 202-508-9100
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                                                                                                                                                                                                                                                                                                                                  ATTORNEY / AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2842 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 19920109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 ADAOKA-LEAALG-----
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                              APPLIÇATION NUMBER:
FILING DATE: 199201
                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: AMINO ACID
                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                              20001-4598
                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-741-940-7
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                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 PPKSDLVPRGSPSQL--QQÆNNITNSKKEMTKLREKVKKAEKEKLDAINRATKLEEERN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 A----QSLVDQTDATATQIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAKTQIAEAQK-KFPDSPILQEAEQM-----VIQAEKDLKNIKPADGSDVPNPGTTVG 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 ALMSLADKLGIASSNSSSSTSRSADVDSTTATAPTPPPPTSDDYKTQAQTAYDTIFTSTS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 LADIQAALVSLQDAVTN----IKDTAATDE-----ETAIAAEWETKNADAIKVGAQI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NDAVSNRDKKKNSETAKTDEVEKQRAAEAAKAVETEKORA----AEA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 TELAKYASDNQAILDSLGKLTSFDLLQTALLQSVANNNKAAELLKEMQDNPVVPGKTPAI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AEKRKAAEAAKAVETEKQRAAEATKV 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 AEAEKOKAAEAAKAVETEKORAAEATKVAEAEKORAAEAMK-----VAEAEKOKAAEA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 ---TKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKO----KAAEATKVAE---- 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 GSKQQGSSIGSIRVSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AEKOKAAEATKVA-----EAEKOKAAEATK------VAEAEKOKAAEATKVAEAEK 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 QAYKAAHK---AEEEKAKTFORLITFESENINLKKRP------------307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 PGPIDETERTPPADLSAQGLEASAANKSAEAQRIAGAEAKPKESKTDSVERWSILRSAVN 66
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                Length 564;
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APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                         54; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                             Score 138.5; DI
Pred. No. 0.01;
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85326/102/DRLO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPA.: 904136
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           527 OKAAEATKVAEAEKOKAAEATKVAEAEKOKAGE 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             403 AKAAGDDSAAAA----LADAQKALEAALGKAGQ 431
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KINZLER, KENNETH
MARKHAM, ALEXANDER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/07741940 Patent No. 5352775
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CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
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Similarity 21.48;
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                                                                                                                                                                                                                : 564 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-115-746-2
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APPLICANT: ALBERT
                                                                                                                                                                                                                                                           TOPOLOGY:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Best Local Simi
Matches 97;
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APPLICANT:
APPLICANT:
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1838 AFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAEL----RKAKENK---ESE 1890
                                                                                                                                       1891 AKVTS----HTELTSNQQSANKTQAIAKQPINRGQPKPILQ-KQSTFPQSSKDIPDRGAA 1945
                                                                                                                                                                                                                                                                                                        1976 --QENNN---KENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLS 2030
                                                                                                                                                                                                                                                                                                                                                                                                     2031 I-----DSEDDLLQECISS-----AMPKKKRPSRLKGDNEKHSPRNMGGILGED-LTLDL 2079
             --TNIKDT--AATDEETAIAAEWETKNADAIKVGAQITELAKYASDNQAILDSL 191
                                                                                                 192 GKLTSFDLLQTALLQSVANNNKAAELLKEM----QDNPVVPGKTPAIAQSLVDQTDATAT 247
                                                                                                                                                                                     248 QIEKDGNAIGDAYFAGQNASGAVENAKSNNSISNIDSAKAAIATAKTQIAEAQKKFPDSP 307
                                                                                                                                                                                                                                                                                                                                                            356 VSMLLDDAENETASILMSGFRQMIHMFNTENPDSQAAQQELAAQARAAKAAGDDSAAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF 1 TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2080 KDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLS 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                416 ADAQKA-LEAALG------KAGQQ--QGILNALGQIASAAVVS 449
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                                                                                                                                                                                                                         1946 TDEKLON-----FAIENTPVCFSHNSSLSSLSDID----
                                                                                                                                                                                                                                                                           308 ILQEAEQMVIQAEKDLKNIKPADGSDVPNPGTTVGGSKQ---
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APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08452654 Patent No. 5691454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARKHAM, ALEXANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAKAMURA, YUSUKE
THLIVERIS, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1001 G Street, NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANAND, RAKESH
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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ADDRESSEE: Banner, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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               142 ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1718 EEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKP 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPTSDDYKTQAQTAYDT-----IFT-----STSLADIQAALVSLQDAV---- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SLADKLGIASSNSSSTSRSADVDSTTATAPTPP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 DETERTPPADLSA-QGLEASAANKSAEAQRIAGAEAKPKE----SKTDSV---
                                                                                                                                                                                                                                                                                                                                               APPLICANT: NAKAMURA, YUSUKE
PEPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
2080 KDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLS 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289 5/197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Banner & Allegretti, LTD 1001 G Street, NW
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                                                                                                     Sequence 7, Application US/08289548A Patent No. 5648212
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IBM PC compatible
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         GRODEN, JOANNA
HEDGE, PHILIP J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino acids
                                                                                                                                                                     ALBERTSEN, HANS
ANAND, RAKESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-1994
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                                                                                                                                                                                                                  CARLSON, MARY
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Matches 105; Conser
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CLONE: APC
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